Identification of S-nitrosylated nuclear proteins in rat cortical neurons

Jacob Anderson

Thesis submitted for the degree of Doctor of Philosophy

Riccio Lab

MRC Laboratory for Molecular Cell Biology

University College London

January 2016

I, Jacob Anderson, confirm that the work presented in this thesis is my own. Where information has been derived from other sources, I confirm that this has been indicated in the thesis.

Abstract

The ability of neurons to modulate gene expression in response to changing environmental conditions, both during development and throughout life, is necessary for proper brain function. Although the mechanisms responsible for transducing extracellular signals into changes in gene expression remain poorly characterized, S-nitrosylation, which is the covalent attachment of a nitric oxide (NO) moiety to cysteine thiols, has been shown to be critical. In the cerebral cortex, S-nitrosylation of histone deacetylase 2 (HDAC2) is essential for gene expression during neuronal development, however few nuclear targets have been identified to date. Progress in this field of research has been hampered by the technical difficulties associated with the detection of S-nitrosylated nuclear proteins. Here, I took a novel approach by enriching for nuclear proteins of rat cortical neurons before inducing S-nitrosylation with nitrosocysteine (CysNO) and isolating S-nitrosylated proteins using S-nitrosothiol Resin Assisted Capture (SNORAC). Mass spectrometry analysis identified 614 S-nitrosylated nuclear proteins, including potential site(s) of S-nitrosylation for 67% of targets. 612 of these proteins are novel potential targets of S-nitrosylation in cortical neurons and 131 have not been shown to be S-nitrosylated in any system. Two hits, the transcription factor CREB and the histone binding protein RBBP7, were further studied and I confirmed endogenous S-nitrosylation in depolarized cortical neurons for both. In addition, I showed that CREB is S-nitrosylated at cysteines 300/310/337 located within the DNA binding domain, whereas RBBP7 is S-nitrosylated at cysteine 166, which is in a WD-repeat region that regulates protein-protein interactions. Overall, this work comprehensively identifies, for the first time, the nuclear proteins that undergo S-nitrosylation in neurons and highlights S-nitrosylation of CREB and RBBP7 as a candidate mechanism by which NO regulates gene expression in mammalian cells.

Acknowledgements

I thank Dr. Antonella Riccio for her expert guidance and support through an extremely interesting and challenging project.

I extend my gratitude to Marco Gaspari at the University of Catanzaro (Italy) for his highly skilled work on mass spectrometry that formed the bedrock of this PhD project and also for providing me with an extremely positive first experience of scientific collaboration.

Next, I would like to thank the students I have supervised (Andreas Pavlou, Sarah Aldous, Marta Iannicelli). In particular, Sarah Aldous deserves special recognition for her effort towards confirming the site of S-nitrosylation of RBBP7.

The Riccio Lab has provided an excellent environment in which to develop scientifically and a genuinely enjoyable place to work. Many thanks to the members of the lab who have been here during my time at UCL: Sarah Aldous, Catia Andreassi, Emily Brookes, Hamish Crerar, Luca Crepaldi, Aniko Ludanyi, Justyna Nitarska, Cristina Policarpi, William Sherlock and Carola Zimmermann.

Thanks for reading and editing drafts of this thesis go to Antonella Riccio, Emily Brookes, Hamish Crerar and Lucie Van Emmenis.

Many thanks to my friends and family for their support.

Contents

Abbreviations

2-DE	Two-dimensional gel electrophoresis
AD	Alzheimer's disease
AMPAR	α-amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid receptor
AP-1	Activating protein 1
Asc	Ascorbate
ATP	Adenosine triphosphate
BAF	Brahma-associated factor
BDNF	Brain derived neurotrophic factor
BH4	Tetrahydrobiopterin
BRG1	Brahma-related gene 1
BRM	Bhrama
Cal	Calmodulin
CaM	Calmodulin binding domain
CAMKII	Ca2+/calmodulin-dependent protein kinase II
cAMP	Cyclic adenosine monophosphate
CBP	CREB binding protein
cGMP	Cyclic guanosine monophosphate
CHD	Chromodomain helicase DNA-binding
COX-2	Cyclooxygenase-2
CREB	Cyclic adenosine monophosphate response element-binding protein
CREB TM	CREB triple mutant (C300/310/337S)
Cys	Cysteine
CysNO	Nitrosylated cysteine
Drp1	Dyamin-related protein 1
DTT	Dithiothreitol
EDRF	Endothelial derived relaxation factor
eNOS	Endothelial nitric oxide synthase
ERK	Extracellular signal-regulated kinase
ESI	Electro-spray ionization
EZH2	Zeste homolog 2
FAD	Flavin adenine dinucleotide
FeNO	Iron nitrosyl species
FMN	Flavin mononucleotide
FSK	Forskolin
GABA	Gamma-aminobutyric acid
GC	Guanylate cyclase
GSNO	S-nitrosoglutathione
GSNOR	S-nitrosoglutathione reductase
HAT	Histone acetyltransferase
Hb	Haemoglobin
HD	Huntington's disease
HDAC	Histone deacetylase
HDAC2	Histone deacetylase 2
HEK293T	Human embryonic kidney 293 large T antigen expansion
iNOS	Inducible nitric oxide synthase
KCL	Potassium chloride
KN1	First nNOS knockout mice (nNOSα and nNOSγ deleted)
KN2	Second nNOS knockout mice (all isoforms deleted)
LTD	Long term depression
LTP	Long term potentiation
MALDI-TOF	Matrix-assisted laser desorption/ionization time of flight
MAPK	Mitogen-activated protein kinase
MBD	Methyl-CpG-binding domain
MEF2C	myocyte enhancer factor 2C
MMP	Matrix mettaloproteinase
MMTS	Methyl methanethiosulfonate
MS	Mass spectrometry
MTA	Metastasis associated protein
NAPDH	Nicotinamide adenine dinucleotide phosphate
NDMA	N-methyl-D-aspartate receptor
NEM	N-Ethylmaleimide
NMDAR	N-methyl-D-aspartate receptor
nNOS	Neuronal nitric oxide synthase
NO	Nitric oxide
NOS	Nitric oxide synthase
npBAF	Neuronal progenitor-specific BAF complex
NuRD	Nucleosome Remodeling and Deacetylation Complex
PD	Parkinson's Disease
PI3K	Phosphoinositide 3-kinase
PKB	Protein kinase B
PLCγ	Phospholipase C gamma
PRC2	Polycolm repressive complex 2
PSD93/95	Post synaptic density protein 93/95
PTM	Post-translational modification
RBBP4/7	Retinoblastoma-binding protein 4/7
RBBP7	C166S RBBP7 cysteine 166-to-serine mutant
SCF	Skp, Cullin, F-box containing protein
Sin3a	Mammalian Sin3a complex
SNO-protein	S-nitrosylated protein
SNORAC	S-nitrosothiol Resin-Assisted Capture
Trk	Tropomyosin-related kinase
Trx	Thioredoxin
TrxR	Thioredoxin reductase

1. Introduction

The 86 billion neurons of the human brain constitute just 0.2% of the total number of cells in the body, yet they are capable of working together to perform tasks of unique complexity, simultaneously orchestrating autonomic functions essential for survival whilst integrating and coordinating responses to the external environment. Understanding how the brain achieves this feat is one of the most interesting, yet challenging, questions now facing biology. In mammals, neurons are generated during embryonic development and, with the exception of neuronal subpopulations in the hippocampus and olfactory bulb, no new neurons are generated later in life. In order for the brain to function correctly, neurons must respond appropriately to a plethora of intracellular and extracellular stimuli during both embryonic development and in the adult brain. A variety of signalling pathways cooperate to ensure that neurons reach their correct destinations and form appropriate connections with neighbouring cells. Once neuronal networks are established, inter- and intra-cellular signalling allows neurons to continually remodel connections in response to environmental stimuli.

Many physiological and pathological processes within the nervous system depend upon changes in neuronal gene expression driven by extracellular stimuli. Though these ‘inducible’ gene targets within neurons are increasingly well understood in regards to their identity and context of activation, the signalling mechanisms that link extracellular stimuli to changes in transcription are still not well elucidated.

1.1 The role of post-translational modifications in cellular signalling

In 1968, Earl Sutherland and colleagues discovered that production of an intracellular molecule was responsible for transduction of extracellular signals (Sutherland et al., 1968). They found that exposure of liver cells to epinephrine stimulated intracellular synthesis of the second messenger cyclic adenosine monophosphate (cAMP) (Sutherland et al., 1968). Since then, thousands of studies have demonstrated the importance of signal transduction across all areas of biology. Cellular signaling largely depends on post-translational modification (PTM) of proteins, in which specific functional groups, that may be chemical or protein in nature, are added to proteins in an enzyme-catalysed manner. A large variety of PTMs have been identified (**Figure 1**), with diverse effects on protein and cellular function.

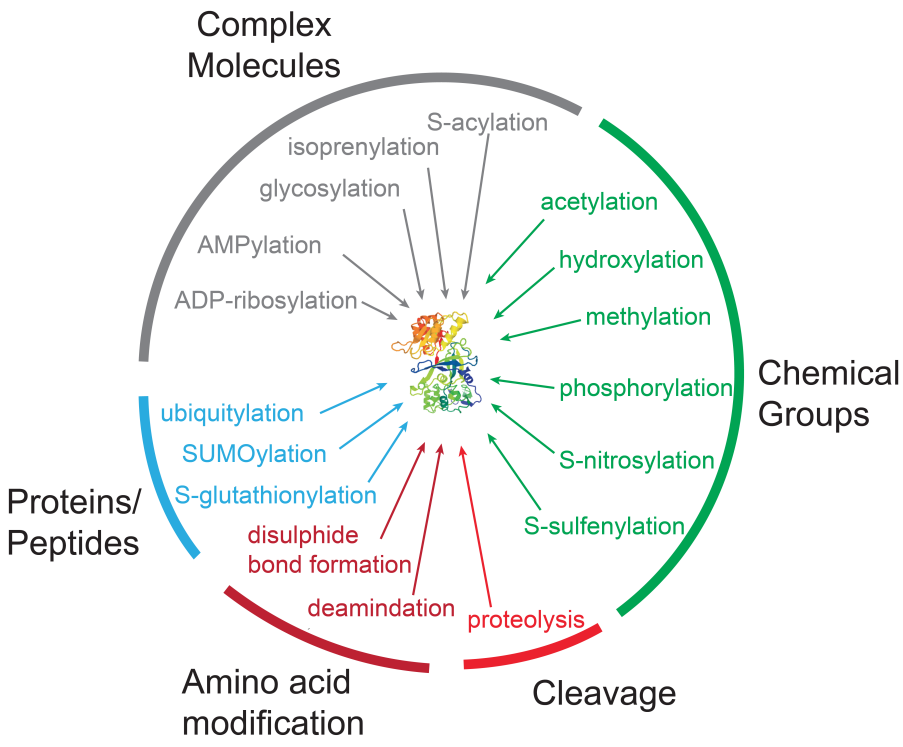


Figure 1. Post-translational modifications in eukaryotic cells. Major classes of post-translational mechanisms active in cellular signaling mechanisms along with key examples.

Deamindation and proteolysis represent irreversible modifications, whereas the remaining modifications are reversible. Figure based upon (Wang et al., 2014) and (Ribet and Cossart, 2010).

The effects of a particular PTM are often protein-specific and depend upon which residue(s) of the protein is modified and whether other PTMs are present, thus endowing the cell with an intricate signaling apparatus. Although many cytoplasmic signaling pathways and associated PTMs have been characterized in neurons, relatively little is known regarding signaling mechanisms within the neuronal nucleus. To date, the majority of the work carried out on transcriptional regulation in neurons has focused on well-studied posttranslational modifications such as phosphorylation and sumoylation. The influence of other, less well-studied, posttranslational modifications on regulation of neuronal gene expression is not yet well elucidated.

1.2 The discovery of nitric oxide as a cellular messenger

Nearly three decades ago, work performed in the laboratories of Robert Furchgott, Louis Ignarro, Salvador Moncada and Ferid Murad culminated in the discovery that nitric oxide (NO; nitrogen monoxide) plays a key role in signal transduction (Ignarro et al., 1987; Palmer et al., 1987). The first suggestion of a biological function for NO arose from studies of the vasodilator nitroglycerin. Although nitroglycerin was known to induce vasodilation through activation of the enzyme guanylate cyclase (GC) and the subsequent increase in intracellular cyclic guanosine monophosphate (cGMP) levels (Katsuki et al., 1977a), the intracellular mechanisms behind GC

activation were unknown. The Murad laboratory discovered that exogenously applied NO activated GC in various tissue preparations, mimicking the action of nitroglycerin (Arnold et al., 1977; Katsuki et al., 1977b). Subsequent work from the Furchgott laboratory demonstrated that a secreted factor released from endothelial cells mediates vascular smooth muscle relaxation, a key event in vasodilation (Furchgott et al., 1984). The identity of this highly unstable factor, termed endothelial derived relaxation factor (EDRF), remained unknown for a number of years. The breakthrough came in 1986 when, upon discovering that the chemical properties of EDRF and NO were identical, the laboratories of Salvador Moncada and Louis Ignarro independently and conclusively identified EDRF as NO (Ignarro et al., 1987; Palmer et al., 1987). This was the first time that an endogenously produced gas had been shown to play a role in physiological signalling. In recognition of their work towards the discovery of NO as a signalling molecule, Ignarro, Furchgott and Murad shared the 1998 Nobel Prize for Medicine or Physiology. The early work carried out by these groups opened up a new field of research and NO is now considered a fundamental messenger that regulates a wide range of processes including platelet aggregation, immune response, synaptic transmission and brain development (review: Hess et al., 2005).

1.3 Nitric oxide synthases

NO is generated in cells by nitric oxide synthase (NOS) enzymes. There are three isoforms of NOS in mammals: neuronal NOS (nNOS, NOS1) (Bredt and Snyder, 1990), endothelial NOS (eNOS, NOS3) (Lamas et al., 1992) and inducible NOS (iNOS, NOS2) (Xie et al., 1992). nNOS and eNOS are

constitutively expressed in a number of cell types (reviews: Fleming and Busse, 2003; Kleinert et al., 2004; Zhou and Zhu, 2009), whereas iNOS is only expressed in response to inflammatory stimuli (Xie et al., 1992). NOS isoforms are structurally related; each contains an N-terminal oxygenase domain and a C-terminal reductase domain, separated by a calmodulin-binding motif. To produce NO, electrons derived from reduced nicotinamide adenine dinucleotide phosphate (NAPDH) are transferred between the reductase and oxygenase domains in a calmodulin-dependent manner, catalysing the conversion of L-arginine and oxygen to L-citrulline and NO (Bredt and Snyder, 1990; Palmer et al., 1988) **(Figure 2)**.

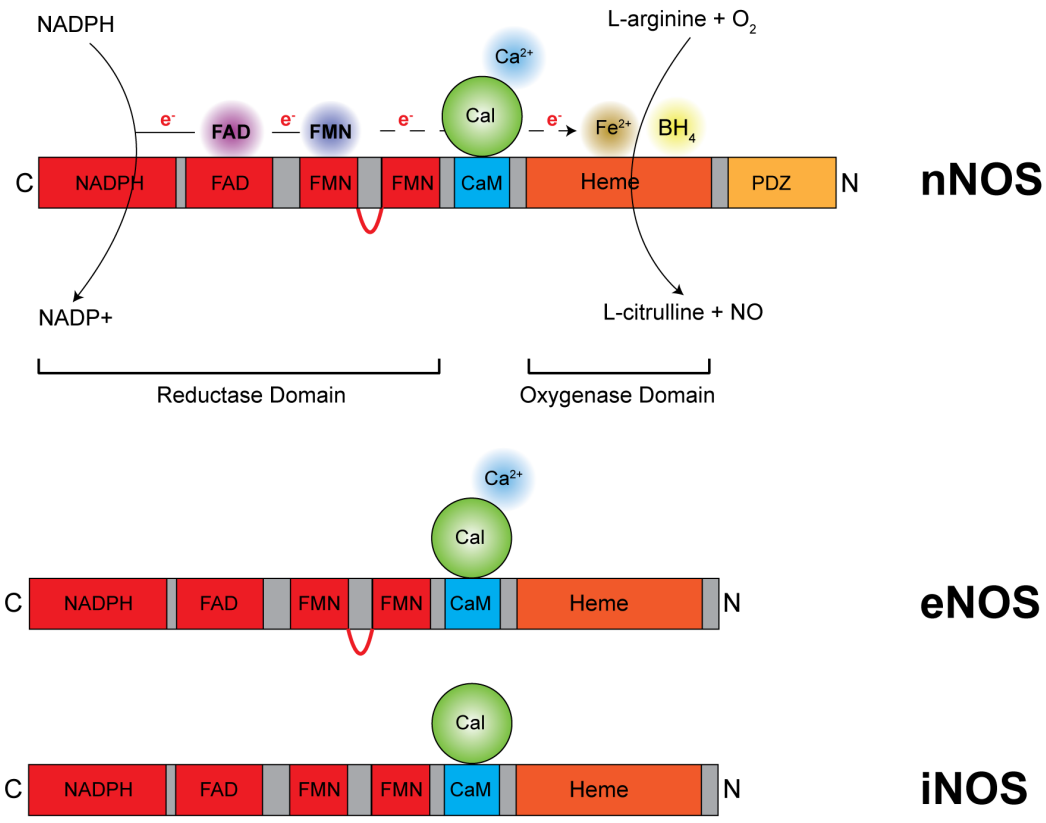


Figure 2. Domain structure and enzymatic activity of nitric oxide synthase enzymes. nNOS, eNOS and iNOS contain reductase and oxygen domains essential for their function

and the general mechanism of nitric oxide production is similar. Electrons (e^-) gained from the reduced form of NADPH are transferred along the reductase domain and passed between the prosthetic groups flavin adenine dinucleotide (FAD) and flavin mononucleotide (FMN). Zinc-dependent dimerisation (not shown) and calmodulin (Cal) binding to the calmodulin binding domain (CaM) are required for the transfer of electrons to the heme iron (in the ferrous form; Fe^{2+}) bound in the oxygenase domain. These electrons, together with electrons from tetrahydrobiopterin (BH_4) prosthetic groups, are required for the conversion of L-arginine and molecular oxygen (O_2) to L-citrulline and nitric oxide (NO) at the active site of the oxygenase domain. Auto inhibitory loops between FMN domains in nNOS and eNOS (pictured as curved red lines) are displaced upon calmodulin binding. Binding of calmodulin is Ca^{2+}-dependent in nNOS/eNOS and Ca^{2+}-independent in iNOS. Figure created using Adobe Illustrator CS4.

The synthesis of NO by NOS enzymes is tightly controlled. Firstly, each NOS isoform requires calmodulin in order to be active. Whilst calmodulin is permanently bound to iNOS (Spratt et al., 2007), calmodulin binding is reversible and calcium-dependent for eNOS and nNOS (Bredt and Snyder, 1990; Förstermann et al., 1991). Accordingly, NO production from eNOS/nNOS is stimulated by an increase in intracellular calcium (Lamas et al., 1992; Lantin-Hermoso et al., 1997) whereas NO production from iNOS is calcium-insensitive (Yui et al., 1991). Secondly, NOS activity is regulated through post-translational modification. For example, nNOS enzymatic activity can be modulated through differential phosphorylation of the enzyme (Bredt et al., 1992). In glutamate-stimulated cortical neurons, protein kinase B (PKB)-dependent phosphorylation of nNOS at serine 1412 increases NO production (Rameau et al., 2007), whereas Ca^{2+}/calmodulin-dependent protein kinase II (CAMKII)-induced phosphorylation at serine 847 inhibits enzymatic activity (Rameau et al., 2007; 2003). eNOS activity is also regulated by PTM; S-sulfhydration of eNOS at cysteine 443 promoters eNOS dimerization and activation (Altaany et al., 2014). Thirdly, NOS enzymes are subject to

transcriptional regulation. This is the most important control mechanism for NO production by iNOS, whose expression is only induced upon inflammatory stimuli (Xie et al., 1992). In addition, whilst eNOS and nNOS are constitutively expressed in many cell types, they too are subject to transcriptional regulation in specific contexts, such as during embryonic development (Bredt and Snyder, 1994; Sherman et al., 1999).

1.4 NO signalling: S-nitrosylation

The original hypothesis for NO-induced vasodilation states that NO produced in endothelial cells migrates in gaseous form to the underlying smooth muscle cells (Palmer et al., 1987). Researchers soon realised, however, that gaseous NO is unlikely to survive the journey due to the abundance of reactive species in the cellular milieu that can rapidly inactivate NO (Blough and Zafiriou, 1985; Palmer et al., 1987). Hence, it was suggested that a carrier molecule of some sort transduces the signal. NO covalently binds to reactive cysteine thiols, in a process known as S-nitrosylation (Ignarro et al., 1979; Oae et al., 1978). The first evidence of a biologically active role for S-nitrosylation was that exogenously generated S-nitrosylated proteins are able to provide the NO moiety needed for the activation of GC (Stamler et al., 1992b). Then, upon demonstration of endogenous S-nitrosylation for the first time (Stamler et al., 1992a), it was suggested that S-nitrosylation itself may directly modulate protein function and represent an alternative regulatory mechanism through which NO exerts its effects.

S-nitrosylation has now been identified as a highly conserved cellular signalling mechanism, present in organisms from bacteria (Hausladen et al., 1996; Seth et al., 2012) to humans (Jia et al., 2014; Stamler et al., 1992a). Like other PTMs, S-nitrosylation affects protein functions, either directly or through modulating protein-protein interactions. The functional consequences of S-nitrosylation depend, in part, on which protein is modified. For example, S-nitrosylation may inhibit enzyme activity, as is the case for pro-apoptotic caspase proteins (Mannick et al., 1999), or result in potentiation of activity, as observed for matrix metalloproteinases (Gu et al., 2002). These effects are often thought to be underpinned by changes in protein structure, given that the crystal structure of four S-nitrosylated proteins has demonstrated that S-nitrosylation induces structural rearrangements ranging from 0.8 to 1.3 angstroms (Marino and Gladyshev, 2010). Phosphorylation, in comparison, can induce changes of up to 50 angstroms (Barford et al., 1991), although modelling suggests that the vast majority of phosphorylation events, and other PTMs, induce changes of less than 2 angstroms (Xin and Radivojac, 2012). In addition, S-nitrosylation can also inhibit the function of certain enzymes through modification of catalytic cysteine residues (Kwiecień et al., 2003; Mannick et al., 1999). In these cases, it is unclear whether structural rearrangements also take place.

1.4.1 Mechanisms

The source of NO moiety needed for S-nitrosylation may derive from either NO itself, higher NO oxides (NOx), metal-NO complexes or other SNO-proteins/peptides. Although the chemical conditions that facilitate S-nitrosylation *in vivo* remain unclear, certain molecules and proteins have been

shown to act as catalysts for the reaction. Transition metals (such as Fe^{2+} and Cu^{2+}) can catalyse S-nitrosylation; Cu^{2+} accelerates the rate of S-nitrosylation of serum albumin from gaseous NO (Stubauer, 1999). In addition, transition metals can also facilitate intra-protein transfer of the NO signal. In haemoglobin (Hb), the NO group is transferred from an iron nitrosyl species (FeNO), that is formed first upon reaction with NO, to cysteine 93 that resides opposite (Gow and Stamler, 1998; Luchsinger et al., 2003). In other cases, S-nitrosylation is catalysed through direct interaction with NOS enzymes. For example, S-nitrosylation of the inflammatory mediator cyclooxygenase-2 (COX-2) is dependent upon iNOS binding (Kim et al., 2005).

1.4.2 Transnitrosylation

Transnitrosylation represents a major mechanism through which the NO moiety is passed between proteins. Upon contact of a S-nitrosylated cysteine with a suitable target cysteine, the S-nitrosylated cysteine is reduced and the NO moiety is transferred from the donor to the receiver (Scharfstein et al., 1994, review: Nakamura and Lipton, 2013). Whilst the mechanisms that facilitate the transfer are still not clear, transnitrosylation is targeted by specific protein-protein interactions (Jia et al., 2014). Proteins such as glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (Kornberg et al., 2010) and S100A8 (Jia et al., 2014) can transnitrosylate several targets, however proteins dedicated exclusively to this function have not yet been identified.

Importantly, transnitrosylation enables propagation of S-nitrosylation signals to cell compartments lacking an endogenous source of NO. For example, nNOS is not detected in the nucleus (Nott et al., 2013; Saini et al.,

2006); however, nuclear proteins undergo S-nitrosylation (Kornberg et al., 2010; Nott et al., 2008; Ryan et al., 2013). A possible mechanism is that nuclear S-nitrosylation depends on the import of specific S-nitrosylated cytoplasmic proteins such as SNO-GAPDH (Kornberg et al., 2010). In this manner, GAPDH is S-nitrosylated in the cytosol by NO synthesised by nNOS (Kornberg et al., 2010). SNO-GAPDH then associates with Siah1 (seven in absentia homolog 1), which contains a nuclear localisation element, allowing transport into the nucleus where SNO-GAPDH S-nitrosylates several targets, including HDAC2 (Kornberg et al., 2010).

1.4.3 Temporal regulation

Because most S-nitrosylation events depend on activation of NOS enzymes, time of onset is often influenced by the kinetics of activation, or transcription, of the specific NOS. iNOS-dependent targets can only be S-nitrosylated once iNOS is expressed (Santhanam et al., 2007). For example, iNOS mRNA is only detected after at least 2 hours of LPS treatment in macrophages (Jacobs and Ignarro, 2001) and, accordingly, iNOS-dependent S-nitrosylation of target proteins shows similar kinetics (Kelleher et al., 2011). In contrast, nNOS-dependent S-nitrosylation occurs on a much quicker timescale. For example, treatment of embryonic cortical neurons with the neurotrophin brain derived neurotrophic factor (BDNF) results in activation of nNOS (Riccio et al., 2006) and protein S-nitrosylation within 10 minutes (Nott et al., 2008).

The removal of the NO group, termed denitrosylation, is also a tightly regulated process. Two enzyme systems have so far been identified as responsible for denitrosylation of substrates *in vivo*. The S-nitrosoglutathione reductase (GSNOR) denitrosylase system specifically denitrosylates S-nitrosoglutathione (GSNO) (Liu et al., 2001), a low molecular weight nitrosothiol present in most cells. GSNO exists in equilibrium with the global pool of SNO-proteins, meaning that changes of GSNO levels can have a profound impact on protein S-nitrosylation (Liu et al., 2001). The thioredoxin system is a second denitrosylase complex that comprises thioredoxin (Trx) and thioredoxin reductase (TrxR) (Benhar et al., 2008). Whilst the mechanism of Trx/TrxR-mediated denitrosylation is still unclear, it has been shown that this system efficiently denitrosylates substrates *in vivo* (Kneeshaw et al., 2014). Finally, denitrosylation may also be achieved by transnitrosylation, a mechanism by which denitrosylation of a substrate is coupled with propagation of the NO signal between proteins.

1.4.4 Specificity

Since the discovery of S-nitrosylation, a fundamental question has been how substrate specificity is achieved. The properties of the amino acid composition immediately surrounding a particular cysteine have been suggested to play a role: increased hydrophobicity (Nedospasov et al., 2000) or the presence of acidic and basic amino acids (Stamler et al., 1997) may render the S-nitrosylation reaction more chemically favourable. However, since cysteines exhibiting these properties are present in the majority of proteins, these features alone cannot account for overall substrate specificity. Instead, substrate and site specificity also depend on the specific interaction

with NOS enzymes or transnitrosylases. For example, upon inflammatory stimulation of monocytes, the transnitrosylase s100a8 is recruited to a consensus sequence present on target proteins (Jia et al., 2014). In this case, the presence or absence of the cofactor s100b determines which cysteine on the target protein is S-nitrosylated. In addition, specificity may also be achieved as a result of the associated stereochemistry associated with a particular S-nitrosylating agent. For example, work from Jonathan Stamler's laboratory has demonstrated that many proteins are differentially S-nitrosylated upon treatment with CysNO versus GSNO (Foster et al., 2009).

1.5 Neuronal nitric oxide synthase

Although nNOS was the first NO-producing enzyme to be identified, the specific signalling pathways triggered upon its activation remain the least well understood. Three catalytically active splice variants of nNOS are expressed in the brain: nNOSα, β and μ (Eliasson et al., 1997; Ihara et al., 2006). nNOSα and μ contain a PDZ domain that facilitates the association with the plasma membrane through interaction with the postsynaptic density protein (PSD) 93 and PSD95 (Brenman et al., 1996a; 1996b; Eliasson et al., 1997). Analyses of transgenic mouse models lacking nNOS have provided several insights into its function. The first, and most widely used, strain of nNOS-knockout mice (named KN1) was generated by deleting the PDZ-encoding exon 2 of the gene. This strategy resulted in the deletion of nNOSα and μ (Huang et al., 1993), whereas nNOSβ remains intact and accounts for 5-10% of residual NOS activity observed (Eliasson et al., 1997). KN1 mice do not show overt defects in overall brain structure (Huang et al., 1993), but exhibit

severe behavioural abnormalities, including increased aggression (Trainor et al., 2007) and impairment of social interactions (Walton et al., 2013). Importantly, KN1 mice also have defects in several paradigms of learning and memory, including long term memory consolidation (Jüch et al., 2009; Pavesi et al., 2013), spatial learning (Walton et al., 2013; Weitzdoerfer et al., 2004), contextual fear learning (Kelley et al., 2009) and working memory (Zoubovsky et al., 2011).

A second nNOS-knockout mouse, named KN2, was generated by deleting exon 6, which codes for the oxygenase domain present in all nNOS isoforms (Gyurko et al., 2002). KN2 mice have so far only been characterised with respect to their striking reproductive defects, such as decreased ovulation rates in females (Gyurko et al., 2002). As wild-type ovaries transplanted into KN2 mice have reduced rates of ovulation, this effect may be CNS-dependent. Furthermore, since ovulation is normal in KN1 mice (Huang et al., 1993), this suggests a significant contribution of nNOSβ to the physiological actions of nNOS.

1.6 Roles of NO in the adult brain

Much work has focused on elucidating the key molecular messengers that underlie signaling events within the brain. A diverse array of individual molecules and signaling pathways have been implicated as involved in neuronal activity, many of which are dependent on a rise of intracellular calcium through either entry into the cell or release from intracellular stores. Even so, it is still not well understood which molecular signaling pathways and

networks are most important for phenomena such as memory formation. nNOS has been proposed as a major effector of calcium dependent changes in transcription in the brain (Riccio et al., 2006). Based on the phenotype of mice lacking nNOS, it is clear that NO mediates signalling events associated with learning and memory. In addition, a number of studies has shown that NO is essential for establishing long-term potentiation (LTP) and long-term depression (LTD), key processes that underlie learning and memory (Barrionuevo et al., 1980; Bliss and Lomo, 1973; Dudek and Bear, 1992; Lomo, 1966; Nabavi et al., 2014). LTP is the increase of synaptic strength that occurs following high frequency stimulation, and represents a major mechanism through which memory is encoded (Bliss and Collingridge, 1993; Nabavi et al., 2014). LTP has mainly been studied in the hippocampus, a brain region that is critical for the storage of long term memories (Scoville and Milner, 1957, review: Lynch, 2004). In hippocampal neurons, nNOS is localised at the postsynaptic density (Aoki et al., 1998) and pharmacological inhibition of NOS results in the inhibition of LTP in hippocampal slices (Böhme et al., 1991; Schuman and Madison, 1991) and in the hippocampus *in vivo* (Doyle et al., 1996). Removal of extracellular NO by haemoglobin also inhibits LTP (Arancio et al., 1996; Schuman and Madison, 1991) and activity-dependent potentiation of presynaptic function is dependent on NO signalling (Stanton et al., 2005). Therefore, it has been proposed that NO may function as a retrograde messenger, which is released post-synaptically and diffuses in the synaptic cleft reaching the presynaptic terminals (Arancio et al., 1996; Schuman and Madison, 1991). In this model, once in the presynaptic terminal, NO activates GC and the signalling events that follow lead to a presynaptic

increase in signaling strength. The initial interest in NO as a retrograde messenger arose from the assumption that NO could freely diffuse across the plasma membrane (PM), however NO transport across the PM has been shown to be a regulated process, dependent on specific channel proteins (Figueroa et al., 2013; Herrera et al., 2006). The role of NO in mediating LTP remains controversial, however, perhaps due to experimental variation caused by species and strain-specific differences in NOS expression (Blackshaw et al., 2003).

In contrast to LTP, LTD is a prolonged decrease in synaptic strength induced by repetitive low frequency stimulation (Barrionuevo et al., 1980; Dudek and Bear, 1992; Ekerot and Kano, 1985; review: Collingridge et al., 2010). The role of nitric oxide in LTD has mainly been studied in the cerebellum, where LTD is associated with motor learning (Aiba et al., 1994; review: Ito, 2001). Pharmacological inhibition of NO signalling prevents LTD in cerebellar slices (Shibuki and Okada, 1991; Stanton et al., 2003). Furthermore, LTD cannot been established in the cerebellum of KN1 mice (Lev-Ram et al., 1997) and these mice exhibit abnormal motor coordination (Kriegsfeld et al., 1999).

The cellular mechanisms that underlie the effect of NO on LTP and LTD are not well defined, though presynaptic activation of GC has been shown to be important in some contexts (Lange et al., 2012; Yang et al., 2007). In addition, S-nitrosylation has also been implicated as a regulatory factor in the process, though its physiological impact has not yet been well defined. In the

pyramidal cells of adult hippocampus and cortex, nNOS interacts with PSD95 (Brenman, Chao, et al. 1996), the major structural component of the postsynaptic density (Sampedro et al., 1981). NO inhibits the clustering of PSD95 and modifies PSD95 by S-nitrosylation (Ho et al., 2011a), though a causal link between these two events has not yet been demonstrated. In addition, nNOS-dependent S-nitrosylation of stargazin, an AMPA receptor auxiliary subunit, increases the surface expression of AMPA receptors *in vitro* (Selvakumar et al., 2009), which may contribute to the positive effect of NO on synaptic strength.

S-nitrosylation has also been functionally implicated in the regulation of glutamate transport at the synapse. nNOS-dependent S-nitrosylation of amino acid transporter 2 (EAAT2) occurs *in vivo* in the brains of wild type mice (Raju et al., 2015). Since glutamate uptake is increased in HEK293T cells expressing a non-nitrosylatable form of EAAT2 (Raju et al., 2015), this suggests that S-nitrosylation of EAAT2 inhibits glutamate uptake. However, this effect remains to be confirmed *in vivo*. Consistent with a role for S-nitrosylation in regulating glutamatergic transmission, several proteins involved in glutamate metabolism undergo S-nitrosylation *in vivo* and KN1 mice have defects of glutamate metabolism (Raju et al., 2015).

1.7 Roles of NO in neurological diseases

NO has been linked to the pathogenesis of various conditions associated with oxidative stress, such as ischaemic stroke (Huang et al., 1994), Alzheimer's disease (AD) (Smith et al., 1997) and Parkinson's disease

(PD) (Liberatore et al., 1999). During oxidative stress, NO reacts with the superoxide anion (O_{2-}) resulting in excessive production of peroxynitrite (ONOO-), a highly toxic derivative of NO (Lipton et al., 1993). Chemical reactions of peroxynitrite with lipids, DNA and proteins have deleterious effects on cellular functions, often culminating in cell death (review: Szabó et al., 2007). The peroxynitrite-mediated addition of nitro groups ($-NO_2$) to tyrosine residues, termed nitration, is known to induce neuronal cell death (Franco et al., 2013) and has long been used as a biomarker for many pathological conditions (Beckmann et al., 1994; Haddad et al., 1994; Kaur and Halliwell, 1994).

S-nitrosylation has also been implicated as a mediator in neurological disease. The conditions in which pathophysiological effects of S-nitrosylation are dominant are not known, however excessive NO production has been suggested as a major cause. In support of this, many neurodegenerative diseases are associated with an increase in iNOS expression (Vodovotz et al., 1996, Hunot et al., 1996). This results in synthesis of NO at levels much higher than observed following the activation of nNOS and eNOS (Moncada et al., 1991; review: Änggård, 1994). S-nitrosylation of the GTPase dyamin-related protein 1 (Drp1) represents a key example of a SNO-protein that contributes to neurodegeneration. S-nitrosylation of Drp1 is increased in post-mortem brains from patients with AD and Huntington's disease (HD) (Cho et al., 2009; Haun et al., 2013) and in mouse models of both diseases (Haun et al., 2013; Akhtar et al., 2016). Analysis of the nitrosomutant form of Drp1 revealed that S-nitrosylation results in hyperactivation of the GTPase activity

of Drp1, which causes mitochondrial fission and synaptic damage (Cho et al., 2009; Haun et al., 2013). As aberrant protein S-nitrosylation has now been detected in several neurodegenerative diseases, targeting S-nitrosylation in these conditions may represent an effective therapeutic strategy.

1.8 NO signalling during cortical development

Whilst the role of NO in the adult brain has been extensively studied, the influence of NO during brain development has received relatively little attention. However, there is clear evidence that NO plays a critical role during brain development, in particular during development of the cerebral cortex.

The cerebral cortex is the outer layer of cerebral tissue responsible for complex cognitive behaviours. Present only in mammals, the cortex is responsible for receiving, integrating and processing sensory stimuli before relaying this information to other brain regions for execution of actions. The cortex plays a central role in higher order brain functions including learning and memory (Hasan et al., 2013), language (Flinker et al., 2015) and behavioural control (Volman et al., 2011). Rodents represent a useful experimental model system for studying the cortex, as they share many features of cortical architecture and function with humans. For example, although the cortex has undergone pronounced expansion and structural changes during mammalian evolution (Finlay and Darlington, 1995; Florio et al., 2015; Stahl et al., 2013), both rodent and human cortices are arranged in an 6-layered structure (reviews: DeFelipe, 2011; Sun and Hevner, 2014), and undergo similar stages of development (reviews: Bystron et al., 2008; Dehay

and Kennedy, 2007). During embryogenesis, asymmetric cell division of neuronal precursor cells generates post mitotic neurons that use radial glia as a scaffold to populate the cortex in an inside-out manner, with newly born neurons forming more peripheral layers (review: Gupta et al., 2002). This process is under the control of a variety of guidance cues (review: Nadarajah and Parnavelas, 2002) and signalling mechanisms (review: Martynoga et al., 2012), including NO and S-nitrosylation (Nott et al., 2013). During embryonic development in rats, nNOS is expressed in the cortex from embryonic day 15 (E15) onwards (**Figure 5**). At E15, nNOS is exclusively expressed in postmitotic neurons in the cortical plate. From E17 to postnatal day 0 (P0), nNOS is enriched in cortical plate neurons and their fibre tracts that project throughout the intermediate zone. Throughout cortical development, nNOS is absent from ventricular zone, the region in which the proliferating apical progenitor cells reside. nNOS levels in cortical neurons decline rapidly during the early postnatal stages and the adult expression pattern is established by postnatal day 15 (P15). In the adult cortex of both rodents and humans, nNOS is only expressed at high levels in subpopulations of GABAergic interneurons that constitute approximately 1% of total neurons (Aoki et al., 1998; Jinno and Kosaka, 2002). In all other cortical neurons, nNOS expression is greatly reduced and restricted to the postsynaptic density of dendritic spines (Aoki et al., 1998).

Cortical development is severely impaired in the KN1 nNOS knockout mice, in which fewer neurons reach the cortical plate and there are significant defects in the arrangement of cortical layers (Nott et al., 2013). Importantly,

the effect of NO in mediating cortical development depends, at least in part, on S-nitrosylation of nuclear and cytoplasmic targets including HDAC2 and GAPDH (Nott et al., 2008; 2013; Riccio et al., 2006; Sen and Snyder, 2011).

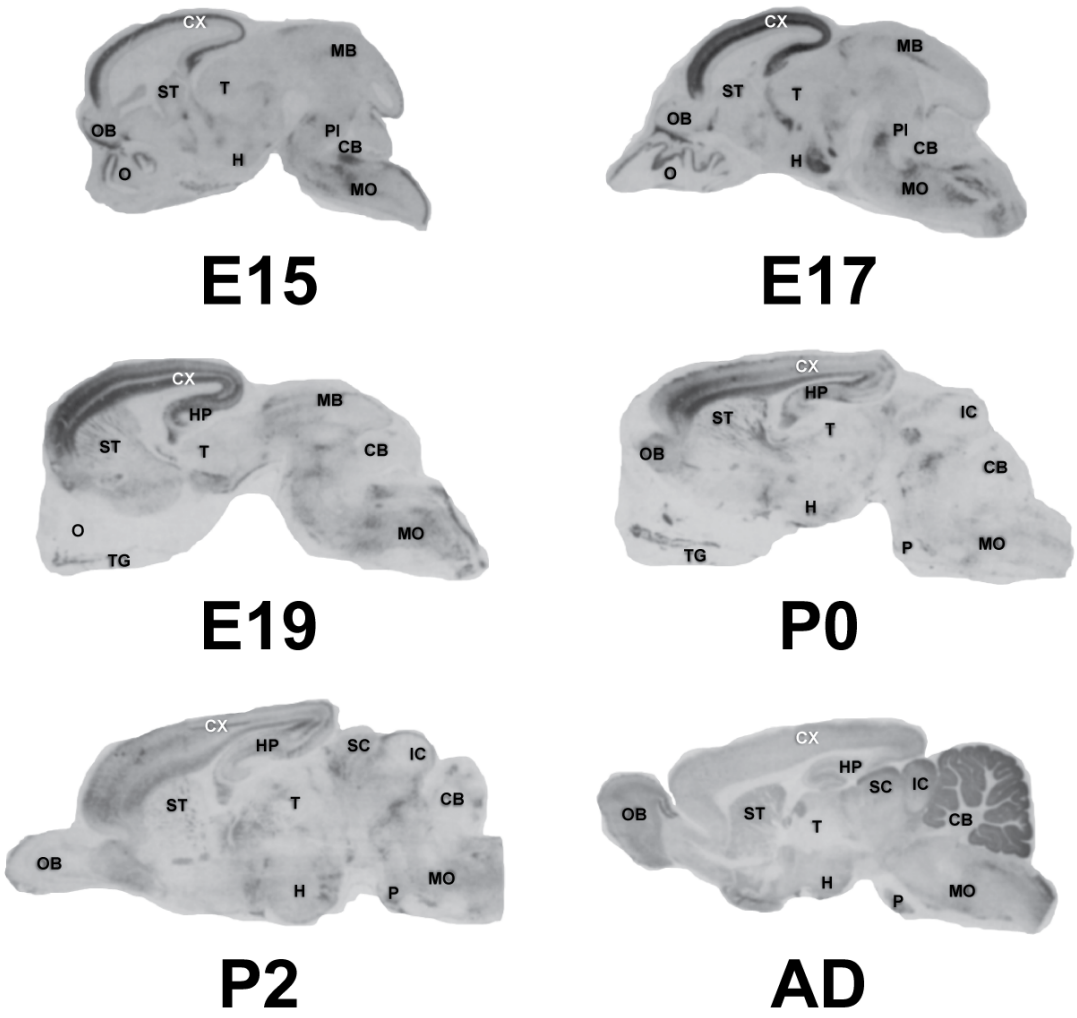


Figure 5. nNOS expression during rat brain development and in the adult. Shown are sagittal sections of rat brain with the indicated developmental stages stained with an nNOS-specific antibody. nNOS is strongly expressed in the cortex (CX) at E15 and expression starts to decline during the early postnatal stages (P0 onwards). The adult (AD) pattern of nNOS expression is established from postnatal day 15 (P15) onwards. Other brain regions are labelled as follows: CB, cerebellum; H, hypothalamus; HP, hippocampus; IC, inferior colliculi; MB, midbrain; MO, medulla oblongata; O, olfactory epithelium; OB, olfactory bulb; P, pons; PI, pineal gland; SC, superior colliculi; ST, striatum; T, thalamus; TG, trigeminal nucleus. Figure is an inverted version (for clarity) from Bredt and Synder (Neuron, 1994).

1.8.1 S-nitrosylation of HDAC2

The first mechanistic insights into the role of S-nitrosylation during cortical development were provided from work completed in our laboratory. S-nitrosylation of HDAC2 was shown to be a key mechanism which regulates the expression of genes involved in the development of the cortex (Nott et al., 2008). In unstimulated embryonic cortical neurons, HDAC2 is bound to the promoters of CREB-dependent genes via multi-subunit repressive complexes. HDAC2 actively deacetylates chromatin and contributes to transcriptional repression. Following exposure to brain derived neurotrophic factor (BDNF), a neurotrophin essential for the growth and development of the nervous system, HDAC2 undergoes S-nitrosylation at cysteines 262 and 274. S-nitrosylated HDAC2 dissociates from chromatin, resulting in an increase in histone acetylation and transcription of CREB-dependent genes (**Figure 6**). Importantly, HDAC2 S-nitrosylation is physiologically relevant, as expression of a non-nitrosylatable form of HDAC2 results in inhibition of dendritogenesis of embryonic neurons *in vitro* (Nott et al., 2008) and severe defects of neuronal migration *in vivo* (Nott et al., 2013).

Whilst SNO-HDAC2 is a key effector of nuclear NO signalling in the cortex, it is likely that several other proteins are S-nitrosylated in developing neurons. For example, the number of S-nitrosylated proteins increases upon treatment of embryonic cortical neurons with BDNF or following exposure of nuclear extracts to NO donors (Nott et al., 2008), however the identity of the majority of these proteins is unknown.

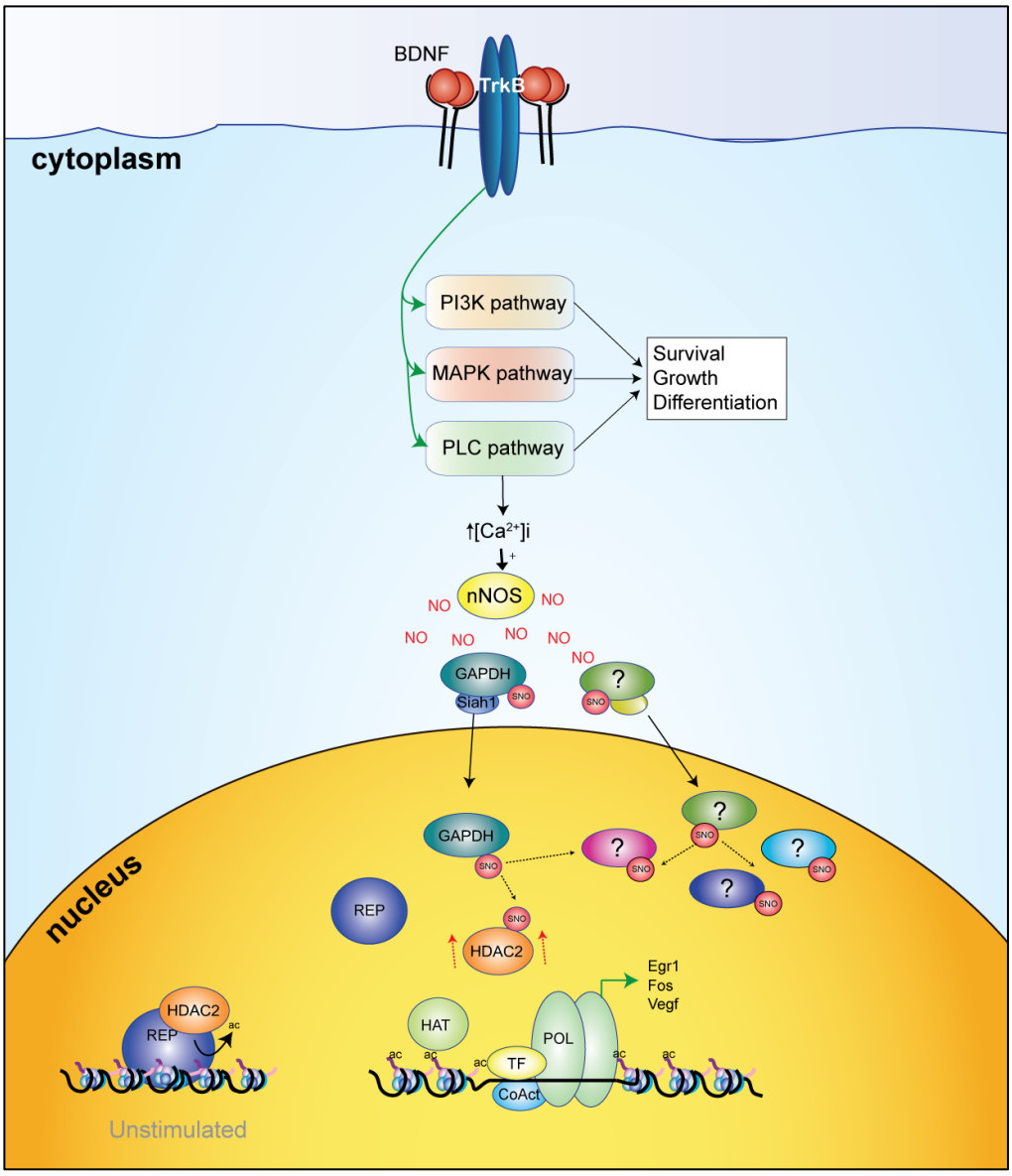


Figure 6. BDNF-induced nuclear S-nitrosylation in cortical neurons. Binding of brain-derived neurotrophic factor (BDNF) to tropomyosin receptor kinase B (TrkB) induces receptor dimerisation and activation of the phosphoinositide 3-kinase (PI3K), mitogen-activated protein kinase (MAPK), and the phospholipase C (PLC) pathways. Calcium released upon PLC activation activates nNOS in the cytoplasm. GAPDH is S-nitrosylated and binds to the protein seven in absentia homolog 1 (Siah1) which facilitates nuclear transport of SNO-GAPDH. Once in the nucleus, SNO-GAPDH trans-nitrosylate HDAC2, inducing its dissociation from chromatin. This results in transcription activation of immediate early genes such as Egr1, Fos and VGF. CoAct, transcriptional coactivator; HAT, histone acetyltransferase; POL, DNA polymerase 2; REP, Repressive complexes; TF, transcription factor.

1.9 S-nitrosylation of additional transcriptional regulators

1.9.1 Transcription factors

The bacterial protein OxyR was the first transcription factor identified as a target of S-nitrosylation (Hausladen et al., 1996). In *E. coli*, S-nitrosylation of OxyR induces DNA binding and activates the transcription of genes that protect against nitrosative stress (Seth et al., 2012). Following this seminal discovery, several S-nitrosylated transcription factors have been identified in mammalian cells (key examples listed in **Table 1**), although few have been confirmed as S-nitrosylated under physiological conditions. Often S-nitrosylation of transcription factors results in inhibition of binding to DNA. For example, it has been proposed that S-nitrosylation of cysteines within the zinc finger DNA binding domains results in zinc release, inducing conformational changes and disruption of the interaction with DNA (review: Kröncke, 2001).

Transcription factor	Location of modified cysteine	Effect
NF-κB p50	DNA binding domain	Inhibition of DNA binding
NF-κB p65	DNA binding domain	Inhibition of DNA binding
AP-1 c-Jun	DNA binding domain	Inhibition of DNA binding
AP-1 c-Fos	DNA binding domain	Inhibition of DNA binding
MEF2C	DNA binding domain	Inhibition of DNA binding
HIF-1α (C533)	Oxygen-dependent degradation domain	Protein stabilization
HIF-1α (C800)	Transactivation Domain	Enhanced binding of cofactor
Sp1	Zinc finger DNA binding domain (proposed)	Inhibition of DNA binding
EGR-1	Zinc finger DNA binding domain (proposed)	Inhibition of DNA binding
Yin Yang 1	Zinc finger DNA binding domain (proposed)	Inhibition of DNA binding
Hepatocyte nuclear factor-4	Zinc finger DNA binding domain (proposed)	Inhibition of DNA binding
Estrogen receptor	Zinc finger DNA binding domain (proposed)	Inhibition of DNA binding
PARP-1	Zinc finger DNA binding domain (proposed)	Inhibition of DNA binding
Myogenin	DNA binding domain (proposed)	Inhibition of DNA binding

Table 1. S-nitrosylated transcription factors. Mammalian transcription factors that are S-nitrosylated, location of the SNO-cysteine and effects of S-nitrosylation (modified from Sha et al, 2012).

S-nitrosylation of transcription factors has only recently been demonstrated in neurons. The pro-survival transcription factor myocyte enhancer factor 2C (MEF2C) undergoes S-nitrosylation when cortical neurons are exposed to toxic concentrations of N-methyl-D-aspartate (NMDA) (Okamoto et al., 2014). SNO-MEF2C has also been detected in post-mortem brains of patients affected by AD and in a patient-derived stem cell model of PD (Okamoto et al., 2014; Ryan et al., 2013). S-nitrosylation of MEF2C occurs at a cysteine contained within the DNA binding domain and contributes to decreased neuronal survival upon toxic stimuli (Okamoto et al., 2014). Hence, these findings suggest that SNO-MEF2C may play a key role in mediating the cell death that occurs in neurodegenerative disorders.

So far, S-nitrosylation of transcription factors has not been demonstrated in physiological situations in neurons and whether nuclear S-nitrosylation occurs in developing neurons, or in response to physiological stimuli in the adult brain, remains unknown. However, several transcription factors that regulate the expression of genes necessary for growth and development of the nervous system contain cysteines that can be modified by oxidation or reduction. For example, the pro-survival transcription factor cyclic-responsive element binding protein (CREB) orchestrates a transcriptional program required for the proper development of the nervous system (Bonni et al., 1999; Mantamadiotis et al., 2002; Riccio et al., 1999; Rudolph et al., 1998; Walton et al., 1999). Several cysteines present in the DNA binding domain of CREB are sensitive to changes in the redox state of the cell and mutations of these cysteines modulate CREB binding to DNA *in vitro* (Goren et al., 2001).

In addition, the Activating Protein 1 (AP-1) transcription factor complex represents another potential nuclear target of S-nitrosylation in neurons. In its active form, AP-1 is a heterodimer that comprises c-Fos and c-Jun and promotes the transcription of genes that regulate neuronal survival and differentiation (Eriksson et al., 2007; Leppä et al., 2001). Interestingly, NO inhibits AP1 binding to DNA *in vitro*, and this event depends on Cys272 and Cys154 located within the DNA binding domains of c-Fos and c-Jun, respectively (Nikitovic et al., 1998).

1.9.2 Epigenetic modifiers

~147 base pairs of DNA are coiled around histone octamers to form nucleosomes, the repeating unit of chromatin (Kornberg, 1974). Epigenetic changes in gene expression occur through modifications of chromatin without alterations in the underlying sequence (perspective: Berger et al., 2009). Epigenetic modifications are stable and heritable in many cell types, with essential roles in maintaining cellular identity (review: Bonasio et al., 2010). In postmitotic neurons, epigenetic modifications have also been shown to be highly dynamic, influencing neuronal function and plasticity (Guo et al., 2011; A. N. Malik et al. 2014; review: Riccio, 2010).

Epigenetic processes act, in part, by modifying chromatin compaction. The compaction state of chromatin is a critical determinant for gene expression; in nucleosome-rich regions, transcription is repressed (Grunstein, 1990; Morse, 1989) as transcription factors and the transcriptional apparatus cannot bind to the densely packed DNA. For transcription to occur, chromatin must undergo a transition to a more open, less nucleosome-dense, structure.

Chromatin modifying enzymes add or remove a variety of post-translational modifications (including methylation, acetylation, phosphorylation, ubiquitination and sumoylation) to the N-terminal tails of histones. Histone modifications can directly affect chromatin compaction by perturbing DNA-histone interactions or altering the affinity between adjacent nucleosomes (review: Kouzarides, 2007). In addition, histone modifications act as docking sites for chromatin modifying and remodelling enzymes that further impact on chromatin structure. The best-characterized histone modification to date is acetylation. Histone acetyltransferase (HAT) enzymes catalyse the addition of a negatively charged acetyl group to positively charged lysine residues on N-terminal histone tails, neutralizing their charge (Hong et al., 1993). This reduces the affinity of histones for the negatively charged DNA (Norton et al., 1989; Vettese-Dadey et al., 1996) and disrupts contacts between adjacent nucleosomes (Shogren-Knaak et al., 2006), increasing the accessibility of DNA to transcription factors. Importantly, acetylated histone residues are recognized by bromodomain-containing proteins that can modify the chromatin further (Filippakopoulos and Knapp, 2014). In general, increased histone acetylation correlates with increased transcription, whereas the removal of the acetyl group by histone deacetylase (HDAC) enzymes is associated with transcriptional inhibition. Interestingly, the HAT CREB binding protein (CBP) is S-nitrosylated *in vitro* in NO-donor treated HEK293 cells (Forrester et al., 2009b), although the functional effect remains to be characterised.

As already mentioned, HDAC2 is S-nitrosylated in cortical neurons (Nott et al., 2008; 2013). In addition, SNO-HDAC2 has been observed in other cell types, including muscle cells and hippocampal neurons (Colussi et al., 2008; Gräff et al., 2014), suggesting that S-nitrosylation of HDAC2 represents a widespread mechanism by which NO regulates transcription. Recently, Graff and colleagues found that HDAC2 is transiently S-nitrosylated in the hippocampus upon recent memory recall in mice (Gräff et al. 2014), an event that correlates with increased histone acetylation and transcription. Strikingly, mice overexpressing the non-nitrosylatable form of HDAC2 in the hippocampus exhibit defects in memory updating; these mice fail to reassign a previously harmful conditioned stimulus as benign (Gräff et al., 2014).

1.9.3 ATP-dependent chromatin remodelers

In addition to chromatin modifications, chromatin structure can be also drastically altered by ATP-dependent chromatin remodeling complexes. This heterogeneous family of multi-protein complexes uses the energy derived from ATP-hydrolysis to mechanically disrupt nucleosomal DNA interactions, resulting in rearrangements in nucleosome spacing, ejection of histones or interchange of histone variants (Narlikar et al., 2013; Son and Crabtree, 2014a). ATP-dependent remodelling complexes may have either activating or repressive effects on transcription (Ho et al., 2009; 2011b).

Two chromatin remodeling complexes have so far been linked with gene expression in neurons, the Brahma-Associated Factor (BAF) complex and the Nucleosome Remodeling and Deacetylation Complex (NuRD). The 2-megadalton mammalian BAF complex consists of at least 15 subunits,

including one of the two possible ATPase subunits, the Bhrama (BRM) or Brahma-related gene 1 (BRG1). Though multiple isoforms of each subunit exist, many are present in the complex in a mutually exclusive manner (Wang et al., 1996). BAF subunits undergo a developmental switch during embryonic development. In neural progenitor cells, the neuronal progenitor-specific BAF complex (npBAF) contains BAF45a/d, BAF53a and BAF55a and is necessary for the transcription of genes that regulate self-renewal. The subunits are replaced in the neuronal BAF complex (nBAF) by BAF45 b/c, BAF53b and CREST, respectively, leading to changes of the transcriptional outcome that underlies neuronal differentiation (review: Son and Crabtree, 2014a). In comparison, the NuRD complex combines ATPase-dependent remodelling with histone deacetylase activity. In neurons, the NuRD complex regulates the expression of genes necessary for synaptogenesis (Yamada et al., 2014) and cortical development (Egan et al., 2013; Knock et al., 2015). NuRD exhibits repressive or activating actions in a gene-specific manner (Potts et al., 2011). In addition, emerging evidence from our laboratory suggests that during cortical development, distinct NuRD complexes are assembled, each eliciting specific transcriptional responses (Nitarska et al, under review). The enzymatic activity of the NuRD complex is provided by the chromodomain helicase DNA-binding (CHD) proteins 3, 4 and 5. CHDs are ATP-dependent DNA translocases capable of moving nucleosomes that, in combination with HDAC1/2, regulate gene expression. Additional non-enzymatic proteins of the NuRD complex include the metastasis associated protein (MTA) 1/2/3, the methyl-CpG-binding domain (MBD) protein 2/3, p66α/β and retinoblastoma-binding protein (RBBP) 4/7. These proteins likely

have structural roles and may also facilitate interaction of the complex with genomic targets. For example, RBBP4 and 7 bind histones, therefore these proteins are candidates for mediating the recruitment of NuRD complexes to chromatin (Murzina et al., 2008; Zhang et al., 2012). Interestingly, the NuRD components MTA2 and RBBP7 have been shown to be S-nitrosylated in screens for S-nitrosylated proteins performed in non-neuronal model systems (Chen et al., 2010; Kohr et al., 2011), suggesting that S-nitrosylation may represent a mechanism by which the assembly of the complex is regulated.

1.10 Identification of S-nitrosylated proteins

S-nitrosylation remains a relatively understudied PTM, in part due to the significant technical challenges posed by the detection of nitrosylated proteins. Whilst pan- S-nitrosocysteine antibodies have been generated, the S-nitrosocysteine moiety has different orientations dependent on the target protein. Hence, it is fortuitous if a pan S-nitrosocysteine antibody (usually raised against SNO-albumin) efficiently recognises a SNO-protein of interest. Moreover, the generation of protein-specific anti-nitrosocysteine antibodies is hampered by the instability of SNO-cysteine under laboratory conditions.

Stamler and colleagues pioneered the first method of detection of S-nitrosylated proteins, which depends upon the release of NO from SNO-cysteine using UV light (Stamler et al., 1992a). Whilst this was important for the first demonstration of S-nitrosylation within cells, use of this complex and labour-intensive technique did not become widespread. A major turning point in the S-nitrosylation field of research came from the work of Samie Jaffrey

and Sol Snyder (Jaffrey, 2001). Jaffrey invented a technique that allows the detection of S-nitrosylated proteins in complex biological samples such as cell lysates. This approach, termed the biotin-switch technique, resolved the problems concerning the lability of the SNO bond by replacing SNO with a stable biotin moiety. Importantly, biotinylated proteins can be isolated using streptavidin beads (Figure 7) and then probed by western blotting using specific antibodies that recognise the protein of interest.

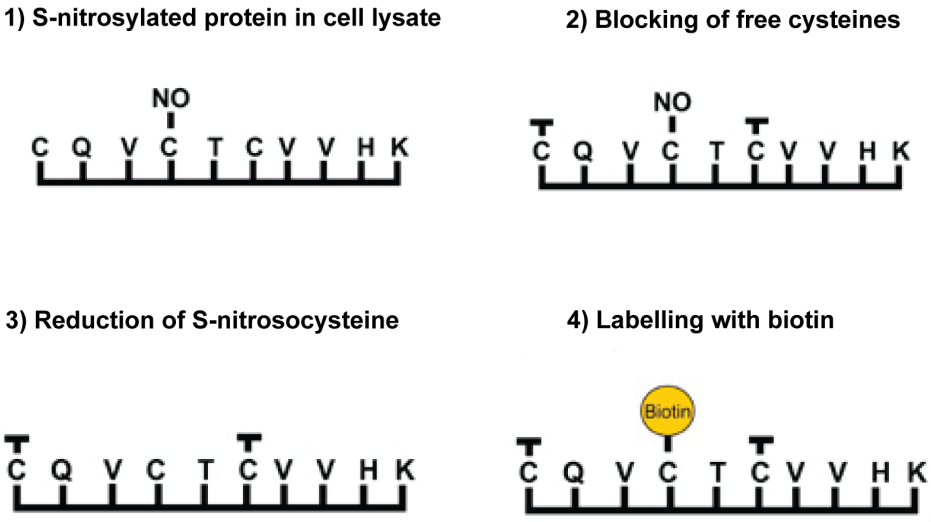


Figure 7. Detection of S-nitrosylated proteins using the biotin switch technique. In cell lysates (1), unmodified cysteines are methylated (blocking step) to render them unreactive (2), S-nitrosylated cysteines are specifically reduced (3) and free cysteines are labelled with biotin (4). Proteins can be pulled down with biotin streptavidin beads and subjected to western blotting. Figure modified from the Dash Lab website at http://www.reading.ac.uk/cellmigration/nitrosylation.htm

1.10.1 Previously published screens

The biotin switch technique can be combined with mass spectrometry analysis, facilitating S-nitrosylated protein identification and, in some cases,

identification of the cysteine(s) that are S-nitrosylated. Several screens have been carried out to date in a variety of mammalian cell types (**Table 2**). Though these screens employ a variety of different S-nitrosylating agents, experimental conditions and cells types, certain key features can be discerned. Most strikingly, whilst some of these screens have detected hundreds of hits, very few proteins involved in gene regulation have been identified. For example, only seven chromatin-binding proteins have been identified as S-nitrosylated to date. This lack of sensitivity is likely due to the bias towards the identification of abundant proteins that appears to be inherent to all forms of biotin switch carried out using whole cell lysates. In regards to the types of proteins identified, often the most annotated gene ontology term is cellular metabolism. It is currently unclear whether S-nitrosylation is more prevalent in proteins involved in metabolism or, instead, that the identification of a large number of S-nitrosylated metabolic proteins is favoured due to the high relative abundance of these proteins within cells. Aside from metabolism, the screens carried out to date have identified S-nitrosylated proteins in a wide range of biological processes, hinting at a far-reaching scope for regulation of protein function by S-nitrosylation.

The screens performed so far have therefore been useful for the identification of cytoplasmic targets of S-nitrosylation, however they offer little information regarding which proteins are S-nitrosylated in the nucleus. Screens leading to the identification of novel nuclear targets of S-nitrosylation will act as valuable resources from which to discover further mechanisms by which NO affects gene expression.

Author	Year	Cell type	Treatment	Duration (mins)	Technique	# proteins (total)	chromatin/chromatin binding protein	transcritpion factor	DNA binding protein
Kuncewicz	2003	Mouse SV40 MES 13 mesangial cell lysates	40μM GSNO	20	Biotin switch and 2-DE	35	0	1	0
Yang	2005	Human aortic endothelial cells	2mM DEANONOate	10	Biotin switch and 2-DE	5	0	0	0
Hao	2006	Rat Cerebellar lysates	5μM GSNO	30	SNOSID (modified biotin switch)	56	0	1	0
Shi	2008	Rat heart extracts	100μM GSNO	30	Biotin switch and 2-DE	10	0	0	0
Huang	2009	Human endothelial cells derived from Ahy 926	1mM GSNO	30	Biotin switch and 2-DE	28	0	0	1
Forrester	2009	HEK293 cell line	500μM CysNO	10	SNORAC. Gel sep. >150kDa proteins only	14	1	1	1
Forrester	2009	Mouse RAW264.7 macrophage cell line	200μM CysNO	10	SNORAC	40	0	1	1
Yi-Ju Chen	2010	Mouse pancreatic MS-1 endothelial cell lysates	1mM SNAP	30	Alkyalting biotin switch and affinity purification	384	5	11	17
Kohr	2011	Mouse heart homogenates	1mM GSNO	30	SNORAC	951	2	18	6
Murray	2012	Human pulmonary arterial endothelial cell lysates	20μM GSNO	15	Modified biotin switch (cysTMT) and affinity purification	180	0	0	2
Scheving	2012	Mouse sciatic nerve	Nerve Inury	24 hours	Biotin switch and 2-DE	57	0	0	0
Doulias	2013	Mouse brain	wild type	-	Organomercury based enrichment	120	0	5	0
Qu	2014	Mouse BV-2 Microglia cell lysates	200μM CysNO	30	Modified biotin switch (iodoTMT) and affinity purification	68	0	0	0
Qu	2014	Mouse BV-2 Microglia cells	100ng/mL LPS	16 hours	Modified biotin switch (iodoTMT) and affinity purification	30	0	2	1
Raju	2015	Mouse brain	wild type	-	Organomercury based enrichment	136	1	1	2
						Unique	**7**	**33**	**40**

Table 2. Screens for S-nitrosylated proteins in mammalian cells. Shown are the results of previously published screens, including the number of chromatin binding proteins, transcription factors and DNA binding proteins identified. For each screen, I carried out gene ontology (GO) analysis using PANTHER (pantherdb.org). See **References** for full citations of each screen.

Aims

A number of studies have shown that protein S-nitrosylation is an important regulatory mechanism through which gene expression is modulated, however which nuclear proteins are S-nitrosylated in neurons remains largely unknown. Therefore, the main aim of my work was to identify novel nuclear targets of S-nitrosylation in cortical neurons. Progress in identifying the targets of S-nitrosylation in neurons has been impeded, in part, due to technical difficulties associated with the detection of S-nitrosylated proteins. The majority of techniques currently used to detect S-nitrosylated proteins can be considered indirect, since they depend upon the chemical modification of the S-nitrosylated cysteine. Therefore, an additional aim of my work was to examine whether endogenous protein S-nitrosylation can be detected in a direct manner in neurons, without prior chemical derivatisation or the use of exogenously-applied nitric oxide donors. The main questions addressed in this thesis are:

1. Which nuclear proteins are S-nitrosylated in cortical neurons?
2. Are neuronal nuclear proteins S-nitrosylated in response to physiological stimuli?
3. Is it possible to detect endogenous S-nitrocysteines on nuclear proteins using a novel technical approach?

This work will bring us closer towards uncovering the nuclear S-nitrosoproteome of cortical neurons, providing a basis from which to study the mechanisms by which S-nitrosylation of nuclear proteins regulates neuronal function. Through identification of novel targets of S-nitrosylation, this work will hopefully contribute towards uncovering additional biological roles of S-nitrosylation in mammalian cells.

2. Materials and Methods

Reagents were purchased from Sigma unless otherwise stated.

4.1 Preparation of E17 cortical neurons

Papain solution for digestion of cortices: 200U of papain (Worthington) was added to 9.8ml of digestion buffer (1 mM Hepes pH 7.4, 20 mM glucose, 82 mM Na_2SO_4, 30 mM K_2SO_4, 6mM $MgCl_2$, 0.25mM $CaCl_2$, 0.001% Phenol Red, 0.126mN NaOH). 100 µL of 200 mM cysteine-HCL was then added to provide the acidic conditions needed for papain activation. Following 10 mins incubation at 37°C, pH was adjusted to 7 using 0.1M NaOH added drop by drop. The solution was filter sterilized and stored at room temperature until use.

Plating procedure and culture conditions: Pregnant Sprague Dawley rats were culled 17 days into gestation, according to home-office approved schedule 1 methods. Embryos were removed then cortices excised from embryonic brains and stored in cold dissection buffer (1x HBSS, 2.5mM Hepes pH 7.4, 30 mM D-glucose, 1 mM $CaCl_2$, 1 mM $MgSO_4$, 4 mM $NaHCO_3$). Dissection buffer was removed completely and the prepared papain solution (see above) was added for 25 mins at 37°C. An initial wash was carried out with plating media (MEM (Life Tech) supplemented with 10% FBS, 5% horse serum and 1 mM glutamine) to ensure papain is inactivated, 3 additional washes were completed to remove remaining papain. Cortices were dissociated via mechanical disruption with a 10ml stripette, before being passed through a cell strainer (40µm, BD falcon). Cells were counted in solutions containing 10% trypan blue solution to identify dead cells; 85% of live cells and above is ideal for high quality preparations. Cells were then plated on 10 cm Nunc dishes (Thermo Fischer) coated with 40 µg/ml poly-D-lysine and 2 µg/ml Laminin (BD Bioscience) at 12.5 million per dish. The following day, media was replaced with supplemented neurobasal (NB with 1x B27 (Thermo Fischer), 1 mM glutamine, 1x penicillin-streptomycin and 10µM fluorodeoxyuridine (FdU) (Merck). The addition of the mitotic inhibitor FdU is necessary so that any proliferating cells that are isolated with the neurons stop dividing. Cells were then kept for 4 days at 37°C, 5% CO_2. Prior to stimulation of cells to induce S-nitrosylation, cells were starved for 16h by adjusting media so that the B27 concentration was 1/3 of normal.

4.2 HEK293T cell culture

HEK293T cells contain a genomic integration of the simian virus 40 large T antigen, rending them more transfectable than their parent HEK293 cell line. HEK293T cells were cultured according to standard conditions listed on the ATCC website for ATCC® CRL-11268™. Cells were not cultured past passage 20.

4.3 Transfection conditions and plasmids

HEK293T cells were transfected at 40-50% confluency using Lipofectamine 2000 (Thermo Fischer) using standard protocol except DNA/lipofectamine ratio of 1 µg DNA/1.25 µL lipofectamine. The CMV myc-CREB plasmid was created by Bonnie Lonze (Ginty Lab).

4.4 Nuclear and cytoplasmic protein extractions

Nuclear and cytoplasmic protein extractions were carried out using the NE-PER kit (Thermo Fischer) according to the manufacturers instructions, except an extra wash of the nuclei with PBS was carried out on the nuclei before addition of buffer NER, to ensure cytoplasmic proteins are removed to the greatest extent possible. In this manner, 1 mL of PBS was added per 100ul packed cell pellet volume and pellets centrifuged at 16000 g for 10 mins 4°C and PBS removed before continuing.

4.5 Working with S-nitrosylation

General Precautions: S-nitrosylation is light sensitive and light can also react with ascorbate to induce artifactual signals (Forrester et al., 2007), so all procedures involving detection of S-nitrosylation were carried out in minimal light conditions; a small light in the opposite corner of the room from where the procedures are taking place. The eppendorf tubes used were brown plastic and falcon tubes were covered externally with foil. No glassware/metalware was used as it may contain contaminating metal species that could interfere with the reaction. All precautions were taken to avoid contamination of the samples with metal at every stage in the process. Polypropylene tubes were used as they are suitable for use with the acetone that is used for CysNO removal and MMTS removal.

NO Donor Preparation: CysNO was prepared fresh each time before use according to (Mallis et al., 2001). Briefly, 25 µL of 4ML HCL (prepared fresh every 4 experiments) was added to 220 µL of 220mM L-cysteine and 220 µL of 220mM $NaNO_2$ and incubated for 10 mins at room temperature, in the dark. pH was then neutralized using 25 µL of 4M NaOH (prepared fresh every 4 experiments). This gives a final concentration of ~100 mM CysNO. Exact final concentration calculated from absorbance at 338nm, of a 1/100 diluted solution, using the formula: $[Abs]_{338}/900 * 100$ (dilution factor) * 1000= CysNO concentration in mM. To create Cys- only controls, 220 µL of water was added in place of $NaNO_2$.

4.6 Detection of S-nitrosylation using the biotin switch technique

Sample acquisition varies for according to the specific experiment, followed by a protocol that is common to all.

Biotin Switch/SNORAC buffers: Buffers were prepared as in Forrester et al, 2009 (Reproduced below for clarity). Sodium ascorbate stock was made to 500 mM. Additional

buffers not mentioned in the original protocol are shown in italic. All buffers and solutions throughout the protocol are prepared using BPC grade water (Sigma W3513)
HEN buffer (100 mM Hepes, 1 mM EDTA, 0.1 mM neocuproine, pH 8.0).
HEN/10 buffer (HEN buffer diluted 10-fold with dH2O).
HEN**S** buffer (HEN buffer with 1% SDS (w/v)).
HEN**S**/10 buffer (HEN/10 buffer with 1% SDS (w/v)).
500 mM sodium ascorbate in HEN buffer.
10% MMTS in N,N-dimethylformamide (v/v).
Elution buffer (HEN/10 containing 1% β-mercaptoethanol (v/v)).
Neutralization buffer (25 mM Hepes, 100 mM NaCl, 1 mM EDTA, 0.5% Triton X-100, pH 7.5).
Wash buffer (neutralization buffer containing 600 mM NaCl).
25% SDS in dH2O (w/v).
70% acetone in dH2O (v/v).
HEN lysis buffer (HEN with 0.2% NP40)
2X MMTS blocking buffer (2% MMTS, 5% SDS in HEN buffer)
NEM blocking buffer stock (200 mM in HEN buffer)
2X western loading buffer (2% SDS, 2% βME, 20% glycerol, 100 mM Tris 6.8, 0.008% bromophenal blue)

Endogenous S-nitrosylation in cortical neurons: 3 plates of E17 cortical neurons per sample (prepared as described above) were treated as appropriate, then washed twice with ice cold PBS and then each harvested in 180 µL of cold HEN lysis buffer. Samples were then homogenized 5x with a 25 gauge needle, centrifuged for 10 mins at 10,000 g 4°C and supernatant collected (~2.5-3 mg of protein per 3 plates). Samples were then split between two eppendorf tubes. Biotin switch common protocol (listed on page 47) followed from this point onwards.

S-nitrosylation of wild-type/mutant constructs in HEK293T cells: A single transfected 6 cm plate of HEK293T cells (70-80% confluency) was used per condition. For in-plate treatment (mycRBBP7 experiments), CysNO was first diluted 1/100 in HEN buffer then added as necessary. Cells were treated for 20 mins then washed once in PBS. Lysates were harvested in 200 µL HEN lysis buffer and homogenized 5 times with a 25G needle. After centrifugation at 10000 g 10mins 4°C, supernatant was saved. CysNO was removed by acetone precipitation. Samples were added directly to 12 mL of -20°C acetone and samples kept at -20°C for a minimum of 1 hour to aid precipitation. Samples were then centrifuged for 10 mins at 2000 g, 4°C and the precipitated protein pellets washed 2x with -20°C 70% acetone (samples centrifuged for 10 mins at 2000 g, 4°C in between washes). Samples were resuspended in 200 µL HEN**S**. At this point, a BCA assay was used to equalize protein amounts to 650 µg and volume made up to 500 µL with HEN. The common protocol for biotin switch (below) followed onwards. For treatment of cellular lysates (mycCREB experiments),

cells were harvested first in 200 µL HEN lysis buffer and homogenized 5 times with a 25G needle. Following centrifugation at 10000 g 10 mins 4°C, supernatant was saved and protein amount (determined with BCA assay) equalized to 750 µg each and volume made up to 500 µL with HEN. CysNO was first diluted 1/100 in HEN buffer then added as necessary. Lysates were treated for 20 mins, then CysNO was removed by acetone precipitation as described above. Samples were resuspended in 200 µL. The common protocol for biotin switch (below) followed onwards

Biotin switch: common protocol: An equal volume of 2X MMTS Blocking Buffer added to each sample. Samples were incubated for 30 mins at 50°C in a waterbath and vortexed every 5 mins to aid denaturation of the proteins (essential for efficient blocking of cysteine thiols). Samples were combined as necessary and added directly to 12 mL of -20°C acetone to precipitate proteins. Next, samples were kept at -20°C for a minimum of 1 hour, after which the supernatant was removed completely. Care was taken not to let pellets dry out, as this impedes resuspension. Samples were resuspended in 220 µL HEN**S** buffer by 3 rounds of repetitive pipetting, with 10 mins in between. Following complete resuspension, sodium ascorbate was added to a concentration of 50 mM, from a freshly prepared 500 mM stock, samples mixed by gentle tapping, and incubated for 5 mins at RT. Then 77 µL of 4 mM Biotin HPDP solution was added to the samples, to make a final concentration of 1 mM Biotin HPDP. Samples were then rotated for 45 mins to allow binding of biotin to the newly reduced cysteine thiols (exnitrosylated). Proteins were precipitated by adding to 12 mL of -20°C acetone, and washed 3 times using -20°C 70% acetone to remove sodium ascorbate and unbound biotin HPDP (samples centrifuged for 10 mins at 2000 g, 4°C in between washes). Samples were then resuspended in 220 µL HEN**S** as before, then 400 µL neutralization buffer added. From this point onwards, the technique was carried out in in the standard light conditions of the lab. Each samples was precleared by incubation with 30 µL bead volume of protein A beads for 1 h at room temperature then centrifuged at 500 g for 5 mins at RT, and supernatant removed. At this point, 40 µL (15.5%) was taken as input and the remainder incubated with 30 µL bead volume of streptavidin agarose beads overnight rotating at 4°C, to capture the peptides that have now been biotinylated. Samples were then centrifuged for 5 mins at 500 g, 4°C, and 4 washes carried out using wash buffer, samples centrifuged at for 5 mins at 500 g 4°C in between washes. Beads were dried using a 29G needle then 40 µL of 2x western loading buffer was added. Samples were then boiled for 5 mins then cooled at RT for 5 mins. Lastly, samples were centrifuged 10,000 g for 2 mins and supernatant collected (100% used per western blot).

4.7 Detection of S-nitrosylation: SNORAC

CysNO treatment of extracts: 400 µg of protein used per sample, CysNO treatment was carried out in the CER1 (cytoplasmic) or NER1 (nuclear) buffer from the NE-PER nuclear and cytoplasmic protein extraction kit. Samples were treated with the appropriate concentration of

CysNO for 20 mins, in the dark, with intermittent mixing. CysNO was removed after treatment. For experiments A-E, CysNO was removed by acetone precipitation; after CysNO treatment, samples were added directly to 12 mL of -20°C acetone and samples kept at -20°C for a minimum of 1 hour to aid precipitation. Samples were then centrifuged for 10 mins at 2000 g, 4°C and the precipitated protein pellets washed 2x with -20°C 70% acetone (samples centrifuged for 10 mins at 2000 g, 4°C in between washes). Samples were resuspended in 200 µL of HENS. For SNORAC screen experiment F, CysNO was removed using P6 spin columns prewashed in HEN buffer.

Blocking of free thiols: Protein amounts were equalized by BCA assay then volume made up to 500 µL with HEN buffer. Experiments A and B were blocked using S-Methyl methanethiosulfonate MMTS using 2X blocking buffer as described in biotin switch common protocol. Experiments C-F blocked using NEM (n-ethylmaleimide). For these experiments, NEM was added from a freshly prepared 200 mM stock (in HEN buffer) to a final concentration of 140 mM. SDS was added from a 20% stock (in distilled water) to a final concentration of 2.44%. NEM blocking was carried out for 30 mins at 50°C. For all experiments, samples were acetone precipitated and washed as described.

Bead preparation: Thiopropyl sepharose 6B resin (GE Healthcare, product code:17-0420-01) was first swelled with 50ml BPC water (250 µg dry weight adequate for 12 samples), followed by 2 additional washes with 50mL BPC water and a final wash with 30mL HEN buffer. Beads were centrifuged at 500 g 10 mins 4°C in between washes. Beads were stored at in HEN buffer at 4°C in a 1:1 ratio (beads: supernatant) and used on the same day as they were prepared.

Incubation with beads: Each protein pellet was resuspended in 220 µL HENS. 14 µL was taken as total input at this point, stored at -20°C. Samples were then split between 2 sets of tubes. In the first set (mass spec analysis samples) 133 µL of sample was added to 60 µL of thiopropyl sepharose 6B bead mix, 60 µL of 500 mM sodium ascorbate, 347 µL of HEN. In the second set (samples for elution) 66 µL of sample was added to 60 µL of thiopropyl sepharose 6B bead mix, 60 µL of 500 mM sodium ascorbate, 413 µL of HEN. Samples were then rotated for 2 hours in the dark at RT.

Washes and elution: beads were washed 4 times with 1 mL HEN, 2 times with HEN/10 (centrifuged at 500 g 5 mins 4°C in between). At this point the beads for mass spectrometry analysis were frozen (conventionally) with 1 mL of HEN/10 buffer and stored at -20°C. Samples for elution were eluted as described in the biotin switch protocol.

4.8 Silver staining and western

Silver staining and western blot was carried out according to standard procedures. ECL Prime (GE Healthcare) or ECL Femto (Thermofischer) was used for western blot detection of proteins isolated by S-nitrosylation.

4.9 Antibodies

CREB1 rabbit monoclonal (New England Biosciences 9197S)
HDAC2 mouse monoclonal (Abcam ab12169)
RBBP7 rabbit monoclonal (Abcam ab3535)
Tubulin mouse monoclonal (Sigma T9026)
C-Myc mouse monoclonal (Santa Cruz sc-56634)

4.10 Gene Ontology Analysis

HEK293T screens: Carried out with PANTHER (pantherdb.org). Exclusive annotations for organelle (each protein assigned one organelle only) were obtained using the 'Functional classification viewed in pie chart' option. Comprehensive GO analysis for cellular component was carried out using the statistical overrepresentation test, displaying all results. Only the raw numbers of each classification were used, statistical analysis was not considered (due to the lack of a suitable background set in this case).

Neuronal screens: Assigned from Uniprot by Proteome Discoverer 1.4 (Thermo Fisher Scientific, Bremen, Germany).

4.11 Motif-X analysis

Motif X (motif-x.med.harvard.edu). Foreground: SNO-peptides associated with S-nitrosylated protein hits. Settings: Extended from IPI Rat Proteome, central character: C, width: 21, significance: 0.000001. Background: IPI Rat Proteome, background central character: C.

4.12 Mutagenesis

Mutagenesis carried out using Quikchange multisite-directed mutagenesis kit (Agilent).

4.13 Software

Graphs prepared using Graphpad Prism. Statistical analysis carried out using Graphpad Prism. Figures compiled using Adobe Illustrator. Venn diagrams made using BioVenn (http://www.cmbi.ru.nl/cdd/biovenn/index.php)

4.14 Mass Spectrometry: CysNO-treated HEK293T cell lysates

Materials and methods for the all the mass spectrometry analysis (including that on neuronal extracts) was written by Marco Gaspari (University of Catanzaro, Italy), who carried out the mass spectrometry. Edited by Jacob Anderson.

Exp 0a: April 2012
Samples:
5. 1mM Cys
6. 1 mM CysNO
8. 1 mM CysNO without sodium ascorbate

Beads thawed at 4 °C, centrifuged at 1 min at 4000 rpm RT. Supernatant was removed from beads. Overnight digestion at 37 °C with 800 ng of trypsin proteomics grade (Sigma) was carried out in 100 µL of 100 mM tris buffer, pH 8.5 (buffer A). Following tryptic digestion, supernatants were saved (samples: **SNO-Proteins**). Beads were then washed three times with 20 mM ammonium bicarbonate in 50% MeOH (v/v) (buffer B). In order to elute formerly cys-nitrosylated peptides, 100 µL of buffer B was added to each sample, followed by the addition of 10 µL of 100 mM DTT (incubation for 1 h at 37 °C). Alkylation of released cysteines was achieved by adding 10 µL of 200 mM iodoacetamide (1h at 37 °C in the dark). The supernatants were recovered, and the beads were washed with 50 µL of buffer B. Supernatants and their respective washes were pooled and evaporated using a vacuum centrifuge (samples**: SNO-peptides**).

An aliquot (40 µL) of each SNO-Protein sample supernatant was purified by reverse-phase (RP) StageTips (Rappsilber et al., 2007). Peptide mixtures were acidified by 0.5% (final concentration) trifluoroacetic acid (TFA) and loaded onto a 200 µL micropipette tip stacked with two layers of a RP exchange resin (C18, Empore extraction disks, Sigma) previously conditioned with a sequential addition of 20 µL of eluent (solution E-RP, 50% acetonitrile / 0.1% formic acid) and 20 µL of solution wash-RP (0.1% TFA). After a washing step of 20 µL of solution wash-RP, elution of tryptic peptides was achieved by adding 15 µL of solution E-RP. SNO-peptides (100% of the sample) were reconstituted and purified by RP Stage tips as described above.

Eluates for both SNO-protein and SNO-peptide samples were evaporated to dryness and resuspended in 20 µL of 0.1% formic acid / 2% acetonitrile. A 5 µL aliquot of each sample was then subjected to nanoLC-MS/MS analysis.

EXP 0b (June 2012)
Samples:
1-2= nuclear extracts
1. 250µM Cys only
2. 250µM CysNO
3. 250µM CysNO without sodium ascorbate
5-7= cytoplasmic extracts
5. 250µM Cys only
6. 250µM CysNO
7. 250µM CysNO without sodium ascorbate

SNO-proteins prepared as for *EXP0a,* except for maximum protein recovery, the ammonium bicarbonate washes was also saved, pooled, evaporated to dryness and resuspended in the

corresponding supernatant solution (samples: **SNO-proteins**). SNO-peptides were prepared as for *EXP0a*

An aliquot of each supernatant (50 µL) from SNO-protein samples was purified by by strong cation exchange (SCX) StageTips (Rappsilber et al., 2007). Digested proteins were diluted with 0.95 mL of 80% acetonitrile / 0.5% formic acid (solution SCX-a) and loaded onto a 200 µL micropipette tip stacked with two layers of a strong cation exchange resin (Empore extraction disks, Sigma) previously conditioned with 20 µL of solution SCX-b (20% acetonitrile / 0.5% formic acid) and 20 µL of solution SCX-a. After two washing steps (20 µL of solution SCX-a, 20 µL of solution SCX-b), elution of tryptic peptides was achieved by adding 14 µL of 500 mM ammonium acetate / 20% acetonitrile (solution E). Eluates were evaporated to dryness and resuspended in 15 µL 0.1% formic acid / 2% acetonitrile. A 5 µL aliquot of each sample was subjected to nanoLC-MS/MS analysis. SNO-peptides were processed as described in EXP 0a.

nanoLC-MS/MS analysis: HEK293T

Nano-LC was performed on an **Ultimate nano-LC system from Dionex (Sunnyvale, CA, USA)**, using a valveless setup (vented column). The peptide mixtures (5 µL) were loaded on an in-house packed 75 µm id, Integra Frit™ (New Objective, Cambridge, MA, USA) trapping column packed with C18 silica particles, 5µm particle size, from Dr. Maisch (Entringen, Germany). Trapping column packing bed length was 1.0 cm; loading flow rate was 10 µm/min of loading pump solvent, consisting of H_2O/ACN/FA/TFA 97.9:2:0.09:0.01 v/v/v/v. After 7 min of column washing, the trapping column was switched on-line to the analytical column, an in-house packed 50 µm id, Pico Frit™ column (New Objective) filled with the same stationary phase as the trapping column but the particle size being 3µm. Peptide separation started at 100 nL/min using a binary gradient. Mobile phase A was H_2O/ACN/FA/TFA 97.9:2:0.09:0.01; mobile phase B was H_2O/ACN/FA/TFA 29.9:70:0.09:0.01 v/v/v/v. Gradient was from 5 to 45% B in 83 min. After 15 min at 100% B, the column was re-equilibrated at 100% in A for 30 min before the following injection.

MS detection was performed on a **QSTAR XL hybrid LC-MS/MS from Ab Sciex (Foster City, CA, USA)** operating in positive ion mode, with nano-ESI potential at 1300V, curtain gas at 15 units, CAD gas at 3 units. Information-dependent acquisition (IDA) was performed by selecting the three most abundant peaks for MS/MS analysis after a full TOF-MS scan from 350 to 1400 m/z lasting 1.5 s. All MS/MS analyses were performed in enhanced mode (1.5 sec/scan, with scan range 80 to 1600 m/z). Threshold value for peak selection for MS/MS was 30 counts. Nano-LC-MS/MS data files were internally re-calibrated after acquisition by using background ions due to polymethylsiloxane traces, detected in the full-scan MS spectrum at medium intensity in absence of eluting peptides. Calibrations *m/z* values were 445.1200, 519.1388, 593.1576, 667.1764, 741.1952 and 815.2140.

Data analysis for HEK293T screens

MS/MS spectra were converted in Mascot Generic Format (mgf) by the Analyst software (Applied Biosystems, version 1.1). A script running on Analyst was used to determine peptide charge state and to perform centroiding and de-isotoping on MS/MS data. Data were searched on the Mascot search engine (www.matrixscience.com), version 2.2.04, against the *Rattus* Protein Sequence database downloaded from the SwissProt/Trembl database (March 2012, 20,359 sequences). In order to estimate false-discovery rate (FDR), the target-decoy database search strategy available within Mascot was adopted. The following search parameters were used: MS tolerance 100ppm; MS/MS tolerance 0.3 Da; fixed modifications methylthio cysteine (for digested proteins), carbamidomethyl cysteine (for SNO-peptides); variable modifications methionine oxidized; enzyme trypsin; max. missed cleavage 1. Protein probability was adjusted in order to have a spectral FDR below 1% in all experiments. For digested proteins, a minimum detection criteria of two peptides per proteins was imposed.

4.15 Mass Spectrometry: CysNO-treated neuronal extracts

EXP A and B (biological replicates): (February 2013)

Set A.

Nuclear extracts

1. 1 mM Cys
4. 1 mM CysNO
5. 1 mM CysNO – ascorbate

Set B

Nuclear extracts

1. 1 mM Cys
2. 1 mM CysNO
4. 1 mM CysNO – ascorbate

SNO-proteins and SNO-peptides eluted and pooled as in Exp0b.

Quantitative analysis: CysNO treated neuronal extracts

The digested proteins samples were subjected to O^{18} labelling as in (Bernaudo et al., 2015). Aliquots of 30 µL of, respectively, samples **A**-4, **A**-5, **B**-1, **B**-2 were evaporated and resuspended in 50 µL of H_2O^{18} 98% pure (Sigma) / methanol 4:1 (v/v). The solution was buffered by the unvolatile tris buffer originally present in the on-beads digestion step. A fresh trypsin aliquot (200 ng in 0.5 µL) was added in order to catalyse the oxygen exchange reaction, which was allowed to proceed overnight at 37 °C. Aliquots of 30 µL of, respectively, samples **A**-1, **A**-4, **B**-2, **B**-4 were evaporated to dryness, resuspended in 30 µL of normal HPLC water, and subjected to a parallel trypsin-catalysed oxygen exchange reaction. Even though in this latter case no change in the molecular weight of control peptides ("light" (L) peptides) was produced, the reaction was allowed to proceed in parallel to the "heavy" (H) labelling reaction in order to avoid any possible source of bias. After labelling, to inactivate trypsin and avoid the phenomenon of back-exchnge, samples were heated for 1 h at 56 °C and boiled for 10 min at 100 °C.

Labelled samples were mixed in a 1:1 ratio as follows: **A**-4(H):**A**-1(L); **A**-5(H):**A**-4(L); **B**-2(H):**B**-4(L); **B**-1(H):**B**-2(L). This arrangement allowed the relative comparison of proteomes isolated from CysNO-treated cells *versus* untreated cells and CysNO-treated cells *versus* CysNO minus ascorbate-treated cells in duplicate analysis with label inversion in the duplicate run for both couples. Mixed samples were purified by strong cation exchange (SCX) StageTips (Rappsilber et al., 2007). Peptide mixtures were diluted with 1.5 mL of 80% acetonitrile / 0.5% formic acid (solution SCX-a) and loaded onto a 200 µL micropipette tip stacked with one layer of a strong cation exchange resin (Empore extraction disks, Sigma) previously conditioned with 20 µL of solution SCX-b (20% acetonitrile / 0.5% formic acid) and 20 µL of solution SCX-a. After two washing steps (20 µL of solution SCX-a, 20 µL of solution SCX-b), elution of tryptic peptides was achieved by adding 7 µL of 500 mM ammonium acetate / 20% acetonitrile (solution E). The eluate was evaporated to dryness and resuspended in 15 µL 0.1% formic acid / 2% acetonitrile. A 5 µL aliquot of each sample was subjected to nanoLC-MS/MS analysis.

For a qualitative analysis of putative nitrosylation sites, SNO-peptides from the evaporated extracts of samples 2 and 4 were dissolved in 200 µL of solution SCX-a, purified by SCX StageTips as described, evaporated to dryness and reconstituted in 10 µL of 0.1% formic acid / 2% acetonitrile. A 5 µL aliquot of the pooled sample was subjected to nanoLC-MS/MS analysis.

Experiment C-E (biological replicates): (August 2015)

Nuclear extracts
Experiment C
7. 100µM Cys
8. 100µM CysNO
9. 100µM CysNO without ascorbate

Experiment D
1. 100µM Cys
2. 100µM CysNO
3. 100µM CysNO without ascorbate

Experiment E
1. 100µM Cys
2. 100µM CysNO
3. 100µM CysNO without ascorbate

Supernatant removed from beads. Overnight digestion at 37 °C with 300ng of trypsin proteomics grade (Sigma) in 100 µL of 100 mM TEAB buffer, pH 8.5 (buffer C). Following tryptic digestion, the supernatants were removed and the beads were washed three times with 20 mM TEAB in 50% MeOH (v/v) (buffer D). The washes of each sample were pooled, evaporated to dryness and resuspended in the corresponding supernatant solution (samples: SNO-proteins). Proteins were reduced further by adding 10 µL of 100 mM DTT (1h at 37 °C) and residual free cysteines were alkylated by adding 12 µL of 200 mM iodoacetamide. After

quenching the reaction with additional 2 µL of 100 mM DTT, complete overnight digestion was achieved by additional 300 ng of fresh trypsin. Samples were labelled according to the standard dimethyl labelling procedure (Boersema et al., 2009). Briefly, samples were subjected to reductive amination by adding 4 µL of 0.6 M sodium cyanoborohydride and 4 µL of either formaldehyde (4% w/v, "light" label) or formaldehyde-d_2 (4% w/v, "medium" label). Samples were labelled as "light" (L) or "medium" (M) and mixed in pairs according to the Table A.

Table A: labelling scheme for dimethyl labelling experiment and generation of M:L pairs.

Sample	**Label**	**M:L pairs**
C-7. NUC cys	L	80 µL of 1-7 (L) + 80 µL of 1-8 (M) 80 µL of 1-9 (L) + 80 µL of 1-8 (M)
C-8. NUC CysNO	M	
C-9. NUC CysNO - asc	L	
D-1. NUC cys	M	80 µL of 2-2 (L) + 80 µL of 2-1 (M) 80 µL of 2-2 (L) + 80 µL of 2-3 (M)
D-2. NUC CysNO	L	
D-3. NUC CysNO - asc	M	
E-1. NUC cys	L	80 µL of 3-1 (L) + 80 µL of 3-2 (M) 80 µL of 3-3 (L) + 80 µL of 3-2 (M)
E-2. NUC CysNO	M	
E-3. NUC CysNO - asc	L	

Digest pairs were diluted to 2.4 mL with SCX-a solution and purified by SCX StageTips as described above. The six eluates were evaporated and peptides resuspended in 12 µL 0.1% formic acid / 2% acetonitrile. A 4 µL aliquot of each sample was subjected to nanoLC-MS/MS analysis with technical duplicates (2 injections per sample).

To extract SNO-peptides, the beads recovered from on-beads digestion were resuspended in 100 µL of buffer C, followed by the addition of 10 µL of 100 mM DTT (incubation for 1 h at 37 °C). Alkylation of released cysteines was achieved by adding 10 µL of 200 mM iodoacetamide (1h at 37 °C in the dark). The supernatants were recovered, and the beads were washed with 50 µL of buffer D. Supernatants and their respective evaporated washes were pooled, labelled by dimethyl labelling and purified as described above. Peptides were reconstituted in 10 µL of 0.1% formic acid / 2% acetonitrile. A 5 µL aliquot of the pooled sample was subjected to nanoLC-MS/MS analysis.

Experiment F : (August 2013)
Nuclear extracts
1. 100µM Cys
2. 100µM CysNO
Cytoplasmic extracts
3. 100µM Cys
4. 100µM CysNO

SNO-proteins were isolated as described in Experiment 1. Digested proteins were prepared and labelled by O^{18} as described above, with minor modifications in starting amounts of samples subjected to isotopic labelling. As before, the volume of the supernatant + evaporated washes recovered from on-beads digestion was 100 µL. Starting amounts for the "heavy" labelling reaction were: 45 µL for samples 1 and 2; 25 µL for samples 3 and 5; 2 x 25 µL for sample 4. Exactly the same amount for each of the five samples was taken for the "light" labelling reaction.

Labelled samples were mixed in a 1:1 ratio as follows: 1(H):2(L); 1(L):2(H); 4(H):3(L); 3(H):4(L). Mixed samples were purified by strong cation exchange (SCX) StageTips as described in Exp 1. Because of the higher amount of protein sample recovered in this experiment, sample fractionation at the peptide level could be achieved (4 fractions). Thus, after tip conditioning, sample loading and washing, stepwise elution of tryptic peptides was achieved by sequential addition of 7 µL of four solutions, all containing 20% acetonitrile, of increasing ionic strength and pH: (i) 60 mM ammonium acetate, 0.5% formic acid; (ii) 120 mM ammonium acetate, 0.5% formic acid; (iii) 250 mM ammonium acetate, 0.5% formic acid; (iv) 500 mM ammonium acetate. The four SCX fractions were evaporated by vacuum centrifugation and resuspended in 8 µL of 0.1% formic acid / 2% acetonitrile. A 6 µL aliquot of each fraction (4 fractions x 6 H:L pairs) was subjected to nanoLC-MS/MS analysis.

For a qualitative analysis of putative nitrosylation sites, SNO-peptides from the evaporated extracts were dissolved in 200 µL of solution SCX-a, purified by SCX StageTips as described, evaporated to dryness and reconstituted in 10 µL of 0.1% formic acid / 2% acetonitrile. A 5 µL aliquot of the pooled sample was subjected to nanoLC-MS/MS analysis.

nanoLC-MS/MS analysis for neuronal extracts

Chromatography was performed on an **Easy LC 1000 nanoscale liquid chromatography (nanoLC) system** (Thermo Fisher Scientific, Odense, Denmark). The analytical nanoLC column was a pulled fused silica capillary, 75 µm i.d., in-house packed to a length of 10 cm with 3 µm C18 silica particles from Dr. Maisch (Entringen, Germany). The peptide mixtures were loaded at 500 nL/min directly onto the analytical column. A binary gradient was used for peptide elution. Mobile phase A was 0.1% formic acid, 2% acetonitrile, whereas mobile phase B was 0.1% formic acid, 80% acetonitrile. Peptides were separated by a gradient elution at a 300 nL/min flow rate, ramping from 5% B to 35% B in 60 min (50 min for SNO-peptides), and from 35% B to 100% B in additional 15 min; after 5 min at 100% B, the column was re-equilibrated at 2% B for 10 mins before the following injection. MS detection was performed on a quadrupole-orbitrap mass spectrometer **Q-Exactive (Thermo Fisher Scientific, Bremen, Germany)** operating in positive ion mode, with nanoelectrospray (nESI) potential at 1800 V applied on the column front-end via a tee piece. Data-dependent acquisition was performed by using a top-12 method (top-8 for SNO-peptide), where the twelve most

abundant ions were automatically selected for HCD fragmentation at normalized collision energy of 25%. Resolution (FWHM), AGC target and maximum injection time (ms) for full MS and MS/MS were 70,000/17,500, 1e6/1e5, 20/60, respectively. MS/MS parameters for detection of SNO-peptides were: resolution 35,000; AGC target 2e5, max injection time 120 ms. MS full scan range was 350-1800 m/z. Mass window for precursor ion isolation was 1.6 m/z. Ion threshold for triggering MS/MS events was 5e4. Dynamic exclusion was 30 s.

Data analysis for neuronal extracts

Data were processed using Proteome Discoverer 1.4 (Thermo Fisher Scientific, Bremen, Germany), using Sequest as search engine and the RATTUS proteome sequence database (http://www.ebi.ac.uk/uniprot) accessed on March 2015. The database was merged with a list of common contaminants named "Common Repository of Adventitious Proteins" retrieved from The Global Proteome Machine website (http://www.thegpm.org/crap/index.html). In total, 27,927 entries were searched. The following general search parameters were used: MS tolerance 15 ppm; MS/MS tolerance 0.02 Da; enzyme trypsin; max. missed cleavages 2; variable modification: oxidised methionine. Additionally, the following search parameters were used, depending on Experiment number: Exp A and B) variable modification: C-terminal ^{18}O labelling; fixed modification: methyl thio-cysteine (MMTS); Exp. C-E) variable modifications: N-ethylmaleimide-cysteine (NEM), carbamidomethyl-cysteine (CAM); fixed modifications (in two parallel searches): (a) N-ter dimethyl (light); dimethyl-lysine (light); (b) N-ter dimethyl (medium); dimethyl-lysine (medium). Exp. F) variable modification: C-terminal ^{18}O labelling; fixed modification: N-ethylmaleimide-cysteine (NEM); For SNO-peptide searches, the following additional parameters were used: Exp. A and F) fixed modification: carbamidomethyl-cysteine (CAM); Exp. C-E) fixed modification: carbamidomethyl-cysteine (CAM); fixed modifications (in two parallel searches): (a) N-ter dimethyl (light); dimethyl-lysine (light); (b) N-ter dimethyl (medium); dimethyl-lysine (medium). Minimum requirement for protein ID for every experiment was 2 peptides at 95% confidence.

4.16 Direct Detection of S-nitrosylation

Sample preparation

Cultured E17 cortical neurons were treated with BDNF (75ng/ml) or KCL (50 mM) for 20 mins. Cells were washed 1x with PBS, then harvested in HEN buffer (100 mM Hepes, 1 mM EDTA, 0.1 mM neocuproine) with 0.2 % NP40. 1 x 10cm plate of neurons (12.5 million cells, approx. 1 mg of protein) was harvested per condition. Samples were homogenized 5x with a 25g needle, then centrifuged at 10000 g and supernatant collected, snap frozen and sent to Marco Gaspari for analysis.

Mass spectrometry analysis: direct detection

Lysates (25 µL) were initially treated by adding 2.5 µL of 50 mM DTT (incubation for 1 h at 37 °C). Alkylation of released cysteines was achieved by adding 3 µL of 100 mM

iodoacetamide (1h at 37 °C in the dark). Excess of iodoacetamide was quenched by additional 0.5 µL of 50 mM DTT. Before the addition of proteomics grade trypsin (500 ng), the solution was diluted to 50 µL total volume with HPLC-grade water. Tryptic digestion was allowed to proceed overnight at 37 °C.

Tryptic peptides were diluted to 1 mL in 80% acetonitrile / 0.5% formic acid (solution SCX-a) and loaded onto a 200 µL micropipette tip stacked with three layers of a strong cation exchange resin (Empore extraction disks, Sigma) previously conditioned with 20 µL of solution SCX-b (20% acetonitrile / 0.5% formic acid) and 20 µL of solution SCX-a. After two washing steps (20 µL of solution SCX-a, 20 µL of solution SCX-b), stepwise elution of tryptic peptides was achieved by sequential addition of 20 µL of six solutions, all containing 20% acetonitrile, of increasing ionic strength and pH: (i) 50 mM ammonium acetate, 0.5% formic acid; (ii) 75 mM ammonium acetate, 0.5% formic acid; (iii) 100 mM ammonium acetate, 0.5% formic acid; (iv) 150 mM ammonium acetate, 0.5% formic acid; (v) 250 mM ammonium acetate, 0.5% formic acid; (vi) 500 mM ammonium acetate. The six SCX fractions were evaporated by vacuum centrifugation and resuspended in 30 µL of 0.1% formic acid / 2% acetonitrile. A 4 µL aliquot of each fraction was subjected to nanoLC-MS/MS analysis. nanoLC-MS/MS analysis was performed as described earlier (SNO-proteins, 60-min gradient).

Data analysis for direct detection

Data were processed essentially as described earlier, except for modifications in settings which were as follows. Variable modification: oxidised methionine, carbamidomethyl-cysteine (CAM), **nitrosyl-cysteine**. Peptide identifications were validated by Percolator (Käll et al., 2007) integrated in Proteome Discoverer. Percolator q-value was set to equal or less than 0.01. An additional constrain was a Xcorr value higher than 1.2.

3. Results

Chapter 1: Identification of S-nitrosylated proteins using SNORAC

To identify novel nuclear targets of S-nitrosylation, I took a proteome-wide, non-biased approach using S-nitrosothiol Resin Assisted Capture (SNORAC) (Forrester et al., 2009b) in combination with mass spectrometry. In this assay, S-nitrosylated proteins are subjected to a series of chemical modifications, culminating in the isolation of S-nitrosylated proteins (**Figure 1**).

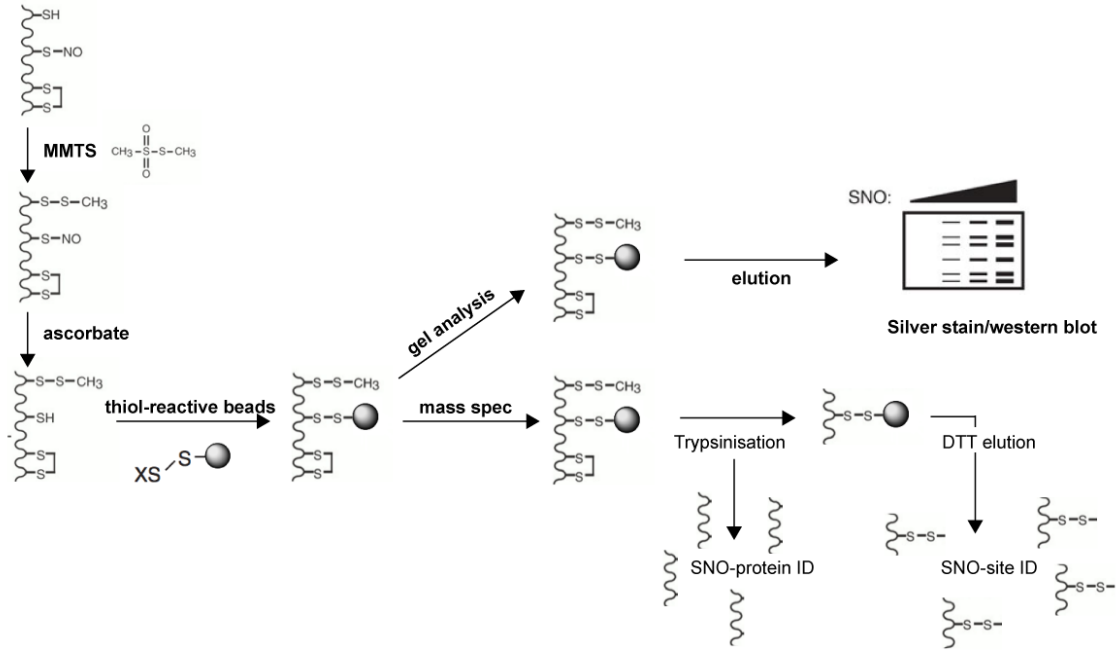


Figure 1. The detection of S-nitrosylated proteins using SNORAC. Methanethiolsulfonate (MMTS) is first used to block free thiol residues on cysteines, rendering them unreactive. Importantly, MMTS does not affect SNO-cysteines or cysteines involved in disulphide bonds. In the following reaction, ascorbate is used to convert S-nitrosylated thiols to free thiols. Free thiols are captured using a thiol-reactive resin. To assess S-nitrosylation, isolated proteins are subjected to SDS-PAGE followed by silver stain or western blotting for specific proteins. In addition, isolated proteins can be analysed by mass spectrometry (MS); firstly, on-resin trypsinisation coupled with MS of the eluted peptides identifies SNO-proteins (SNO-protein ID). The fragments containing the exnitrosylated cysteines are then eluted with DTT, allowing their identification by MS. Figure adapted from (Jaffrey and Snyder, 2001) and (Forrester et al., 2009).

This study represents the first effort to identify S-nitrosylated nuclear proteins in cortical neurons using an unbiased approach. I used the NO donor S-nitrosocysteine (CysNO) to induce S-nitrosylation in rat embryonic cortical neuronal nuclear extracts. Upon CysNO treatment of protein extracts, S-nitrosylation occurs through transnitrosylation, in a manner that is independent of specific cellular stimuli. Thus, screens carried out in this way provide a representation of the proteins within a cell or compartment that are potentially S-nitrosylated, termed the S-nitrosoproteome. My overall aim during the screening process was to identify, in the greatest detail possible, the nuclear S-nitrosoproteome in cortical neurons.

Validation of SNORAC in CysNO-treated HEK293T cell lysates

Cultured cortical neurons have a measurable level of endogenous nitric oxide signalling in non-stimulated conditions, therefore I first tested SNORAC in HEK293T cells, which do not have known endogenous sources of NO. Cell lysates from HEK293T cells were treated with 1 mM CysNO and SNORAC was used to isolate S-nitrosylated proteins. Samples were split in two fractions; one set was separated using SDS-PAGE and subjected to silver staining to visualise total proteins, whilst the corresponding sample set were analysed by mass spectrometry. In each experiment, a control group was treated with unmodified cysteine (Cys) (for preparation details, see **Methods**). When HEK293T cell lysates were exposed to Cys, a number of protein bands were detected by silver staining (**Figure 2**, lane 1). Given the absence of NO signalling in this model system, these bands may represent proteins in which blocking by MMTS was incomplete and/or proteins that bind the resin in a

non-specific manner. Treatment with CysNO resulted in the isolation of a much greater number of proteins (**Figure 2**, lane 2).

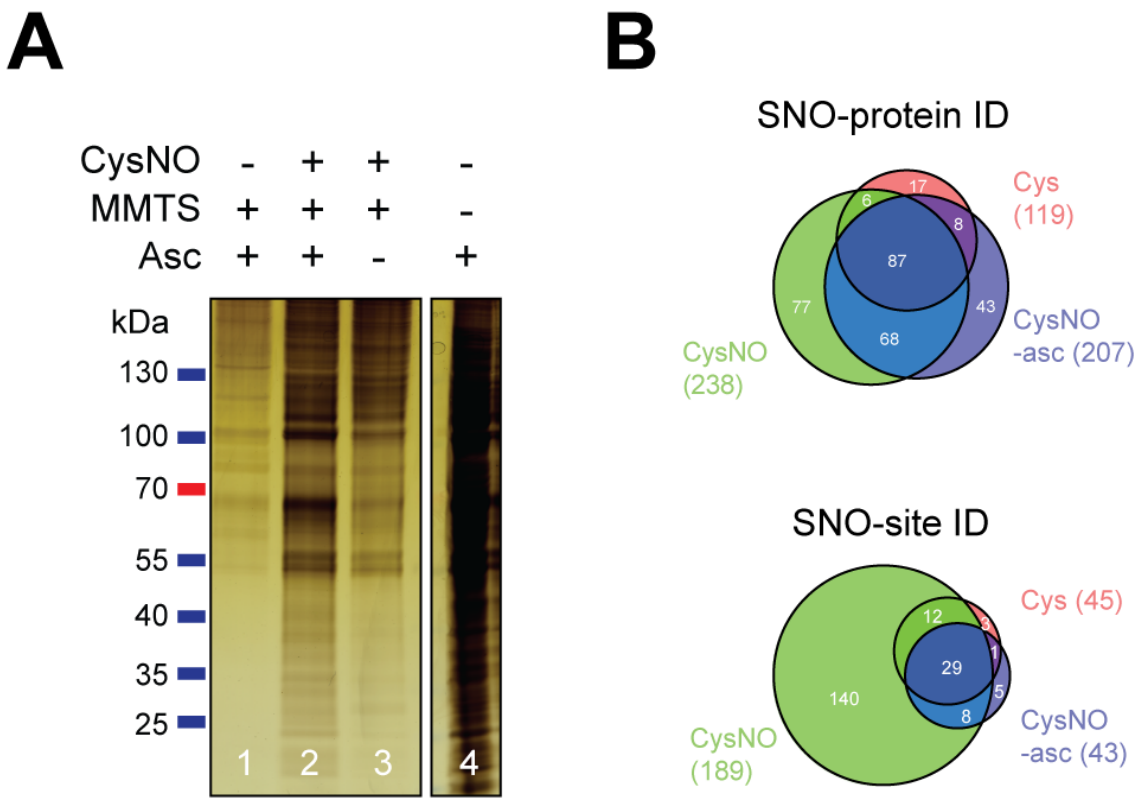


Figure 2. Detection of S-nitrosylated proteins in HEK293T cell lysates treated with CysNO. A. HEK293T cell lysates (500 µg protein per sample) were treated as shown, and subjected to SNORAC. Isolated proteins were separated by SDS-PAGE and detected by silver staining. Samples were treated for 20 mins with either 1 mM of cysteine only (lane 1) or 1 mM of the nitric oxide donor CysNO (S-nitrosylated cysteine) (lane 2). As a control, the S-nitrosylation-specific reducing agent sodium ascorbate was omitted in a CysNO-treated sample (lane 3). As an additional control, the thiol blocking reagent MMTS was omitted (lane 4). **B.** Summary of mass spectrometry results (nano-LC MS/MS). Top: number of SNO-proteins detected after on-resin trypsinisation. Bottom: number of SNO-sites identified upon DTT-elution of cysteine containing peptides.

The use of the reagent sodium ascorbate in SNORAC is necessary to convert S-nitrosothiols to free thiols so that these proteins can bind the thiol-reactive resin. Upon omission of sodium ascorbate in CysNO-treated

samples, there was a reduction in both number and intensity of protein bands detected (CysNO-asc; **Figure 2**, lane 3). This indicates that the proteins detected in samples treated with CysNO represent S-nitrosylated proteins. Another key methodological step during SNORAC is the blocking of free thiols on cysteines to prevent non-specific binding to the thiol reactive resin. This is achieved using an alkylating agent, such as MMTS. Upon omission of MMTS, there is saturation of the silver stain signal (**Figure 2**, lane 4). This signal is far greater than that detected in the Cys control, indicating that MMTS is capable of blocking free thiol groups.

For the mass spectrometry analysis (nano-LC MS/MS, performed by Dr. Marco Gaspari, University of Catanzaro, Italy), proteins were eluted in two steps (as shown in **Figure 1**). During the first step, proteins bound to the resin were treated with trypsin and the resultant peptides identified by mass spectrometry. We found 77 proteins that were exclusively present in CysNO treated samples (**Figure 2B**, SNO-Protein ID). Importantly, 69 (89.6%) of these proteins were previously identified targets of S-nitrosylation (as assessed using the dbSNO database for protein S-nitrosylation; dbSNO.mbc.nctu.edu.tw). Although this result was encouraging, as it demonstrated that SNORAC is suitable for the identification of S-nitrosylated proteins, we did not find any nuclear proteins (as assessed by PANTHER gene ontology analysis for organelle; pantherdb.org). This result may be due to the high relative abundance of cytoplasmic proteins, compared to nuclear proteins, in these samples.

During the second step, the peptide fragments containing the (former) S-nitrosylated cysteines were eluted and identified by mass spectrometry. 140 cysteine-containing peptides (equating to 123 SNO-sites on 90 proteins) were identified in CysNO only (**Figure 2B**, SNO-site ID), of which 74% were previously identified (dbSNO).

Here, I confirmed that SNORAC is a suitable method for the detection of S-nitrosylated proteins in CysNO-treated cellular extracts. This important step determined the initial conditions, which were then modified to identify nuclear targets of S-nitrosylation.

Validation of SNORAC in CysNO-treated HEK293T nuclear extracts

In order to identify nuclear S-nitrosylated proteins, I enriched for nuclear proteins before carrying out CysNO-treatment and SNORAC. Initial experiments on HEK293T cytoplasmic extracts were first carried out to confirm that 250 µM CysNO is a suitable concentration to induce efficient S-nitrosylation. Nuclear extracts of HEK293T cells were then treated with 250 µM Cys, 250 µM CysNO or 250 µM CysNO-asc, and subjected to SNORAC (**Figure 3**). Cytoplasmic extracts were also included for comparison. In both nuclear and cytoplasmic extracts, 250 µM CysNO resulted in an increase of both the number and intensity of protein bands detected, when compared to Cys (**Figure 3**, lanes 2 and 5). Omission of sodium ascorbate completely abolished the effect of CysNO, confirming the specificity of the assay (**Figure 3**, lanes 3 and 6). For both nuclear and cytoplasmic extracts, corresponding samples for Cys, CysNO and CysNO-asc were sent for mass spectrometry (nanoLC-MS-MS). Analysis of SNO-proteins from nuclear extracts revealed

that 38 proteins were S-nitrosylated upon CysNO treatment (**Figure 3**, SNO-protein ID), 35 (92.1%) of these have been previously identified as S-nitrosylated nuclear proteins (dbSNO). 60 proteins were also identified upon Cys treatment of nuclear extracts, however these likely represent proteins that bind to the resin non-specifically as only 31% are known SNO-proteins and most do not contain cysteines (e.g. 4 detected histone H1 variants). Nuclear and cytoplasmic SNO-proteins were largely distinct; only 2 (5.4%) of the SNO-proteins identified in nuclear extracts were also found in cytoplasmic extracts.

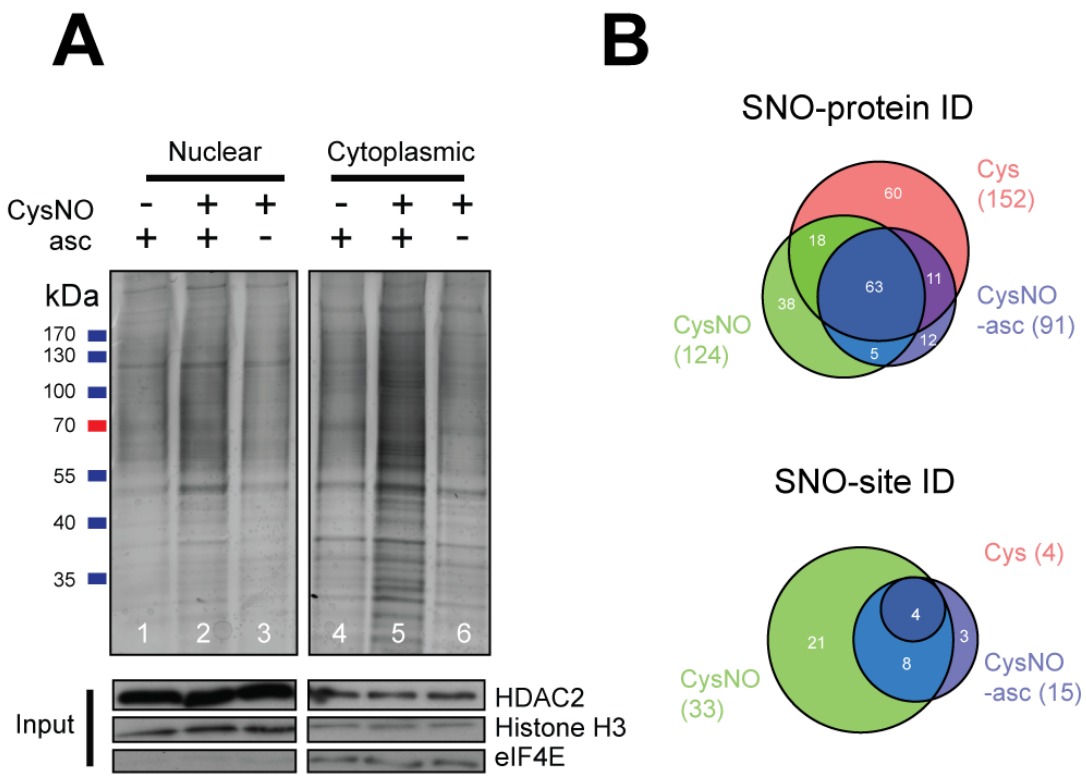


Figure 3. Detection of S-nitrosylated proteins in CysNO-treated nuclear and cytoplasmic extracts of HEK293T cells.

A. Nuclear and cytoplasmic proteins were extracted from HEK293T cells and 500 µg of protein per sample were treated with 250 µM Cys (lanes 1 and 5) or 250 µM CysNO (lanes 2 and 6) for 20 mins. As a control, sodium ascorbate (asc) was omitted in a CysNO sample in both the nuclear and cytoplasmic extracts (lanes 3 and 7). SDS-PAGE followed by silver staining was used to detect proteins isolated by SNORAC. Input fractions (1.5%) were separated by SDS-PAGE and western blots were carried out using antibodies against the

nuclear proteins histone deactylase 2 (HDAC2) and histone H3 as well as the predominantly cytoplasmic protein eIF4E (Figure 6, bottom). **B.** Summary of mass spectrometry results for the nuclear samples. Top: number of SNO-proteins detected after on-resin trypsinisation. Bottom: number of SNO-sites identified upon DTT-elution of cysteine fragments.

PANTHER gene ontology analysis of S-nitrosylated nuclear proteins indicated nine exclusive annotations for organelle with four proteins (44.44%) assigned to the nucleus, one (11.11%) as chromosomal, two to the cytoskeleton (22.2%), and the remaining two assigned to the endoplasmic reticulum and the Golgi. GO analysis for the cellular component, which includes proteins that are present in more than one organelle, identifies 27 nuclear S-nitrosylated proteins (**Table S1**). Hence, nuclear extraction prior to CysNO treatment greatly improves the detection of S-nitrosylated nuclear proteins using SNORAC. Four of the nuclear proteins identified in this analysis are novel targets of S-nitrosylation (nucleolar protein 56; NOP56, replication initiator 1; REPI1, Small ubiquitin-related modifier 2; SUMO2 and SWI/SNF-related matrix associated actin-dependent regulator of chromatin subfamily D member 2; SMRD2; each marked with ★ on **Table S1**). These novel targets of S-nitrosylation have diverse cellular functions. NOP56 is an RNA binding protein involved in ribosome biogenesis (Gautier et al., 1997), whereas REPIN1 is an ATP-dependent DNA helicase involved in DNA replication (Dailey et al., 1990) with an undefined role in neurons. SUMO2 is ubiquitin-like protein that can be covalently attached to lysine residues on target proteins during the process of SUMOylation to regulate protein function (review: Gareau and Lima, 2010). Interestingly, in unstimulated hippocampal neurons, SUMO2 binding inhibits aggregation of the prion-like protein cytoplasmic polyadenylation element-binding protein 3 (CPEB3) (Drisaldi et

al., 2015), which drives the *de novo* protein synthesis necessary for long-term memory consolidation (Fioriti et al., 2015). Upon neuronal stimulation, SUMO2 binding is inhibited and aggregation of CPEB3 facilitates translation of mRNAs. Here, we show for the first time that a member of the SUMO-family of protein is S-nitrosylated, however S-nitrosylation of the SUMO-ligase PIAS2 (Protein inhibitor of activated STAT2) has been demonstrated before (Kohr et al., 2012). In both cases, the functional effect of their S-nitrosylation is as-of-yet unknown. SMARCD2 (also known as BRG1-associated factor 60B; BAF60B), the final novel target of S-nitrosylation identified during this analysis, is a member of the multisubunit BAF (Brg/Brm-associated factors) chromatin-remodeling complex. Due to their ability to bind transcription factors (Debril et al., 2004), BAF60 proteins have been suggested to regulate the interaction of BAF complexes with target genes. BAF60B previously been shown to be regulated postranslationally; in HeLa cells, activation of Rac GTPases triggers a signaling pathway which leads to ubiquitination and degradation of BAF60B (Lorès et al., 2010). The only other BAF family member known to be S-nitrosylated is SMARCC2 (also known as BAF170) (Lam et al., 2010; Li et al., 2012), a protein important for the early stages of cortical development (review: Son and Crabtree, 2014b), however the functional effect of this S-nitrosylation is also not yet known.

Identification of novel nuclear targets of S-nitrosylation in neurons

Having confirmed that SNORAC is suitable to identify novel nuclear targets of S-nitrosylation, I carried out SNORAC on CysNO treated extracts obtained from rat cortical neurons. For these experiments, we made two

modifications to the mass spectrometry methodology. Firstly, we switched to a quantitative mass spectrometry approach (O^{16}/O^{18} labelling) so that relative amounts of each protein can be accurately measured. This is an important modification, as some S-nitrosylated proteins (that bind the resin with high affinity in CysNO-treated groups) may also bind the resin in control conditions. Accurate quantification of relative protein amounts was necessary to confidently identify S-nitrosylated proteins (≥2 fold changes in response to CysNO treatment, when compared to Cys). Secondly, we used a mass spectrometer with a vastly increased sensitivity (see **Methods**) that allowed us to identify the putative S-nitrosoproteome of the neuronal nucleus to the greatest degree possible.

Two concentrations of CysNO were used to treat neuronal nuclear extracts; initially, two experiments were performed using 1 mM CysNO (experiments A and B). Then, upon confirmation of the success of this approach, four additional experiments with 100 μM CysNO were carried out (experiments C-F). The 100 μM concentration of CysNO was chosen after previous experiments established that this is the lowest concentration by which a robust increase in S-nitrosylation is detected by silver staining. S-nitrosylation was confirmed by silver staining and western blotting for HDAC2, a known target of S-nitrosylation (**Figure 4**, A and B). In addition, cytoplasmic proteins were treated with CysNO to obtain a comparative dataset. In this case, S-nitrosylation was confirmed by tubulin western blotting (**Figure 4**, C).

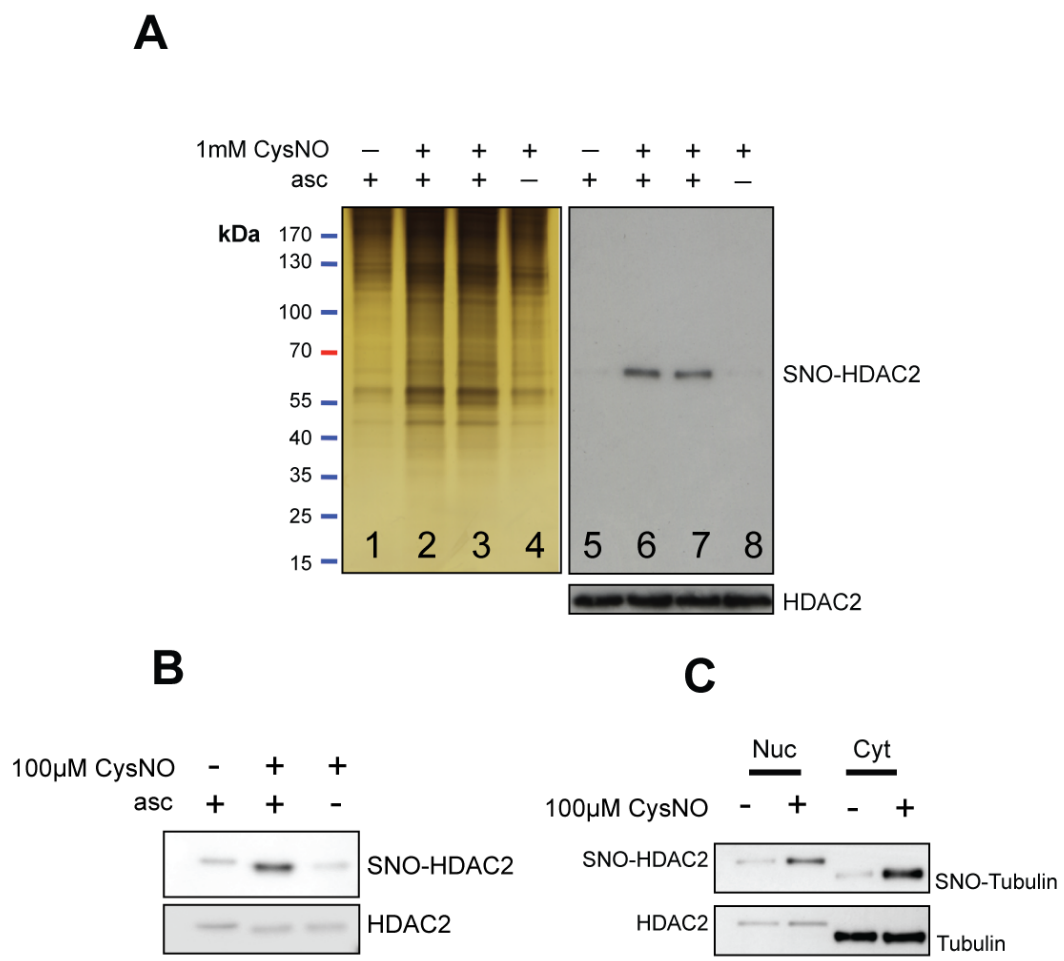


Figure 4. Detection of S-nitrosylated proteins in CysNO-treated neuronal extracts.
A. Nuclear proteins were obtained from embryonic rat cortical neurons (cultured for 4 days) and 400 µg of protein per sample was treated either with 1 mM Cys (lane 1) or 1 mM CysNO (lanes 2 and 3) for 20 mins, and subjected to SNORAC (n=2). Sodium ascorbate (asc) was excluded (lane 4) for control purposes. SNORAC isolated proteins and inputs were separated by SDS-PAGE and detected by either silver staining (left) or western blotting (right) using a HDAC2 specific antibody. **B.** 400 µg of neuronal nuclear proteins were treated with 100 µM Cys or 100 µM CysNO and subjected to SNORAC (n=3). The omission of sodium ascorbate confirmed the specificity of the assay. Isolated proteins and inputs were separated by SDS-PAGE followed by western blotting for HDAC2. **C.** 400 µg of either nuclear or cytoplasmic proteins were treated with 100 µM Cys or 100 µM CysNO and subjected to SNORAC (n=1). Isolated proteins and inputs were separated by SDS-PAGE followed by western blot for HDAC2 and tubulin.

Samples were subjected to trypsinisation on-resin and the resultant peptides analysed by quantitative mass spectrometry using $^{16}O/^{18}O$ labelling (ESI-QUAD TOF MS). For each comparison, samples were labelled with

either light (^{16}O) or heavy (^{18}O) oxygen before being mixed and analysed by mass spectrometry. The characteristic mass shifts produced upon labelling with ^{16}O and ^{18}O permits the identification of labelled peptides. The calculation of the heavy/light ratio for individual peptides allows the quantification of relative amounts of labelled peptides. For experiments A-E, two comparisons were carried out: 1) CysNO vs Cys, and 2) CysNO vs CysNO-asc, whereas for experiment F, only CysNO vs Cys was compared. ≥2 fold changes of protein amounts were considered significant. In 9 out of 11 comparisons, most proteins were enriched in CysNO versus controls (**Figure 5**). Experiment D was excluded from further analysis as >50% of proteins detected were not enriched upon CysNO treatment (**Figure 5**, D).

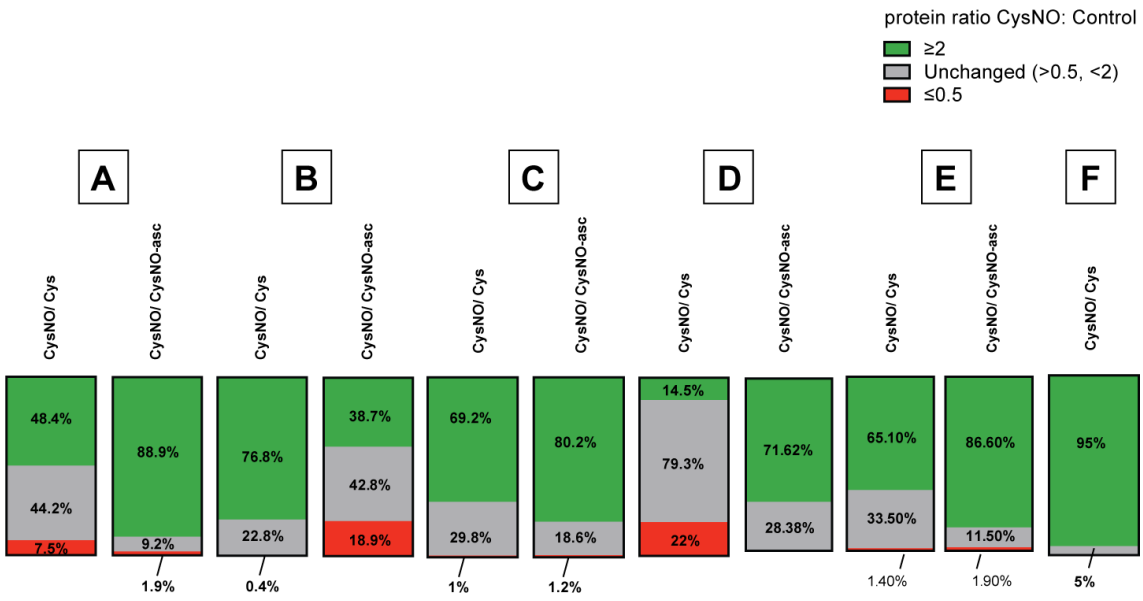


Figure 5. Mass spectrometry summary: CysNO-treated nuclear extracts

Relative proportion of proteins detected and enriched either ≥2 fold in CysNO groups (green), unchanged (grey) or enriched ≥2 fold in controls (red). CysNO concentration in experiments A and B is 1 mM CysNO and 100 μM in experiments C-F.

I first asked whether proteins that are enriched in CysNO vs Cys matched those proteins enriched in CysNO vs CysNO-asc, as CysNO-induced S-nitrosylated proteins should be present in both. Encouragingly, I

found that 85% of the proteins enriched in CysNO vs Cys only were also enriched in CysNO vs CysNO -asc. Of note, comparative analysis of this type does not include endogenously S-nitrosylated proteins that are not CysNO-responsive. Furthermore, there is a 78% overlap between proteins enriched in 1 mM and 100 µM CysNO (**Figure 6B**). S-nitrosylated proteins from these samples were considered alongside one another for subsequent analysis.

A

Treatment	# proteins detected ≥2 fold enriched in cysNO	% of total	# proteins detected unchanged	% of total	# proteins detected ≥2 fold in control	% of total	total number of proteins detected
1mM CysNO/Cys (Exp A)	448	**48.4**	409	**44.2**	69	**7.45**	926
1mM CysNO/CysNO-asc (Exp A)	1046	**88.9**	108	**9.18**	22	**1.87**	1176
1mM CysNO/Cys (Exp B)	751	**76.8**	223	**22.8**	4	**0.41**	978
1mM CysNO/CysNO -asc (Exp B)	371	**38.2**	416	**42.8**	184	**18.9**	971
100µM CysNO/Cys (Exp C)	276	**69.2**	119	**29.8**	4	**1.0**	399
100µM CysNO/CysNO -asc (Exp C)	344	**80.2**	80	**18.6**	5	**1.2**	429
100µM CysNO/Cys (Exp E)	142	**65.1**	73	**33.5**	3	**1.4**	218
100µM CysNO/CysNO -asc (Exp E)	323	**86.6**	43	**11.5**	7	**1.9**	373
100µM CysNO/Cys (Exp F)	1283	**95**	67	**4.96**	0	**0**	1350
Average	554	**72.1**	171	**24.2**	33.1	**3.79**	758

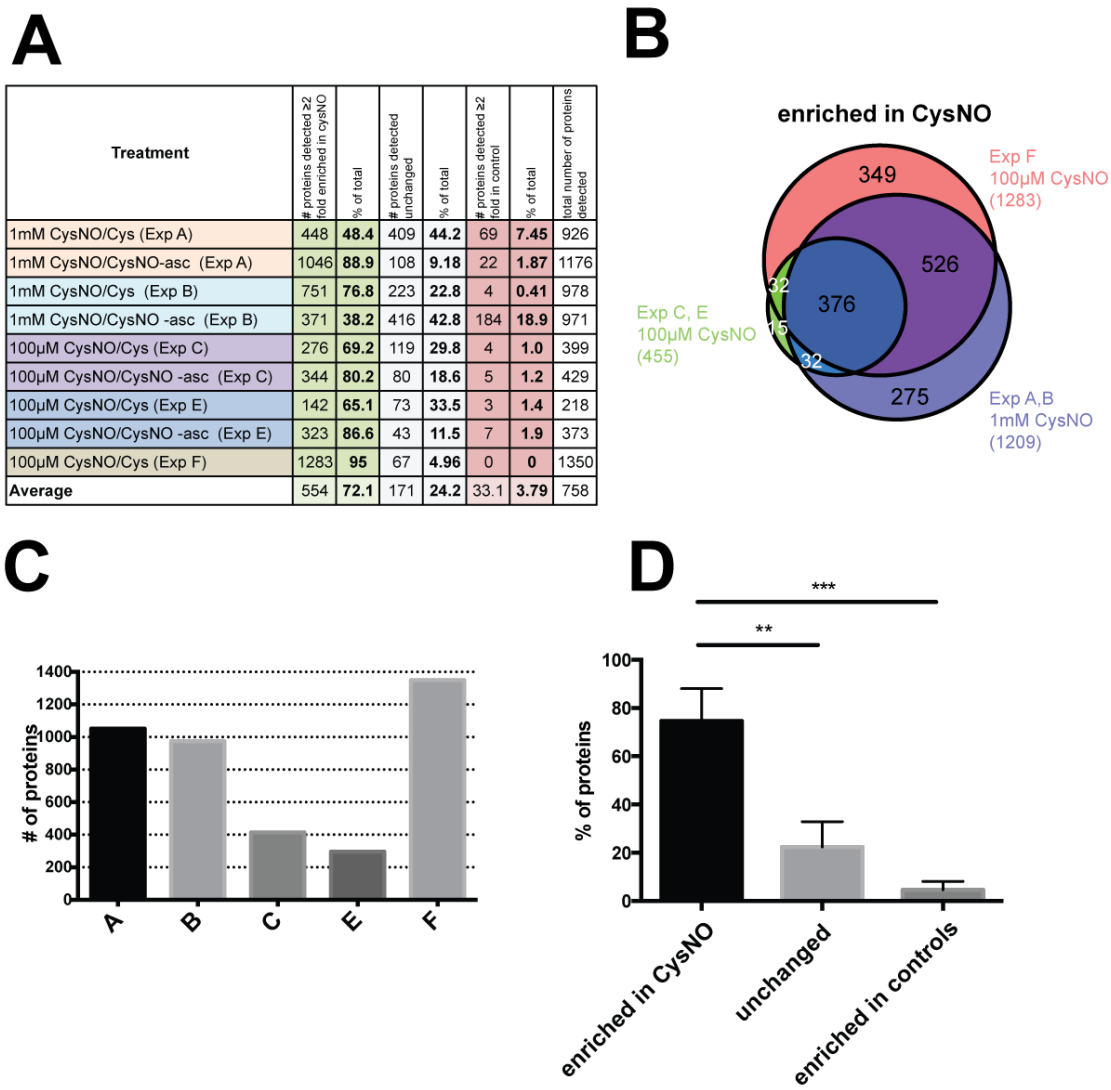


Figure 6. Screen summary: CysNO-treated neuronal nuclear extracts

A. Summary table of quantitative data for each experiment. **B.** Comparison of the number of proteins detected as ≥2 fold enriched in CysNO versus control groups in at least one experiment. Experiments C and E are depicted separately from F to show the difference in the number of enriched proteins detected. **C.** Total number of proteins detected in each experiment by mass spectrometry. **D.** Percentage of proteins detected by mass spectrometry as enriched in CysNO (≥2 fold; CysNO vs controls), unchanged (<2, >0.5; CysNO vs

controls), or enriched in controls (≤ 0.5 fold; CysNO vs controls). ** p<0.01, *** p<0.001 (One way ANOVA, compared to 'enriched in CysNO', Uncorrected Fischer's LSD)

Whilst there is substantial variation in the total number of SNO-proteins detected per experiment (**Figure 6A** and **6C**), most proteins are enriched in CysNO groups (**Figure 6D**) confirming the validity of the approach. I decided that proteins must fulfill the following criteria in order to be considered as targets of S-nitrosylation:

1) enriched ≥2 fold in CysNO versus control samples (Cys or CysNO minus asc), identified in at least three experiments
2) not enriched ≥2 fold in any control sample

In this manner, in order to consider a protein S-nitrosylated, it must be detected at least once as S-nitrosylated upon treatment with the lower (100 μM) concentration of CysNO. 267 (13.8%) of the 1930 unique proteins detected were excluded as they were enriched in a control group, 1049 (54.35%) were excluded because they were enriched only in one or two experiments or unchanged. The remaining 614 proteins (31.81%) were considered as S-nitrosylated neuronal nuclear proteins (**Table S2**; proteins ranked alphabetically). The vast majority (612) of the hits are novel potential targets of S-nitrosylation in cortical neurons and 131 (38.1%) are entirely novel targets of S-nitrosylation in any system (marked with ★ in **Table S2**). Hence, using SNORAC on CysNO-treated nuclear extracts, we identified many novel nuclear potential targets of S-nitrosylation in cortical neurons.

Comparative analysis of nuclear and cytoplasmic S-nitrosylated proteins

In cytoplasmic extracts, 640 proteins were found to be enriched ≥2 fold upon CysNO treatment (**Table S3**). When this dataset was compared with S-nitrosylated nuclear proteins, I found that they were largely distinct with only 15.6% of the proteins present in both datasets. GO analysis showed major differences between exclusive (single term mentioned) and total (term mentioned alongside others) annotations for cellular component (**Figure 7A** and **B**). As expected, GO analysis revealed that nucleic acid binding proteins represent the most annotated term for nuclear S-nitrosylated proteins (30.20%), whilst in cytoplasmic extracts only 7% of the proteins were annotated as such (**Figure 8**). Therefore, the nuclear extracts were compositionally largely distinct from cytoplasmic extracts in regards to both protein identity and GO annotation.

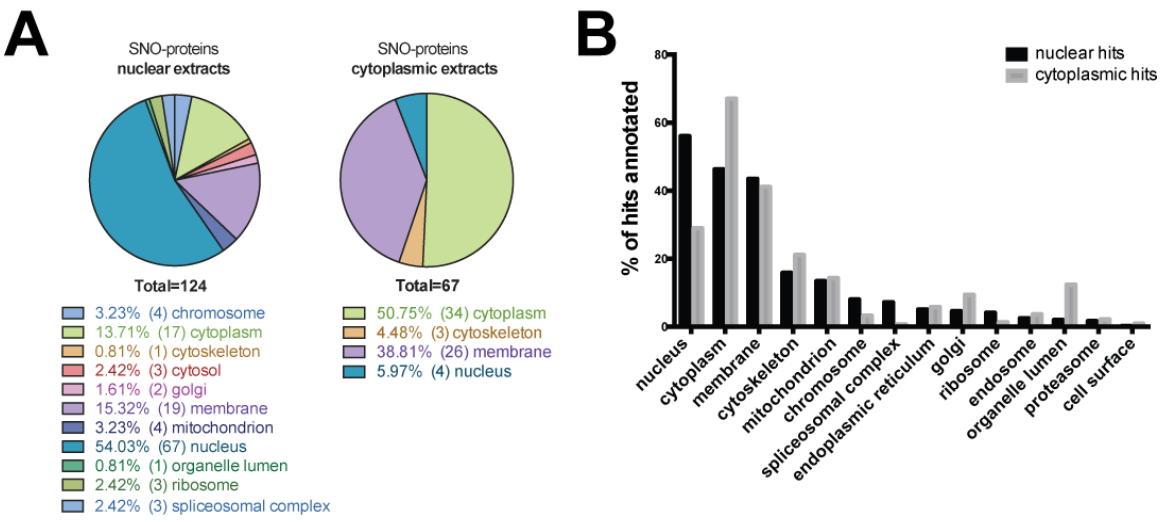


Figure 7. GO analysis of S-nitrosylated proteins identified in CysNO-treated neurons: Cellular Component.

A. Exclusive annotations. Displayed is the number of times a particular term was assigned in instances where no other term was present. **B.** Total annotations. The percentage of

annotated hits that were assigned each particular term. This includes the majority of instances in which multiple terms were assigned.

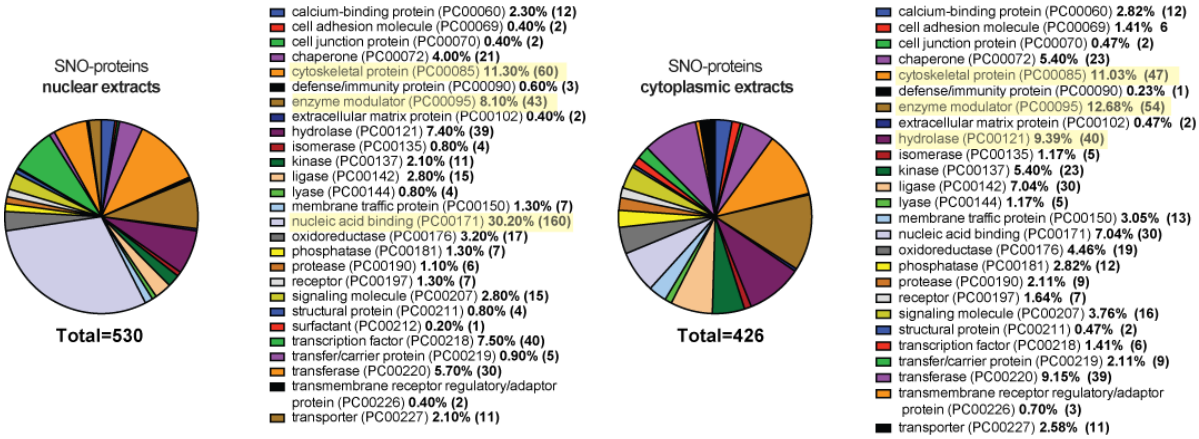


Figure 8. GO Analysis of S-nitrosylated proteins identified in CysNO-treated neurons: Protein Class.

S-nitrosylated hits were annotated using PANTHER GO analysis for Protein Class. 530 annotations were made for S-nitrosylated proteins identified in CysNO-treated nuclear extracts and 426 exclusive annotations were made for S-nitrosylated proteins from CysNO-treated cytoplasmic extracts. The three most commonly annotated terms for each are highlighted in yellow.

Nuclear S-nitrosylated proteins are involved in a wide range of biological processes (**Table S4**; terms ranked according to number of annotations) including metabolic function (293 proteins, 63%), transcription (61 proteins, 13%; listed in **Table S5**) and chromatin organisation (20 proteins, 4.3%; listed in **Table S6**). The majority of S-nitrosylated proteins were identified as involved in metabolism (level 1 GO term; metabolic process, GO:0008152). Further GO classification (level 2 GO analysis) of these proteins revealed that 69.9% of the total annotations refer to primary metabolic processes, 10.4% to nitrogen compound metabolic processes, 6.8% to phosphate-containing metabolic processes, 5.2% to biosynthetic processes, 4.2% to catabolic processes, 3.1% to generation of precursor metabolites and energy and 0.5%

to coenzyme metabolic processes. Of the proteins involved in primary metabolic processes, the two most common annotations (level 3 GO analysis) were regarding nucleobase-containing compound metabolic processes (49.6% of total annotations) and protein metabolic processes (37.3% of total annotations). Hence, many of the S-nitrosylated proteins identified here are involved in either DNA/RNA or protein metabolism. This is in concordance with hits from previous S-nitrosylation screens in which many hits were shown to be involved in metabolic processes (Kohr et al., 2011; Raju et al., 2015). Apart from examples examining the role of S-nitrosylation on transcription (Nott et al., 2008; 2013; Ryan et al., 2013), the functional role of S-nitrosylation on RNA metabolism has not been addressed. Data is also scarce regarding the role of S-nitrosylation on DNA metabolism. S-nitrosylation of O6-alkylguanine-DNA alkyltransferase (AGT), a key DNA repair protein, has been detected during inflammatory responses in the livers of GSNOR knockout mice (Wei et al., 2010). As this event correlates with proteosomal degradation of AGT, this has lead to the speculation that S-nitrosylation induces degradation of AGT and may contribute to carcinogenesis in these mice (Wei et al., 2010).

In regards to the S-nitrosylated targets involved in protein metabolism, several ribosomal subunits were detected as S-nitrosylated in our screen on CysNO-treated nuclear extracts (**Table S2**, hits 10-17 and 20-27). The presence of ribosomes in nuclear extracts can be accounted for since ribosomes are assembled within the nucleolus and are also present in the outer nuclear membrane (review: Marshall and Wilson, 1997). Although

ribosomal proteins have been identified in many screens for protein S-nitrosylation, across multiple cell types (Chen et al., 2010; Kohr et al., 2011; Qu et al., 2014; Zaręba-Kozioł et al., 2014), the functional role of S-nitrosylation on ribosomal function has not been elucidated. Interestingly however, NO has previously been linked to protein metabolism in the brain; glutamate metabolism is impaired in the brains of nNOS-/- mice (Raju et al., 2015). The mechanism behind this NO-dependent effect *in vivo* remains to be determined.

Protein targets of S-nitrosylation are involved in transcriptional regulation

Since the range of GO annotations obtained when carrying out the analysis in this manner (Functional classification analysis, pantherdb.org) may simply be a reflection of the relative abundance of the proteins, I asked whether particular GO terms are over or under represented in S-nitrosylated nuclear proteins, when compared to nuclear proteins in general. We first generated a background dataset by subjecting unprocessed nuclear protein extracts to mass spectrometry analysis (nano LC-MS-MS, carried out by Marco Gaspari). The resulting dataset, consisting of 191 nuclear proteins, was used as a background list to perform GO statistical overrepresentation analysis of S-nitrosylated protein hits. Changes in relative frequency of annotations with P values of <0.05 (-log10(P) of 1.3 and above) were considered significant (**Figure 9**).

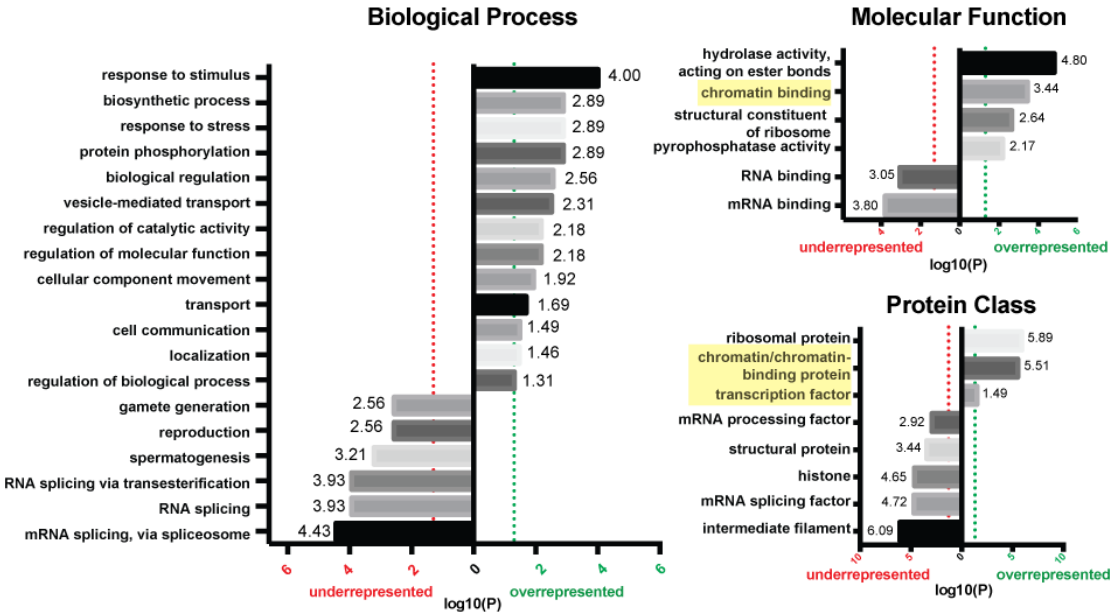


Figure 9. GO Overrepresentation analysis of S-nitrosylated nuclear proteins

Statistical analysis of terms over- or underrepresented in S-nitrosylated hits versus neuronal inputs were calculated using PANTHER. Overrepresentation test performed with Bonferroni correction for multiple testing (pantherdb.org). –log10(P) values of 1.3 (dotted lines) and above are considered statistically significant.

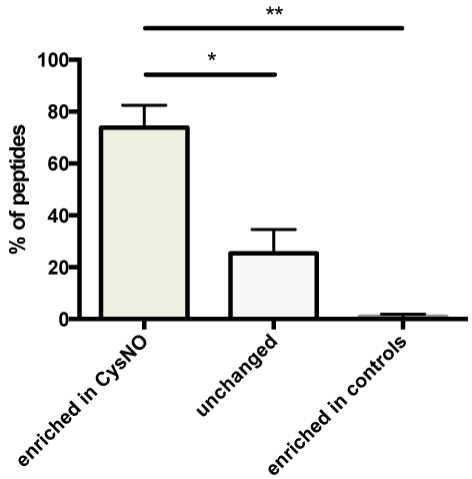
Terms relating to transcriptional regulation are significantly overrepresented in S-nitrosylated nuclear proteins. GO analysis of molecular function revealed a significant enrichment for the term chromatin binding (-P)=3.44), whilst GO analysis of protein class revealed that chromatin binding proteins (-log10(P)= 5.51) and transcription factors (-log10(P)= 1.49) were significantly enriched in S-nitrosylated hits. 10 (58.8%) chromatin binding proteins and 24 (60%) transcription factors have never previously been shown to be S-nitrosylated (marked with ★ in **Table S5** and **Table S6).**

Identification of S-nitrosylated nuclear peptides

In order to identify the site(s) of S-nitrosylation on nuclear proteins, we analysed the peptides that remained bound to the resin following the first round of trypsinisation. As shown in **Figure 1**, these peptides should harbour

the cysteine(s) that were initially S-nitrosylated. We performed quantitative mass spectrometry analysis using dimethyl labelling on peptides obtained from experiments C-E (neuronal nuclear extracts exposed to 100 µM CysNO). Peptides from Cys samples were labelled with a light dimethyl tag (L), whereas peptides from CysNO samples were labelled with a medium dimethyl tag (+4 Da; M) and peptides from CysNO-ascorbate samples with a heavy dimethyl tag (+8 Da, H). Samples were mixed and subjected to mass spectrometry to determine the relative amount of each peptide. 74% of the peptides per experiment were enriched ≥2 fold in CysNO (**Figure 10**, A), confirming the suitability of SNORAC for identifying S-nitrosylated peptides. However, the amount of SNO-peptides detected varied substantially (**Figure 10,** B) and far fewer SNO-peptides than SNO-proteins were detected per experiment (average 34 SNO-peptides versus 261 SNO-proteins per experiment).

A



B

Experiment	Treatment	# of peptides enriched in CysNO	% of total	# peptides detected as unchanged	% of total	# of peptides enriched in controls	% of total
100uM exp C	CysNO vs Cys	54	**84.4**	10	**15.6**	0	**0.0**
100uM exp C	CysNO vs CysNO -asc	53	**79.1**	13	**19.4**	1	**1.5**
100uM exp D	CysNO vs Cys	5	**55.6**	4	**44.4**	0	**0.0**
100uM exp D	CysNO vs CysNO -asc	47	**73.4**	17	**26.6**	0	**0.0**
100uM exp E	CysNO vs Cys	2	**66.7**	1	**33.3**	0	**0.0**
100uM exp E	CysNO vs CysNO -asc	41	**83.7**	6	**12.2**	2	**4.1**
	average	34	74	9	25	1	1
	standard dev.	23.8	11.1	6.0	12.1	0.8	1.7

Figure 10. Quantitative analysis on SNO-peptides: Experiments C-E

SNO-peptides were eluted from resin and subjected to dimethyl labeling. 71% of peptides contained cysteines and all peptides that did not contain cysteines were excluded. **A.** The

average proportion of cysteine-containing peptides per experiment that were enriched in CysNO (≥2 fold versus controls), unchanged (<2, >0.5 in CysNO versus controls) or enriched in controls (≥2 fold versus CysNO). * p<0.05, ** p<0.01 (One way ANOVA, compared to 'enriched in CysNO', Uncorrected Fischer's LSD). **B.** The number of cysteine-containing peptides detected in each experiment as enriched in CysNO, unchanged or enriched in controls.

To increase the sensitivity of our assay, SNO-peptide analysis was carried out in a non-quantitative manner using nuclear extracts exposed to 100 μM CysNO (experiment F). I found that 60% of the peptides detected contained cysteines and that the peptide size ranged from 5 to 39 amino acids in length, with an average length of 13 amino acids (Stdev=4). 3332 cysteine-containing peptides were detected in CysNO, 227 in the Cys control and 855 peptides in both. The CysNO peptide dataset from experiment F was used to compile the SNO-sites of S-nitrosylated proteins. Firstly, 265 peptides that contain more than one cysteine were removed, to avoid ambiguity regarding the site of S-nitrosylation. In total, 1253 unique SNO-sites were assigned across 409 proteins (**Table S7**). I included the 855 peptides detected in both Cys and CysNO, as this dataset overlapped with the 87 SNO-peptides from experiments C-E that were quantitatively validated (49/87 identical; 56.32%).

Next, I assessed how the newly identified SNO-sites compared to previously published sites. Both qualitative data from experiment F and quantitative data from experiments C-E were analysed. To this end, I selected 10 proteins present in both SNO-peptide datasets for which published SNO-site data are available. In experiment F, 46 SNO-sites were identified for these 10 proteins, of which 21 (45.7%) matched previously published sites

(dbSNO; 33 in total). In experiments C-E, 13 SNO-sites were identified for these proteins and nine (69.2%) match previously published datasets.

Amino acid composition of SNO-peptides

To investigate whether certain amino acids surrounding SNO-cysteines were differentially represented, I compared the relative occurrence of each amino acid in resin-bound peptides relative to their occurrence in the proteome. As expected, cysteines were overrepresented (2 fold) in my samples compared to the proteome. Other notable changes included arginine (overrepresented 1.5 fold) and tyrosine (1.8 fold underrepresented) (**Figure 11**, A). I next investigated if relative enrichments or depletions of certain amino acids correlated with cysteine nitrosylation or represented stretches of amino acids that promoted binding to the resin irrespective of cysteines. Hence, the same analysis was carried out for the bead bound fragments that do not contain cysteines. Because several amino acids were over or underrepresented in these non-cysteine containing peptides (**Figure 11**, B) this dataset was used as background. Normalisation using this background dataset resulted in fragments in which there were no notable changes in amino acid frequency, apart from cysteine (**Figure 11**, C).

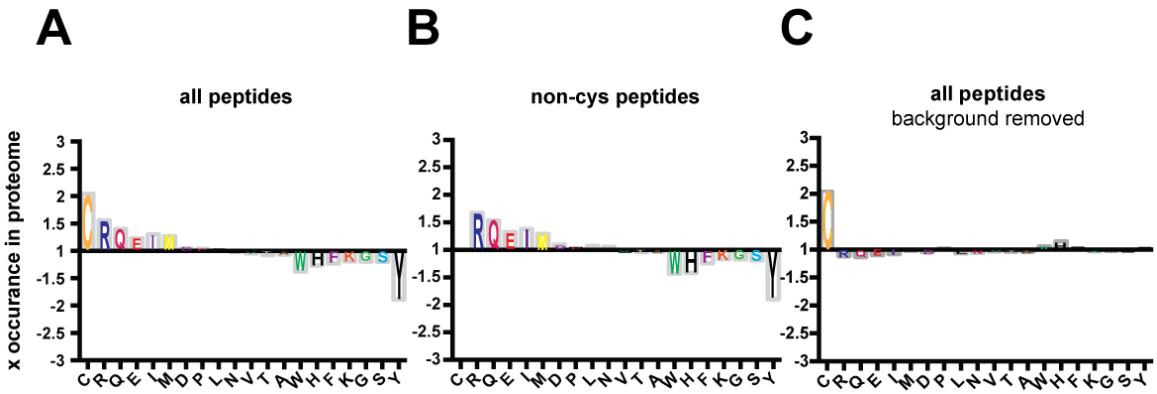


Figure 11. Analysis of relative occurrence of amino acids in regions surrounding S-nitrosylated peptides.

A. The relative occurrence of each amino acid in all resin-bound peptides was calculated and then compared to the relative occurrence of each amino acid in the vertebrate proteome (information from University of Tennessee, http://www.tiem.utk.edu/~gross/bioed/webmodules/aminoacid.htm). Data expressed as fold changes of relative occurrence versus the proteome. **B.** The relative occurrence of each amino acid in non-cysteine containing peptides (i.e. background) was calculated as for A, except cysteine occurrence was set to the level of the proteome (1x). **C.** Amino acid composition of non-cysteine containing peptides was subtracted from all peptides to obtain data relevant to SNO-peptides only.

Motifs containing acidic or basic amino acids are associated with S-nitrosylated cysteines

Given that there are no changes in the overall frequency of amino acids surrounding S-nitrosylated cysteines, I next asked whether any amino acid motifs are associated with S-nitrosylated peptides. Motifs take into account the relative position of each amino acid to the modified cysteine within the linear sequence. Motif-X (motif-x.med.harvard.edu) was used to extend cysteine-containing fragments associated with S-nitrosylated nuclear proteins so that they were 21 amino acids in length (using the IPI rat proteome). The fragments were arranged to contain the detected cysteine as the central amino acid (273 of the 1656 peptides were excluded as they contain more

than one cysteine). Motif analysis was performed to identify amino acid motifs surrounding the central cysteine, using the rat proteome (IPI rat proteome) as background (motif-x; see **Methods** for complete parameters). Using this approach, five motifs were identified, which included the amino acids lysine (K) and glutamic acid (E) (**Figure 12**). In total, these motifs were associated with 426/1383 (30.8%) of SNO-peptides.

#	Motif	Motif Score	Foreground Matches	Foreground Size	Background Matches	Background Size	Fold Increase
1.	........K.C.....	8.93	101	1061	15482	308484	1.90
2.	.........C.....K....	9.36	92	960	14013	293002	2.00
3.	.K........C.....	7.89	83	868	13766	278989	1.94
4.	....K.....C.....	6.64	70	785	12292	265223	1.92
5.	.........C.....E....	6.56	79	715	15318	252931	1.82

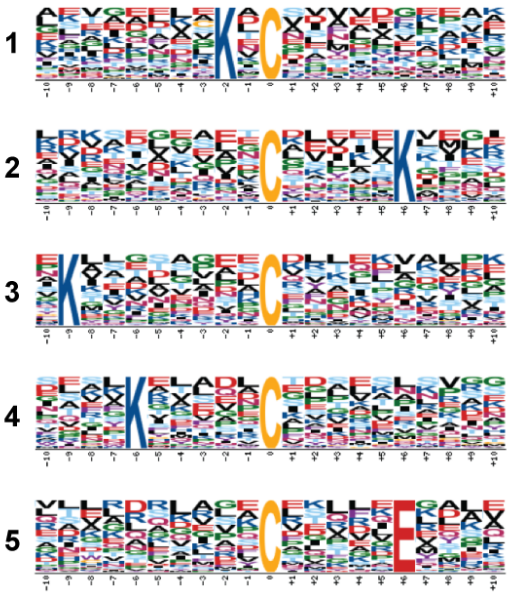


Figure 12. Analysis of SNO-motifs.

Cysteine-containing peptides associated with nuclear SNO-proteins were subjected to SNO-site analysis using motif X (see **Methods**) and the IPI rat proteome as background. Left: summary table. Right: graphical representation of the motifs; the size of the letters refers to the probability of the occurrence of that amino acid. Full size letters (as for cysteine, C, lysine, K and glutamic acid, E) indicate their involvement in a specific motif.

Summary: Chapter 1

My data indicates that SNORAC is a technique suitable for the identification of S-nitrosylated proteins from CysNO-treated rat neuronal nuclear extracts. I identified 614 S-nitrosylated proteins, 131 of which represent novel targets of S-nitrosylation in any system. In addition, putative

SNO-sites were identified for 409 SNO-proteins, along with several acid/base motifs that may render a cysteine more prone to S-nitrosylation.

GO analysis revealed that the S-nitrosylated protein dataset identified here contains proteins that are involved in diverse cellular processes. Though terms associated with metabolic processes represent the most common GO annotations for biological process, statistical overrepresentation analysis revealed that terms associated with transcription and chromatin regulation were amongst the most overrepresented in the S-nitrosylated protein dataset. This suggests an important regulatory role of nitric oxide-dependent post translational modifications in regulating gene expression in neurons. Of note, several novel targets of S-nitrosylation identified here are transcription factors that are known to have important roles in neurons such as cyclic AMP-responsive element-binding protein 1 (Creb1) and neurogenic differentiation factor 2 (neurod2). One limitation of this dataset is that the S-nitrosylated proteins were isolated CysNO-treated nuclear extracts; therefore not all of these sites may be S-nitrosylated in an endogenous setting. To address this point, confirmation of S-nitrosylation of individual proteins must be carried out in relevant cell culture systems and *in vivo.* Since we identified the sites of S-nitrosylation for the majority of S-nitrosylated protiens identified, this allows S-nitrosomutants to be generated that can be used in future studies to explore the role of S-nitrosylation in regulating neuronal nuclear function.

Chapter 2: Endogenous S-nitrosylation of nuclear factors in cortical neurons

The SNORAC screen identified several proteins involved in transcriptional regulation and chromatin remodelling (**Tables S5** and **S6**). Since the role of S-nitrosylation in regulating neuronal gene expression remains relatively unexplored, I first asked whether the proteins identified from the screen are endogenously S-nitrosylated in cortical neurons. I initially focused on two proteins that regulate transcription which have never been identified as targets of S-nitrosylation in neurons: cAMP response element binding protein 1 (CREB), a transcription factor with a well-defined and multifaceted role in neuronal functions and retinoblastoma-binding protein 7 (RBBP7), a histone binding protein involved in several chromatin remodeling complexes in neurons.

CREB

The transcription factor CREB is critical for stimulus-induced transcription in a wide range of contexts and cells types (Altarejos and Montminy, 2011; 1988). CREB transcriptional activity is essential for survival at both the organismal and the cellular level; mice lacking CREB have severe heart and brain defects during embryogenesis and die during the perinatal stages (Rudolph et al., 1998), whilst brain-specific deletion of CREB, in combination with deletion of closely related family member CREM (cAMP response element modulator), results in widespread apoptosis of neurons (Mantamadiotis et al., 2002). In neurons, CREB binds DNA at cAMP-response element (CRE) sequences located at the promoters and enhancers of many

genes involved in both development of the nervous system and neuronal plasticity (Kim et al., 2010; Riccio et al., 2006; Sasaki et al., 2000; Tao et al., 1998a). CREB transcriptional activity is dependent, at least in part, on stimulus-induced posttranslational modifications of the protein. In neurons, a variety of neurotrophins, neurotransmitters and neuropeptides activate the enzyme adenylate cyclase, causing production of the potent second-messenger cAMP from ATP (Kakiuchi and Rall, 1968; Wang and Storm, 2003). cAMP, in turn, activates a number of protein kinases including protein kinase A which phosphorylates CREB at serine 133 (Gonzalez and Montminy, 1989a). This phosphorylation event is required for binding of the essential coactivator CREB-binding protein (CBP) (Parker et al., 1996), although additional signals are required to recruit CREB to DNA. In neurons for example, nitric oxide signaling is required for CREB binding (Kakiuchi and Rall, 1968; Riccio et al., 2006). Upon BDNF-signalling in neurons, S-nitrosylation of histone deacetylase 2 (HDAC2) results in its dissociation from chromatin (Nott et al., 2008) which facilitates CREB DNA-binding (Riccio et al., 2006). Whether NO modifies CREB during this process is unknown; S-nitrosylation of CREB has never been assessed.

CREB is S-nitrosylated in cortical neurons

SNORAC of CysNO-treated neuronal nuclear extracts detected S-nitrosylation of CREB in three of the five experiments (**Table S2**, hit number 105). In the remaining two experiments, CREB was not detected in any condition. I first asked whether CREB is S-nitrosylated in embryonic cortical neurons treated with CysNO. Rat cortical neurons were left untreated or

treated with CysNO (200 μM for 20 mins) and subjected to either SNORAC or biotin switch assay. The biotin switch technique differs slightly from SNORAC in that ascorbate-reduced thiols, instead of being directly bound to thiol-reactive beads, are labelled with biotin and pulled down using streptavidin beads. Therefore, I treated data obtained with the biotin switch and SNORAC as equivalent. Proteins isolated by SNORAC/biotin switch were analysed by western blot using a CREB-specific antibody to assess S-nitrosylation of CREB. Exposure of cortical neurons to CysNO resulted in a robust S-nitrosylation of CREB (**Figure 12**).

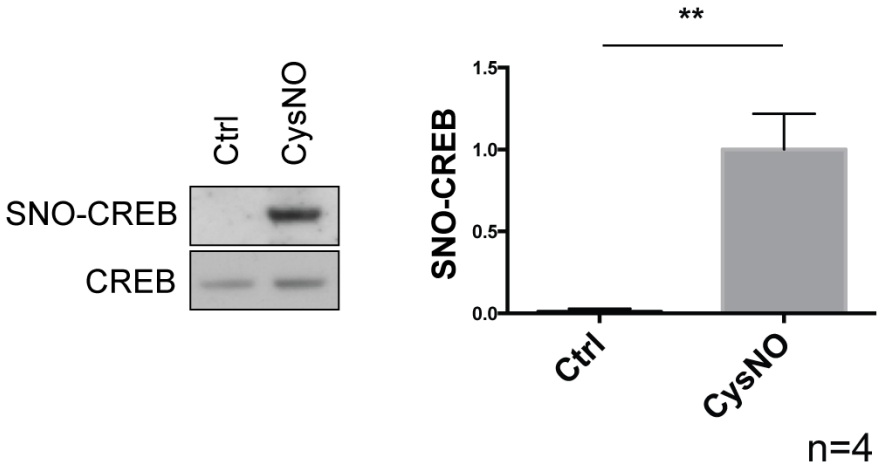


Figure 12. S-nitrosylation of CREB in neurons upon CysNO treatment.
Rat cortical neurons cultured for 4 days were either treated with CysNO (200 μM for 20 mins) or left untreated and subjected to SNORAC (n=2) or biotin switch (n=2). Isolated proteins were separated by SDS-PAGE and western blot analysis was carried out using an CREB antibody (left). Densitometry analysis on the western blots (right) was performed using ImageJ. SNO-CREB signals first adjusted according to CREB inputs. Values for SNO-CREB in CysNO were then set to 1 for normalization (Paired t test, **P=<0.01).

To ask whether CREB S-nitrosylation occurs in response to physiological neuronal stimulation, cortical neurons were exposed to brain-derived neurotrophic factor (BDNF) or depolarised with KCL. BDNF is a

neurotrophin known to be essential for the growth, development and plasticity of mammalian nervous systems (Barde et al., 1982; Park and Poo, 2013). Binding of BDNF to TrkB receptors results in receptor dimerisation, autophosphorylation and the activation of a wide variety of intracellular signalling pathways, including the MAPK/ERK, PLCγ and PI3K pathways (Glass et al., 1991; Huang and Reichardt, 2003). Upon BDNF stimulation of cortical neurons, the associated rise in intracellular calcium results in enzymatic activation of nNOS and triggers an increase in nuclear protein S-nitrosylation (Riccio et al., 2006). KCL-induced depolarisation of neurons is a commonly used experimental approach to model the transcriptional response to neuronal activity (Buzas et al., 1998; Kim et al., 2010; Malik et al., 2014). Upon neuronal depolarisation, calcium influx through L-type calcium channels triggers a host of intracellular signalling pathways that culminate in transcription of several hundred genes (Greenberg et al., 1986; Morgan and Curran, 1986; Xiang et al., 2007). Activity-dependent gene expression mediates a broad range of neural functions including neuronal differentiation, survival (Ghosh et al., 1994a), synapse maturation (Stryker and Harris, 1986) and learning and memory (Agranoff et al., 1967). Activation of nNOS occurs in response to neuronal activity (Fontana et al., 1997) and the expression of several activity-induced genes have been shown to be dependent on nitric oxide signalling (Li et al., 2004); however, activity-dependent S-nitrosylation of nuclear proteins has never been demonstrated.

Cultured cortical neurons were treated with either vehicle (PBS), BDNF (75 ng/ml) or KCL (50 mM) for 20 mins, then S-nitrosylated proteins were

isolated from cell lysates using SNORAC/biotin switch. Isolated proteins were then analysed by western blotting using a CREB-specific antibody. Using this approach, SNO-CREB was clearly detected upon treatment with KCL or BDNF (**Figure 13**). KCL treatment resulted in a 4.39 fold increase (SEM=1.0) of CREB S-nitrosylation, when compared to vehicle-treated neurons. Statistical analysis (One-way ANOVA, compared to Ctrl column, Uncorrected Fischer's LSD) indicated that this result tends towards significance (p=0.167). In addition, densitometry analysis revealed a 3.29 fold increase (SEM=1.1) of SNO-CREB levels upon BDNF treatment (p=0.048). Thus, endogenously produced nitric oxide released upon physiological stimulation is capable of inducing S-nitrosylation of CREB in neurons.

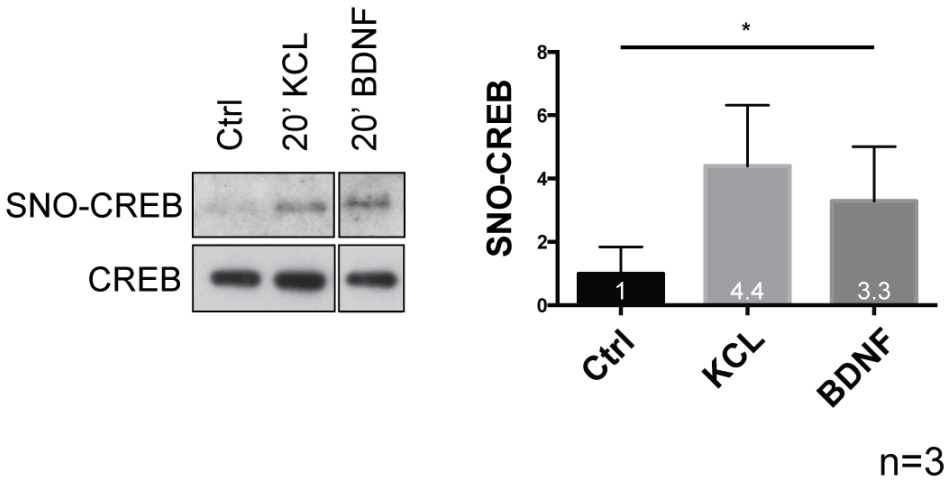


Figure 13. Endogenous S-nitrosylation of CREB in neurons

E17 rat cortical neurons (4 days in vitro) were exposed to KCL (50 mM for 20 mins) BDNF (75ng/ml for 20 mins) or left untreated and subjected to SNORAC (n=2) or biotin switch (n=1). Densitometry analysis of the western blots was carried out (right) using ImageJ. SNO-CREB was normalized to input levels of CREB and expressed as fold change relative to control. KCL treatment resulted in a 4.4 fold increase of SNO-CREB relative to untreated (P=0.04; One-way ANOVA, compared to 'Ctrl' column, Uncorrected Fischer's LSD) while BDNF treatment resulted in a 3.3 fold increase (p=0.12).

Next, I sought to identify which CREB cysteine(s) are modified by S-nitrosylation. CREB belongs to the bZIP family of transcription factors, along with the closely related cAMP response element modulator (CREM) and activating transcription factor 1 (ATF1) (Lonze and Ginty, 2002). bZIP transcription factors are characterised by a bZIP domain, comprising a C-terminal basic region that mediates DNA binding and a leucine zipper region essential for dimerisation (Landschulz et al., 1989; O'Shea et al., 1991). Two isoforms of CREB are expressed in rodents: CREB1α (considered the canonical sequence; 36.6 kDa) and CREBΔ (35.1 kDa). Aside from the bZIP domain, both isoforms contain a kinase-inducible domain (KID) which is phosphorylated and regulates the binding of coactivators (Chrivia et al., 1993) and two glutamine rich domains (Q1 and Q2) important for transactivation (Mayr et al., 2005). CREB1α and CREBΔ only differ structurally by the absence in CREB1Δ of a 13-amino acid domain, known as the alpha domain **(Figure 14).**

Because the peptides obtained upon trypsinisation were common to all isoforms, it was not possible to determine which CREB isoform was S-nitrosylated. Furthermore, CREB SNO-peptides were not detected. This is likely due to the fact that trypsinolysis around cysteines 90, 300, 310 and 337 results in peptide fragments of 65, 3, 5 and 6 amino acids, respectively (predicted with PeptideCutter; ExPASy). In our experiments, we detected SNO-peptides ranging from 5 to 39 amino acids in length (average of 13 amino acids, Stdev= 4) making the trypsinised fragments containing cysteines 90 and 337 out of range. Moreover, out of 4444 peptides in total, only 1

peptide of 5 amino acids length and 30 peptides of 6 amino acids length were detected (0.023% and 0.67% of total peptides, respectively). This may explain why cysteine-containing CREB peptides could not be identified during our analysis. To discover the sites of S-nitrosylation on CREB, I focused on CREB1α due to both its relative abundance and well-defined role in neurons, when compared to the lesser known CREB1Δ. There are four cysteines in CREB1α, three in the BZIP domain (C300,C310,C337) and one (C90) in the alpha domain. All cysteines are conserved between rat, mouse and human CREB1α.

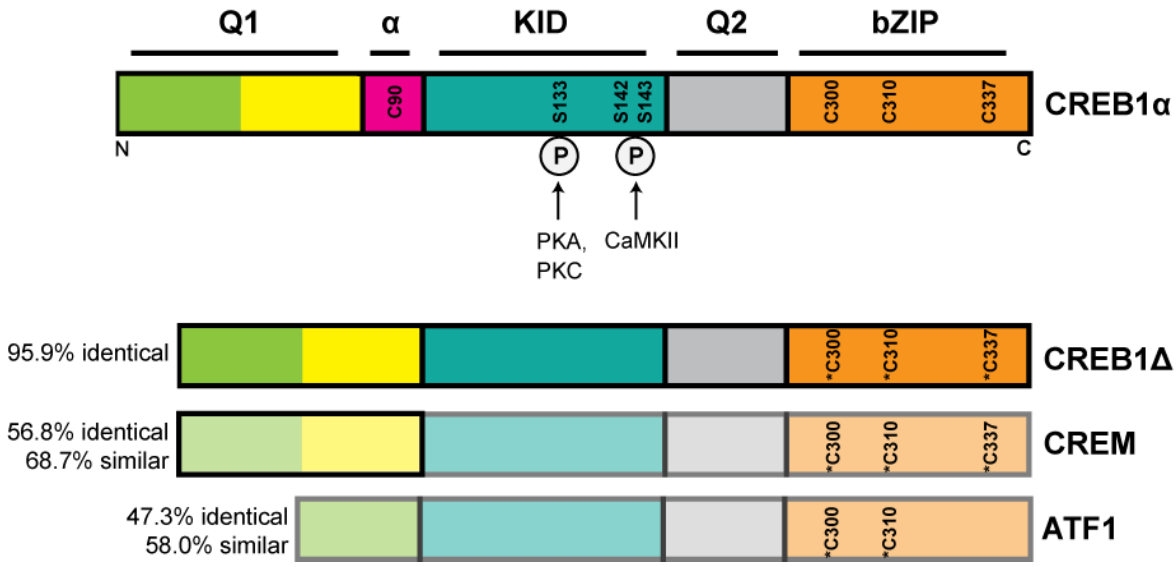


Figure 14. Structure of CREB and related bZIP transcription factors.

Q1= glutamine rich region 1, α= alpha domain, KID= kinase inducible domain, Q2= glutamine rich region 2, bZIP= bZIP domain. Cysteines of CREB1 are annotated (C90, C300, C310, C337), along with equivalent cysteines on related proteins (denoted with * prefix). Phosphorylated serines are also shown (S133, S142, S143) along with their respective kinases (protein kinase A (PKA), protein kinase C (PKC) and Ca^{2+}/calmodulin-dependent protein kinase II (CaMKII)). cAMP responsive element binding protein 1 alpha (CREBα) and delta (CREBΔ) are shown, with the closely related cAMP responsive element modulator (CREM) and Cyclic AMP-dependent transcription factor ATF-1 (ATF1). Cysteine locations, sequence similarity and sequence identity were obtained with Clustal Omega (EMBL-EBI).

To investigate which CREB cysteines are S-nitrosylated, I used an existing plasmid containing a myc-tagged form of mouse CREB1α (99.1% identical to rat) under the control of a CMV promoter. Together with Catia Andreassi (Riccio Lab), I made a series of mutant forms of CREB in which the cysteine(s) under investigation were mutated to the non-nitrosylatable amino acid serine. Serine was chosen due to its structural similarity to cysteine; the only difference between the two amino acids is the presence of a thiol (SH) group in cysteine instead of a hydroxyl (OH) group in serine. We generated single mutants of each cysteine (C90S,S300S,C310S,C337S), a double mutant of the cysteines C300 and C310 in the bZIP domain (C300S/C310S) and a triple mutant (TM) in which all cysteines of the bZIP domain are mutated (C300S/C310S/C337S). DNA vectors were transfected in HEK293T cells and cell lysates were exposed to CysNO (500 μM for 20 mins) before carrying out the biotin switch technique. I found that whilst CREB is S-nitrosylated upon treatment with CysNO (**Figure 15,** lane 2), mutation of single cysteines did not affect S-nitrosylation. Similarly, SNO-CREB levels were not affected in C300/C310S mutant (**Figure 15,** lane 7). The CREB mutant that exhibited the greatest decrease of SNO-CREB when compared to wild type CREB was the bZIP cysteine triple mutant (C300/310/337S) in which CREB S-nitrosylation was reduced to 43% of control (**Figure 15,** lane 8; S.E.M=0.18). Hence, cysteines 300,310 and 337 are the most likely sites of S-nitrosylation on CREB.

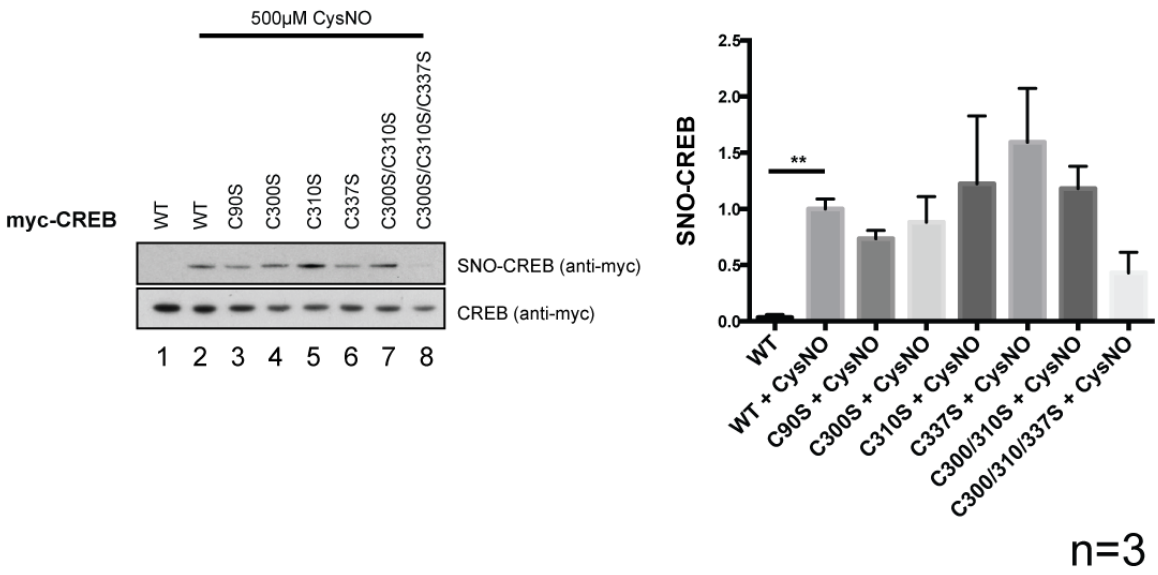


Figure 15. Identification of S-nitrosylated cysteines of CREB.

Myc-tagged wild type CREB or CREB cysteine-to-serine mutants expressed in HEK293T cells for 48h then cell lysates were exposed to CysNO (500 μM for 20 mins) and subjected to biotin switch assay. Isolated proteins were separated by SDS-PAGE followed by immunoblotting with using a myc antibody. Densitometry analysis was carried out using image J. SNO-mycCREB was normalized to input levels of mycCREB and expressed as fold change relative to wild type mycCREB. **p<0.01 One-way ANOVA, compared to 'WT + CysNO' column, Uncorrected Fischer's LSD.

To determine whether cysteine S-nitrosylation may induce conformational changes of CREB, I investigated the crystal structure. Although the full-length CREB protein has not been crystalised, the crystal structure of mouse CREB bZIP domain (identical to rat and human) bound to the CRE sequence of the somatostatin promoter, in dimerised form, has been solved (Schumacher et al., 2000; **Figure 16, A**). Interestingly, in this structure, cysteines 300, 310 and 337 have been switched to serines. As suggested by Lou and colleagues (Luo et al., 2012) these cysteine-to-serine mutations may have been carried out to prevent spontaneous disulphide bond formation that would otherwise hinder crystalisation.

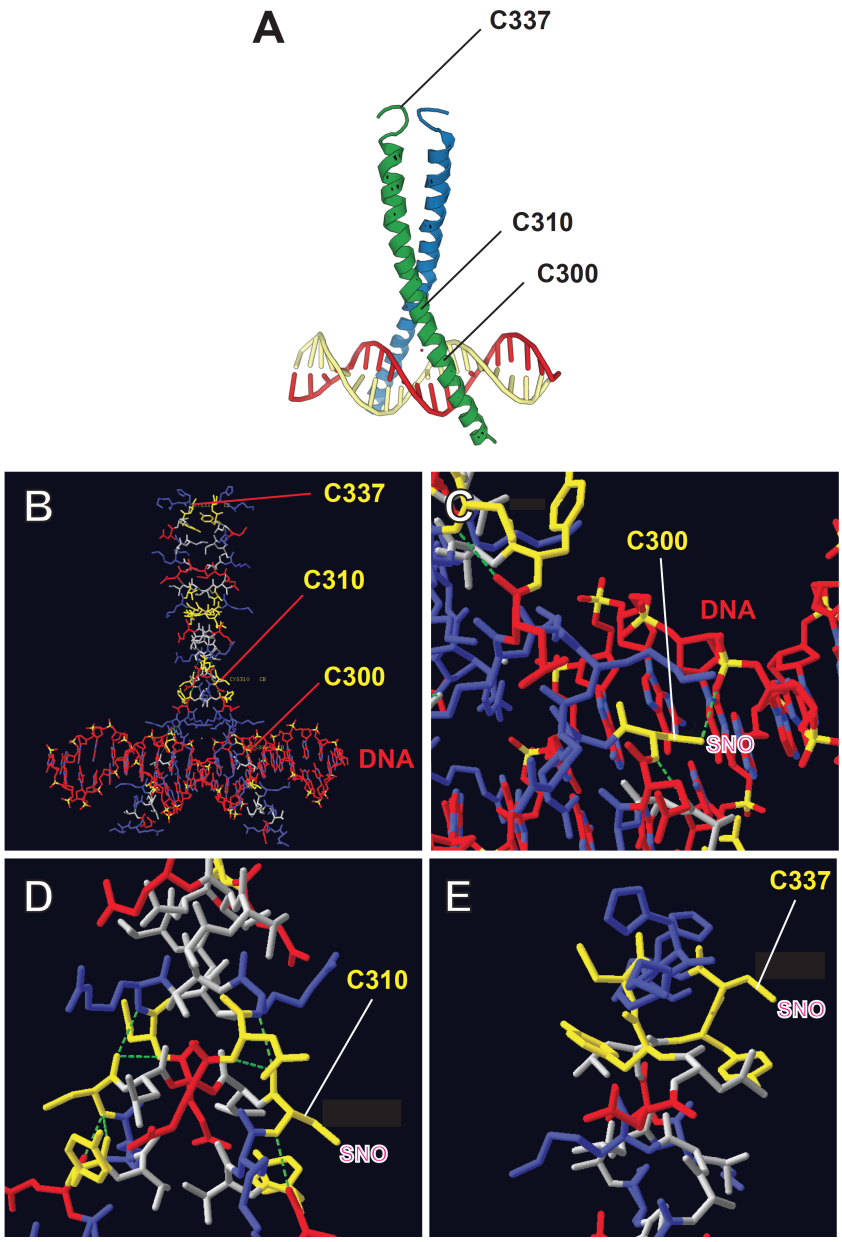


Figure 16. Crystal structure of dimerised CREB bZIP domain binding somatostatin-CRE. Shown is the published structure for dimers of bZIP domains (CREB residues 283-341) that were crystalised as a protein-DNA complex with a synthetically-produced somatostatin CRE sequence (Schumacher et al., 2000). Location of cysteines are marked, however the crystalised form contains serines in place of cysteines. A. Cartoon view. Spiral indicates alpha helix, green and blue represent one bZIP domain each. Structure visualised using PV Javascript protein viewer on the RSCB protein data bank website (10.2210/pdb1dh3/pdb). B-E. Backbone view, visualized using Swiss-PdbViewer. Using the mutation tool, serines 300,310 and 337 were switched for cysteines. Amino acids are coloured according to their properties: acidic; red, basic; blue, polar; yellow, neutral; grey. Green dotted lines represent hydrogen bonds. Prospective location of S-nitrosylation labeled SNO. B. View of CREB bZIP dimer bound to DNA. C-E; Locations of cysteines 300, 310 and 337.

From the structure, it is evident that these cysteines are spatially distinct, with cysteine 300 found in close proximity to DNA whilst C310 and C337 are close to sites of interaction with the opposing CREB molecule. Analysis of a modified crystal structure of CREB, in which serines 300, 310 and 337 were mutated back to cysteines, revealed that the thiol group of cysteine 300 is predicted to form a hydrogen bond with the underlying DNA sequence **(Figure 16,** C**)**, hence S-nitrosylation at this point may modulate CREB DNA-binding through disrupting this bond. The thiol groups of cysteines 310 and 337 are predicted to face away from the protein **(Figure 16,** D and E**)**, therefore S-nitrosylation may affect interaction with cofactors. Alternatively, in each case, the addition of the NO group may cause a conformational change, modifying protein structure and leading to modulation of the contacts between dimers or between CREB and DNA.

Serine 133 phosphorylation is unaffected in the bZIP cysteine triple mutant

Although CREB cysteines may not be essential for bZIP dimerisation and DNA binding under crystalised conditions, I remained concerned that mutation of three cysteines in CREB TM may render the protein non-functional. In this case, the effect of S-nitrosylation would be difficult to assess since it would be impossible to distinguish between S-nitrosylation-mediated effects and the effect of cysteine mutation on protein structure. Thus, I asked whether CREB TM is phosphorylated at serine-133, an event necessary for CREB transcriptional activation (Gonzalez and Montminy, 1989a), in response to physiological stimuli. To induce CREB phosphorylation, HEK293T cells were transfected with either WT or TM CREB and treated with the adenylyl

cyclase agonist forskolin (Seamon and Daly, 1981). Western blotting of cell lysates using a CREB phosphoserine 133-specific antibody detected phosphorylation of both the wild type and the triple mutant form of CREB following forskolin treatment. (**Figure 17**, low exposure). Forskolin treatment also caused S133 phosphorylation of endogenous CREB (**Figure 17**, high exposure).

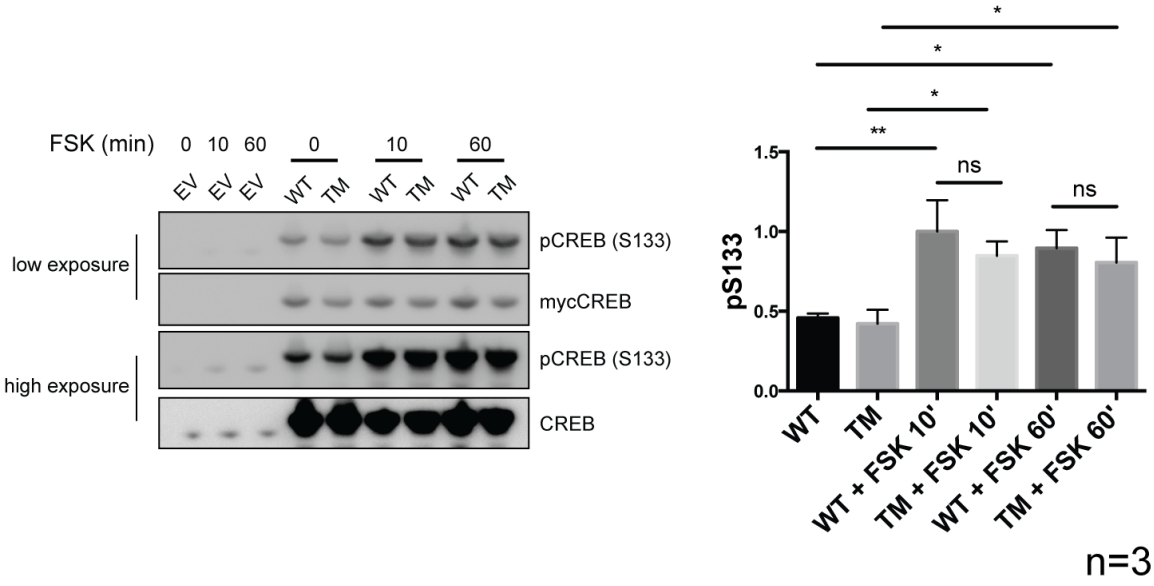


Figure 17. FSK-induced phosphorylation is unaffected in CREB C300/310/337S. HEK293T cells were transfected with empty vector (EV), myc-tagged wildtype (WT) or C300/C310/C337 (triple mutant; TM) CREB and after 48h they were treated with forskolin (50 μM for 10 or 60 mins). Proteins from cell lysates were separated by SDS-PAGE followed by western blotting using a CREB phosphoserine 133 antibody. Expression levels of transfected plasmids were assessed with myc antibody while endogenous CREB levels were assessed using a CREB antibody. Densitometry analysis on western blots was carried out using image J; pS133 signals were normalized to mycCREB, and expressed as fold changes of phospho WT mycCREB at 10' FSK. One-way ANOVA was used to compare the means of each treatment, Uncorrected Fisher's LSD (*= $p<0.05$,**= $p<0.01$ ns= not significant).

When cells were treated with forskolin, I did not observe significant differences between S133 phosphorylation of WT and TM CREB. Hence, mutation of 3 cysteines in the bZIP domain of CREB does not affect FSK-

induced serine 133 phosphorylation, implying that the triple mutant CREB is potentially transcriptionally active.

In summary, CREB is S-nitrosylated upon stimuli that activate NO signalling in neurons. Mutation analysis of CREB cysteines suggests that C300, C310 and C337 are all S-nitrosyated. Because the cysteines are located within the DNA-binding domain of CREB, it is conceivable that CREB S-nitrosylation may affect its binding to chromatin.

Retinoblastoma binding protein 7 (RBBP7)

RBBP7 was first identified as a protein that binds the tumour suppressor retinoblastoma (Rb) in HeLa cells (Qian and Lee, 1995) and inhibits cell proliferation (Guan et al., 1998; Zhang et al., 2007). In post-mitotic neurons, the physiological significance of RBBP7 is as-of-yet unknown. However, along with the closely related RBBP4, RBBP7 is known to be a core component of a number of chromatin-modifying complexes (**Figure 18**).

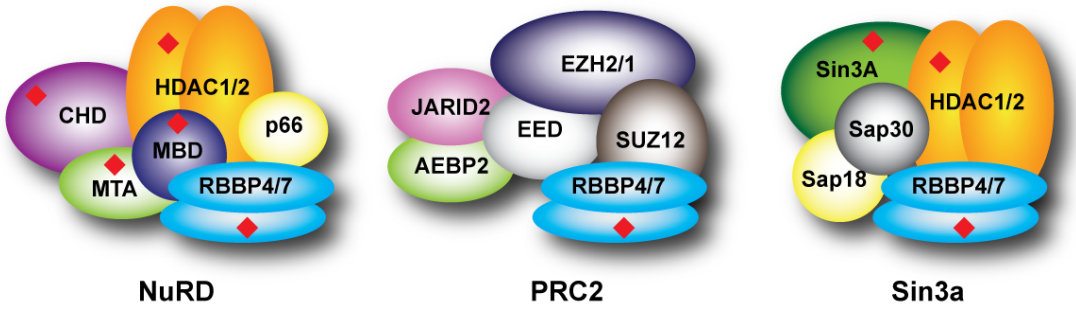


Figure 18. RBBP7 is a subunit of a number of chromatin modifying complexes. RBBP4 and 7 are the core histone-binding components of several multisubunit chromatin-modifying complexes. NuRD; nucleosome remodeling and deacetylase complex, PRC2; polycolm repressive complex 2, Sin3a; mammalian Sin3a complex. Proteins marked ◆ were identified as S-nitrosylated in our screens.

The NuRD complex is unique in that it couples ATPase-dependent chromatin remodeling and histone deacetylation (Xue et al., 1998). Although NuRD was initially characterised as a transcriptional repressor (Kehle et al., 1998; Xue et al., 1998), it is now evident that it may function as either a repressor or an activator of gene expression (Miccio et al., 2010; Nitarska et al, under review). In the cortex, NuRD regulates several stages of cortical development (Egan et al., 2013; Knock et al., 2015; Nitarska et al, in prep) and promotes synaptogenesis in the postnatal cortex (Yamada et al., 2014).

The PRC2 complex is a histone methyltransferase complex involved in gene silencing through trimethylation of lysine 27 on histone H3 (H3K27me3) via the methyltransferase enhancer of Zeste homolog 2 (EZH2) (Viré et al., 2006). In non-neuronal cells and in neuronal precursors, PRC2 keeps pro-neural genes in a repressed state (Mohn et al., 2008; Pengelly et al., 2013). In post mitotic neurons, the EZH2-containing PRC2 complex is not expressed at high levels (Pereira et al., 2010). However, a distinct EZH1-containing PRC2 complex has recently been identified in mature hippocampal neurons (Henriquez et al., 2013), though the functional role of this complex is not yet clear.

The Sin3a complex has only been functionally characterized in non-neuronal cells. In pluripotent embryonic cells, the Sin3a complex is a key regulator of cell cycle control and apoptosis, exerting pro-proliferative and pro-survival effects that are critical during early embryonic development (embryonic days 3.5- 6.5 in mice) (Cowley et al., 2005; Dannenberg et al.,

2005; McDonel et al., 2012). The Sin3a complex has also been shown to play a role in adult tissues, such as in the mouse epidermis, where it exerts anti-proliferative effects (Nascimento et al., 2011). Whether the Sin3a complex is important during neuronal differentiation, or in adult neuronal function, is unknown. However, similar to PRC2, the Sin3a complex is known to repress neuron-specific gene transcription in non-neuronal cells (Roopra et al., 2000). Interestingly, most subunits of the Sin3a and NuRD complex were identified as targets of S-nitrosylation (marked with ◆ in Figure **18**).

RBBP4 and 7 interact with histones H3 and histone H4 (Migliori et al., 2012; Murzina et al., 2008; Zhang et al., 2012), and specific members of each chromatin-modifying complex (Smits et al., 2012; Zhang et al., 1998b). Even though RBBP4 and RBBP7 share high sequence homology (**Figure 19**), studies performed using a non-neuronal cell type suggests that they have different effects on gene expression; RBBP4 inhibits estrogen-dependent gene expression in MCF-7 cells, whilst RBBP7 either represses or activates transcription in a gene-specific manner (Creekmore et al., 2008).

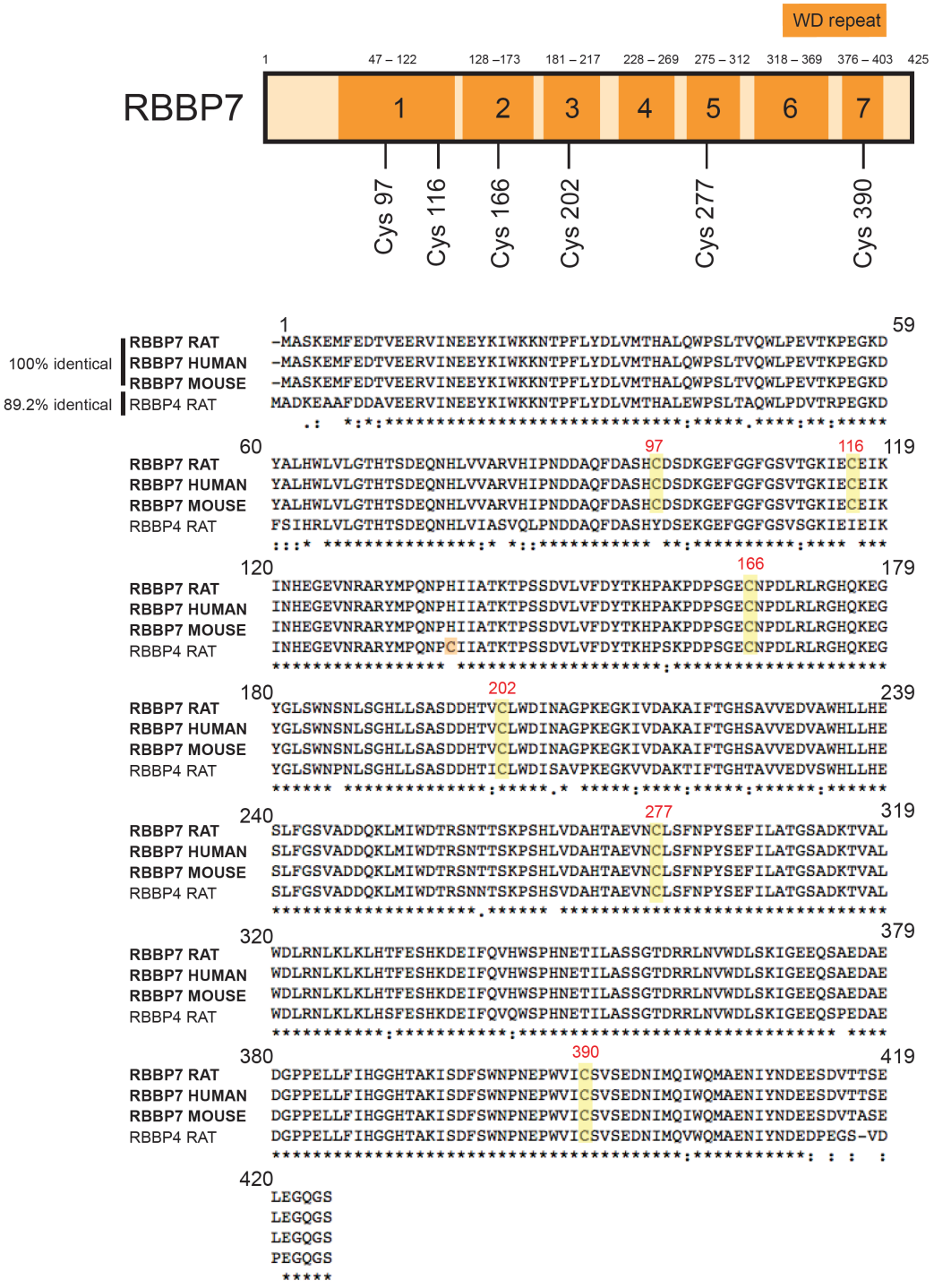


Figure 19. RBBP7 structure and sequence homology. Top. RBBP7 contains 7 WD-repeat domains, composed of short motifs of approximately 40 amino acids ending in a tryptophan-aspartic acid dipeptide. Bottom: sequence homology between rat, human and mouse RBBP7 and rat RBBP4. Sequence alignment carried out using Clustal Omega (Embl-Ebi).

RBBP7 is S-nitrosylated in cortical neurons

S-nitrosylation of RBBP7 was detected in four out of five experiments (**Table S2**, hit number 238). In the remaining experiment, RBBP7 was not detected in any condition. I first asked whether RBBP7 is S-nitrosylated in neurons treated with CysNO (200 µM). Indeed, S-nitrosylation of RBBP7 was clearly detected in rat cortical neurons exposed to CysNO (**Figure 20**, A). To test whether S-nitrosylation takes place in response to physiological stimuli, cortical neurons were treated with KCL (50 mM for 30 mins). I observed that KCL strongly increased RBBP7 S-nitrosylation in neurons (**Figure 20**, B).

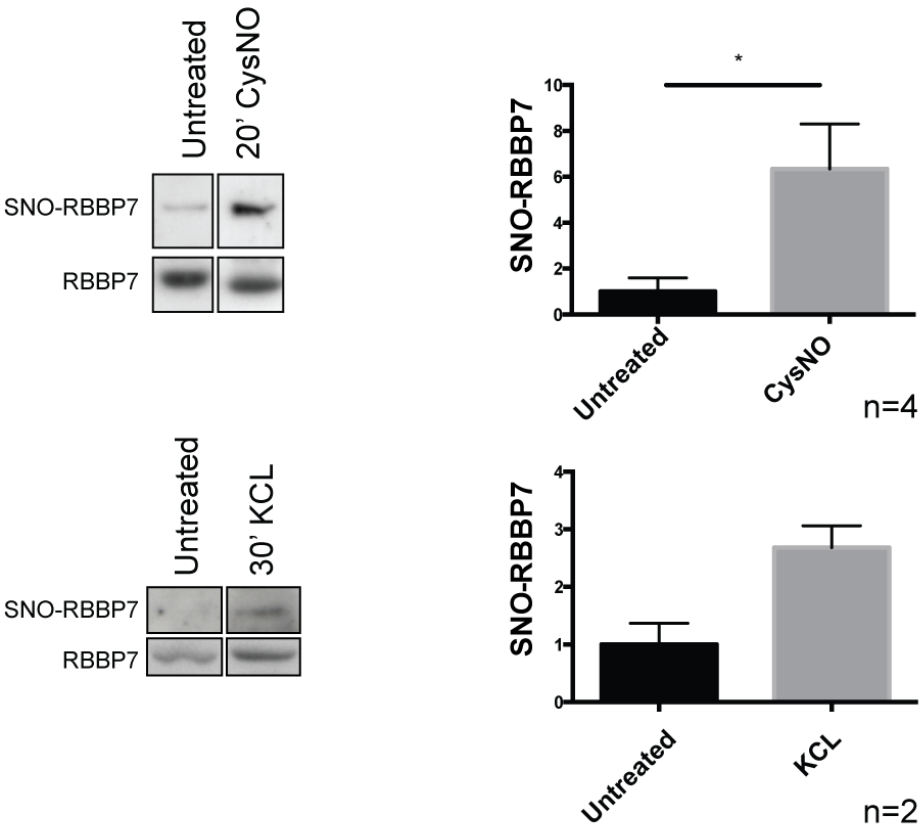


Figure 20: S-nitrosylation of RBBP7 in neurons. Cortical neurons were cultured for 4 days and treated with CysNO (200 µM for 20 mins) (A) or 50 mM KCL for 30 mins (B). S-nitrosylated proteins were isolated using biotin switch and protein isolates separated by SDS-

PAGE and then analyzed by western blotting using an RBBP7-specific antibody. For densitometry analysis (Image J), SNO-RBBP7 was first adjusted according to input levels and then normalized to untreated. SNO-RBBP7 signals first adjusted according to RBBP7 inputs. Values for SNO-RBBP7 in CysNO were then set to 1 for normalization (Paired t test, *P=<0.05).

Next, I investigated which cysteine(s) on RBBP7 are modified by S-nitrosylation. RBBP7 contains seven WD domains that encompass most of the protein (**Figure 19**, top). WD domains are composed of repetitive motifs (~40 amino acids in length), termed WD40 repeats that end with a tryptophan-aspartic acid (WD) dipeptide (Fong et al., 1986; van der Voorn and Ploegh, 1992). Due to their prevalence in proteins with no intrinsic enzymatic activity, WD domains are thought to provide platforms for protein-protein interactions (Stirnimann et al., 2010).

There are six cysteines on RBBP7, which are conserved between rat, human and mouse. Moreover, 4 cysteines are also present in the closely related RBBP4 protein (**Figure 19**, bottom). In a previous study, cysteine 166 was identified as a site of S-nitrosylation of RBBP7 in cardiac cells (Kohr et al., 2011). Importantly, cysteine 166 was also identified in the SNO-peptide analysis in neurons (**Table S7**, hit number 238). Wild type rat RBBP7 was cloned into the myc-tagged mammalian expression vector (CMV-myc) and site-directed mutagenesis was performed to mutate cysteine 166 to serine (C166S). HEK293T cells were transfected with vectors expressing wild type or C166S RBBP7 for 48h, then exposed to CysNO for 20 mins, followed by biotin switch and western blotting using an anti-myc antibody. S-nitrosylation of WT RBBP7 was detected upon CysNO treatment and completely abolished

when cysteine 166 was mutated (**Figure 21**). What role might C166 S-nitrosylation play? The crystal structure of mouse RBBP7 (100% homology to rat) has been solved (**Figure 22**), revealing that the seven WD domains form a seven-bladed beta helical propeller structure (Murzina et al., 2008). Cysteine 166 is on the peripheral surface of WD domain 2 (marked with an arrow in **Figure 22**). The propeller structure is normally found in WD-domain containing proteins (Wall et al., 1995) and may play a key role in tethering the components of multisubunit complexes through protein-protein interactions (Garcia-Higuera et al., 1996; Martínez-Balbás et al., 1998). Unfortunately, the role of WD2 in RBBP7-containing complexes is unknown, although it is conceivable that S-nitrosylation of cysteine 166 may contribute to determine the composition of RBBP7-containing complexes or their interaction with DNA.

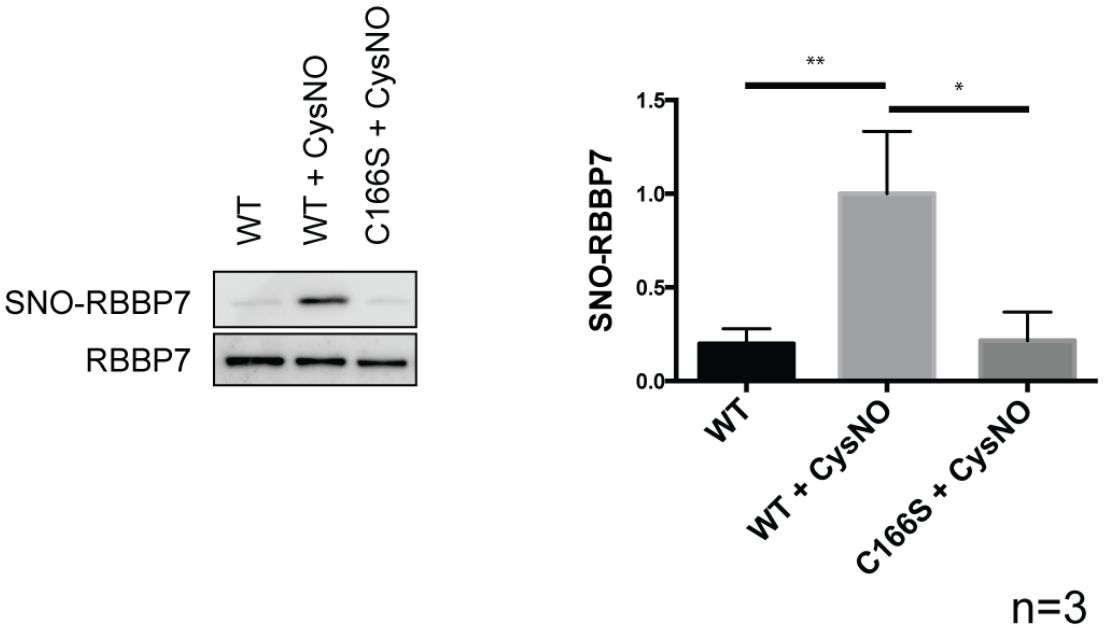


Figure 21. RBBP7 is modified by S-nitrosylation at cysteine 166. Myc-tagged vectors expressing wild type (WT) or cysteine 166 mutant (C166S) RBBP7 were transfected in HEK293T cells. After 48 hours, cells were treated with Cys or CysNO (500 μM for 20 mins)

and lysates were subjected to the biotin switch technique. Protein were separated by SDS-PAGE and subjected to western blotting using a myc antibody. For densitometry analysis, SNO-signals were first normalised to total inputs and expressed as fractions of SNO-RBBP7 in cells transfected with WT RBBP7 and treated with CysNO. One-way ANOVA, compared to 'WT + CysNO' column, Uncorrected Fischer's LSD. Experiment performed by Sarah Aldous (Riccio Lab).

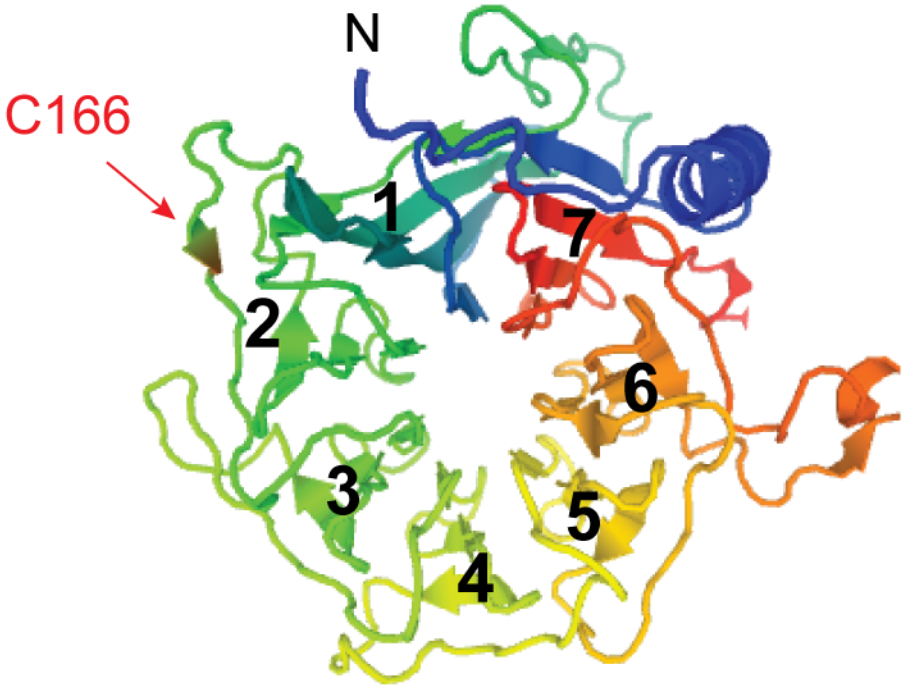


Figure 22. Crystal structure of RBBP7. Solved crystal structure of full-length murine RBBP7 (resolution: 2.6 Angstroms) shown in a top-down view with respect to the N terminal tail (blue). The 7 WD domains are numbered, arrows within the structure indicate beta strands and the single alpha helix is represented by a coil. Position of cysteine 166 is indicated and highlighted in red. Model visualized using SWISSMODEL at proteinmodelportal.org, based on template 3cfvB for Uniprot ID Q60973.

Summary: Chapter 2

I confirmed that CREB and RBBP7 are endogenously S-nitrosylated in a stimulus-inducible manner in neurons. Moreover, I identified the site(s) of S-nitrosylation for both. The non-nitrosylatable mutants that I have generated

will facilitate further studies into the physiological significance of CREB and RBBP7 S-nitrosylation.

In order to ascertain whether S-nitrosylation of CREB affects its interaction with chromatin, the binding of wild type CREB versus nitrosomutant (C300/310/337S) CREB should be assessed by chromatin immunoprecipitation (ChIP) experiments. Lentiviral-based expression of myc-tagged wild type or nitrosomutant CREB in rat cortical neurons followed by ChIP using an anti-myc antibody would allow CREB binding to key gene targets (fos, jun, egr1, vgf) to be assessed under basal conditions and conditions that induce CREB S-nitrosylation. If these experiments determine that there is a S-nitrosylation-dependent change in CREB DNA binding, then to assess whether this affect is due to a direct effect on the ability of CREB to bind DNA, an electrophoretic mobility shift assay (EMSA) could be carried out on purified CREB protein that is either untreated or S-nitrosylated by CysNO. If the binding of CREB to a target promoter is affected by CysNO treatment, then we may reason that S-nitrosylation directly affects CREB DNA binding. Alternatively, the interaction of CREB cofactors may be regulated by S-nitrosylation. To assess this, coimmunoprecipitation (CoIP) experiments on neurons expressing wild type or nitrosomutant CREB should be carried out.

To assess whether RBBP7 S-nitrosylation affects its interaction with chromatin, ChIP experiments should be carried out in a similar manner to those for CREB. In this case, the genomic loci at which RBBP7 binds are unknown, however RBBP7 is a component of several HDAC2 containing

complexes, therefore HDAC2 gene targets may first be assessed. Alternatively, ChIP-seq analysis using DNA isolated from cortical neurons upon immunoprecipitation of either wildtype or nitrosomutant (C166S) RBBP7 would be necessary. CoIP experiments, in which the interaction of binding partners is assessed, would be informative as to whether S-nitrosylation of RBBP7 affects cofactor binding.

The physiological relevance of the S-nitrosylation of CREB and RBBP should also be addressed. KCL and BDNF both induce dendritogenesis in cortical neurons (Crepaldi et al., 2013; Kwon et al., 2011). The effect of S-nitrosylation of CREB or RBBP7 on dendritogenesis can be addressed by expressing nitrosomutant forms of each protein in cultured cortical neurons and assessing how KCL/BDNF-induced dendritogenesis is altered. Furthermore, the effect of CREB/RBBP7 S-nitrosylation during cortical development could be assessed by *in utero* electroporation of embryonic rat cortices with nitrosomutant forms of each construct. By assessing the migration of the electroporated cells, the effect of S-nitrosylation of CREB/RBBP7 on migration of cortical neurons can then be determined. To establish whether S-nitrosylation of either CREB/RBBP7 in the cortex has an effect on behavior, knock-in mice that express the nitrosomutant forms of CREB/RBBP7 in cortex would need to be generated. These nitrosomutant mice can then be behaviourally characterized and their performance on cortex-dependent forms of memory assessed.

Chapter 3: Direct detection of S-nitrosylated cysteines by mass spectrometry

At present, most techniques used for the detection of S-nitrosylated proteins stem from the biotin-switch technique. Although there are slight differences in the labelling, blocking and pulldown steps (review: Foster, 2012), all methods use a series of chemical modifications during which the NO group is lost from the SNO-cysteine. The biotin switch technique is highly specific if performed under the correct conditions (Forrester et al., 2007), however it still provides an indirect assessment of protein S-nitrosylation. More compelling evidence may be gained from the direct detection of S-nitrosylated cysteines using mass spectrometry (Mirza et al., 1995). This approach is very challenging due to the labile nature of the S-NO bond. NO is usually lost when subjected to the high energy of the lasers used for peptide protonation during MALDI-TOF mass spectrometry (Kaneko and Wada, 2003). Interestingly, electro-spray ionisation (ESI) mass spectrometry allows the detection of intact S-nitrosylated cysteines, which exhibit a +29Da mass shift, compared to their non-nitrosylated controls (Mirza et al., 1995). This technical approach, herein termed direct detection, has been successfully employed to identify S-nitrosylation sites on individual SNO-proteins (Lee et al., 2007; Mirza et al., 1995; Wang et al., 2008) and has recently been used to identify S-nitrosylated proteins in bacteria (Li et al., 2014; Yang et al., 2014).

Direct detection of S-nitrosylated proteins in neurons

Endogenous S-nitrosylation in neurons has never before been demonstrated without chemical derivatization of SNO-cysteines. To directly

detect endogenous S-nitrosylation, rat cortical neurons were treated with either BDNF (75 ng/ml) or CysNO (200 μM) for 20 mins and cell lysates were snap frozen and sent for analysis by ESI-mass spectrometry (Dr. Marco Gaspari, University of Catanzaro, Italy). 42 of the 27835 peptides (0.15%) detected in neurons treated with CysNO were found to be S-nitrosylated (**Table S8**). For BDNF-treated neurons, 28554 peptides were detected in total and 56 (0.20%) exhibited the +29Da shift in mass that indicates that they are S-nitrosylated (**Table S9**). While the overall number of S-nitrosylated peptides is low, the sensitivity of this assay is in agreement with previously published reports (Li et al., 2014; Yang et al., 2014)**.**

S-nitrosylated nuclear factors are identified by direct detection

Analysis of the S-nitrosylated proteins revealed that cytoskeletal proteins were the most represented class, although several transcription factors were also identified (**Figure 23**, marked with ★ in **Tables S8** and **S9**). This is an extremely important result as it represents the first direct evidence that S-nitrosylation is taking place in the nucleus. GO analysis of the proteins S-nitrosylated upon BDNF treatment indicated that two proteins are transcription factors (Zinc finger protein 157 (zfp157) and Zinc finger protein 513 (znf513), **Table S9**, hit numbers 25 and 39). In addition, Zinc finger protein 2 (Zfp2) was assigned as a transcription factor by manual analysis (**Table S9**, hit number 26). The functional role of these proteins in neurons is unknown, however S-nitrosylation is known to target zinc finger proteins and regulate their binding to DNA (Berendji et al., 1999; Kröncke, 2001). We found that the transcription factor Homeo box D13 (Hoxd13) is also S-nitrosylated

following CysNO treatment (**Table S8**, hit number 11). Although the role of Hoxd13 in neurons is unknown, other members of the homeobox family of transcription factors play important roles during embryonic brain development (Park et al., 2007).

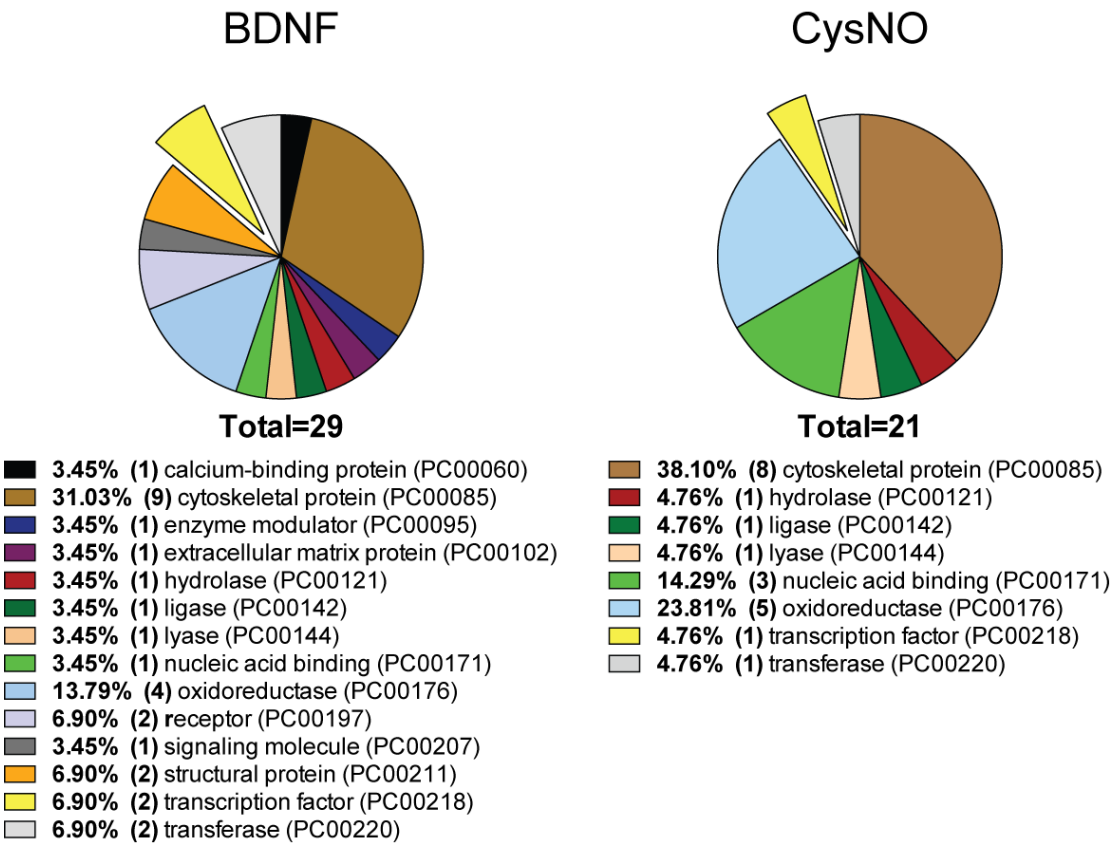


Figure 23. Protein class of proteins identified by direct detection as S-nitrosylated in neurons. PANTHER GO analysis for protein class of proteins identified by direct mass spectrometry analysis. Only annotated proteins are shown.

Comparison of S-nitrosylated proteins identified by direct detection analysis of BDNF and CysNO-treated neurons

To compare proteins detected in BDNF and CysNO-treated neurons, I assigned protein-level identifications using Uniprot ID. 16 proteins (31.6% of

total proteins) were identified in both CysNO and BDNF-treated neurons (marked with • on **Tables S8** and **S9**). Next, I asked whether the same site(s) were identified in the shared hits and found that 16/23 sites (69.6%) were identical between BDNF and CysNO-treated neurons. In BDNF-treated neurons, 56 SNO-sites relate to 39 proteins, 16 of which (41%) were previously identified as S-nitrosylated proteins. Of 32 sites of S-nitrosylation, four (12.5%) match previously published sites, while 28 (87.5%) are potentially new sites of S-nitrosylation in these proteins. In CysNO-treated neurons, 42 SNO-sites were identified on a total of 32 proteins, 21 of which (65.6%) are known targets of S-nitrosylation. Five of 27 sites (18.5%) match known SNO-cysteines, while 21 (77.8%) are novel sites of S-nitrosylation.

Finally, I asked whether proteins identified by direct detection of S-nitrosylation were also found by the SNORAC screens and found that 13/57 (22.8%) proteins were also identified in the SNORAC screens on CysNO-treated nuclear and cytoplasmic extracts. SNO-peptide data from SNORAC was available for six of these proteins in total. For these proteins, 51 sites were identified by SNORAC and eight sites by direct detection. Three out of eight sites (37.5%) identified by direct detection were also identified using SNORAC.

Summary: Chapter 3

These data represent the first attempt to directly identify S-nitrosylated proteins in neurons and provide the first direct evidence that nuclear factors are modified by S-nitrosylation. The approach used here represents a

promising basis on which further work may be built to improve the sensitivity of direct detection of protein S-nitrosylation in neurons.

Of the 13 proteins that are shared between the direct detection experiments and the SNORAC screens, 8 (62%) are proteins that are present in both nuclear and cytoplasmic CysNO-treated extracts, 3 (23%) are present in nuclear extracts only and 2 (15%) in cytoplasmic extracts only. It is possible that these proteins may be detectable by direct detection due to their high abundance in the samples. For example, 5/13 (38%) of the detected proteins relate to isoforms of tubulin. In addition, 11/13 (95%) of these proteins have been previously shown to be S-nitrosylated, which may also indicate that these proteins are particularly amenable to detection. In order to improve the sensitivity of this approach, certain methodological approaches may be considered. Firstly, treating the samples immediately prior to their detection by mass spectrometry may avoid degradation of the signal. Secondly, the use of a higher amount of starting material may increase the number of S-nitrosylated protein identifications. As a negative control, ascorbate should be added to one sample to reduce S-nitrosothiols.

A major advantage of this approach over prototypical methods for detection of S-nitrosylation is that direct detection does not require the chemical reduction of S-nitrosothiols. As an alternative to this approach, a direct labeling approach such as SNOTRAP (SNO trapping by triarylphosphine) could be attempted (Seneviratne et al., 2013). In this methodology, S-nitrosylated residues are bound in a direct and specific

manner by a triarylphosphine moiety linked to biotin. Trypsinisation followed by pulldown of biotin-bound peptides, upon streptavidin binding, allows identification of SNO-sites by mass-spectrometry. This approach has recently been used to identify S-nitrosylated cortical proteins in a mouse model of Alzheimer's disease (Seneviratne et al., 2016), however has not yet been attempted in cultured cortical neurons or cortical lysates from embryonic brains.

3. Discussion

Protein S-nitrosylation has emerged as an important mediator of the biological activity of nitric oxide in many contexts and is now established as a physiological mode of signalling. In neurons, nuclear S-nitrosylation plays an important role in the transduction of extracellular stimuli to changes in gene expression during neuronal development (Nott et al., 2008; 2013) and in the adult brain (Gräff et al., 2014). Strikingly however, few nuclear targets of S-nitrosylation in neurons have been identified.

In this study, I identified 614 proteins that are S-nitrosylated in nuclear extracts from cortical neurons. This is the first screen that specifically focuses on S-nitrosylation of nuclear proteins and the first time that S-nitrosylation has been investigated in neurons in an unbiased manner. The vast majority of SNO-proteins identified are novel targets of S-nitrosylated in neurons and 131 proteins were not known to be S-nitrosylated in any system. I demonstrated that several proteins involved in transcriptional regulation and chromatin remodeling are modified by S-nitrosylation, including CREB and RBBP7, for which I confirmed endogenous S-nitrosylation in response to physiological stimuli. Importantly, I also identified the cysteines that are modified by S-nitrosylation in these proteins. These important findings will allow the investigation of the functional consequences of CREB and RBBP7 S-nitrosylation and whether this impacts transcription of target genes. Lastly, I provide the first evidence that intact S-nitrocysteines can be directly detected on endogenous neuronal proteins, further demonstrating that S-nitrosylation occurs under physiological conditions in neurons.

Comparison to previously published screens

There are two main characteristics that set our screen apart from previous attempts: the large number of total SNO-proteins identified and the distinct composition of these proteins. In our SNORAC screen, we detected 614 proteins, the second highest number of proteins ever identified in a single screen and over 10-fold higher than the median average of 57 (**Table 2**, Introduction). The reasons for the higher sensitivity are unclear; however, there is evidence suggesting that the technique used to detect S-nitrosylation has a significant impact. For example, biotin switch approaches that rely on gel excision of proteins separated by two dimensional electrophoresis (Biotin switch and 2-DE) consistently lead to the detection of fewer than 60 S-nitrosylated proteins independent of either cell type or S-nitrosylating agent used (**Table 2**, Introduction). In contrast, the highest number of proteins detected in any one experiment was 951, using SNORAC on GSNO-treated rat myocardium (Kohr et al., 2011). Additional methodological components may also be important, since only 40 SNO-proteins were detected in the initial SNORAC screen performed by Jonathan Stamler's group (Forrester et al., 2009b). Certainly, the sensitivity of the mass spectrometer used plays a fundamental role in determining the sensitivity of the assay. Initial analysis of SNO-proteins led to the detection of 2.5 fold fewer proteins (data not shown), when compared to the analysis of the same samples performed using a more sensitive mass spectrometer (**Methods**). Furthermore, it is likely that cell-type specific differences in protein denitrosylation systems also contribute to differences in the number of proteins detected between screens. For example, denitrosylation of caspase-3 is 40% more efficient in rat brain lysates than rat

liver lysates (Benhar et al., 2008). In addition, whether the screen has been carried out on proteins that have been S-nitrosylated in an endogenous setting or from samples treated exogenously likely has a significant impact on the number of proteins detected, though this is hard to discern many methodological differences such as cell type and techniques for isolation of S-nitrosothiols are often also present. The second, and most striking, difference between our screen and those previously published is the number of transcriptional regulators that we found to be S-nitrosylated (95), which is higher than all the published screens combined (80). This major improvement in sensitivity is most likely due to the successful enrichment of nuclear proteins, as demonstrated during the initial experiments performed using cellular and nuclear extracts of HEK293T. Although we used CysNO-treated nuclear extracts, our approach allowed the identification of proteins that are also S-nitrosylated endogenously in neurons. Firstly, several previously known intracellular targets of S-nitrosylation in neurons were also detected by our SNORAC experiments, including GAPDH (Hara et al., 2005), HDAC2 (Gräff et al., 2014) and nucleophosmin (Lee et al., 2012). Secondly, two neuronal targets of S-nitrosylation, CREB and RBBP7, were found to be true hits as they were endogenously S-nitrosylated in neurons. I cannot, however, rule out that a proportion of our hits are not S-nitrosylated under physiological conditions. Therefore, the results of the screen have provided a set of proteins that are “nitrosylatable” in the nuclear nucleus of cortical neurons, yet this result should be confirmed in intact cells.

In regards to the S-nitrosylated transcriptional regulators identified in our screen versus those previously published, 3/15 (20%) of the chromatin binding proteins, 6/40 (15%) of the transcription factors and 6/40 (15%) of the DNA binding proteins have previously been shown to be S-nitrosylated in mammalian species. This could be due to species- or cell type specific differences in protein S-nitrosylation, though comparative analyses of this type have not yet been performed. However, as many of these studies have been carried out *in vitro*, on donor-treated cell lysates for example, the impact of species-dependent differences in S-nitrosylation is likely to be negligible in these cases. Instead, a major contributory factor may be variations in protein expression between organisms, or between different tissues within the same organism. For example, analysis from Vaquerizas and colleagues on transcription factor expression data from different human tissues has shown that approximately 25% of transcription factors are expressed in only 1 or 2 tissues (Vaquerizas et al., 2009).

Here, we identified 1253 unique SNO-sites across 409 proteins. An important consideration is how these sites compare to sites of S-nitrosylation *in vivo.* This can be assessed by comparing the sites identified in our screen compared a screen carried out *in vivo,* such as that carried out on endogenous S-nitrosylation in wild type mouse brain by Raju and colleagues (Raju et al., 2015). Overall, there were 27 shared protein targets of S-nitrosylation between both screens. Raju and colleagues identified 45 sites of S-nitrosylation for these 27 proteins, in comparison to the 98 we identified. Of the 45 *in vivo* sites of S-nitrosylation, 27 (60%) were also identified in our

screen. Hence, our screen also identified an additional 71 sites of S-nitrosylation. These may represent sites that are not S-nitrosylated *in vivo* in the mouse brain, or sites that are S-nitrosylated only upon specific cellular stimuli. To address this, further *in vivo* screens are needed to assess changes in protein S-nitrosylation in the brain in response to different physiological and pathological stimuli.

Specificity in S-nitrosylation: the linear acid/base motif

Since the discovery of S-nitrosylation, researchers have set out to determine how specificity is achieved, given that not all cysteines can be modified by means of S-nitrosylation. Which factors determine the cysteine(s) that have the potential to be modified by NO? Several studies have focused on the identification of linear amino acid sequence motifs common to S-nitrosylated cysteines, reporting overrepresentation of acidic and basic residues within +/- 10 amino acids of the site of S-nitrosylation (Doulias et al., 2010; Greco et al., 2006; Kohr et al., 2011; Lee et al., 2011; Marino and Gladyshev, 2012). Here, I identified five amino acid linear motifs that were associated with 40% of SNO-cysteines, four motifs containing the basic amino acid lysine and one containing glutamic acid (**Figure 12**). Similar to previous studies, we identified several different acid/base motifs, ruling out the existence of a universal linear sequence motif for S-nitrosylation. Given that 60% of S-nitrosylated cysteines were not associated with any SNO-motifs, our data support the hypothesis that although acid/base motifs in the surrounding linear sequence may be indicative of the “nitrosylatability” of a certain cysteine, they are not the sole factor that determines the specificity of cysteine

S-nitrosylation. Indeed, some studies have failed to find SNO-motifs altogether (Hao et al., 2006). It must also be noted that sequence-based approaches do not take into account the tertiary structure of the protein, therefore critical information may be lost. Interestingly, a three dimensional SNO-motif, consisting of acidic and/or basic residues within 8 angstroms of the SNO-cysteine, has been found to be more predictive of cysteine S-nitrosylation (Marino and Gladyshev, 2010).

S-nitrosylation of chromatin remodelling complexes

Several subunits of ATP-dependent chromatin remodeling complexes were found to be S-nitrosylated in our screen, including seven of the 20 members of the neuronal BAF complex and nine of the 12 possible members of the NuRD complex (**Tables S10 and S11**). It is now established that the composition of chromatin remodeling complexes is associated with distinct transcriptional responses during both embryonic development (Olave et al., 2002; Nitarska et al, under review) and in response to neuronal activity (Wu et al., 2007). The mechanisms by which the composition of these complexes is regulated in neurons however, remain unknown. Given the large proportions of subunits modified by S-nitrosylation, it is possible that this may be one of the mechanisms through which subunit composition is regulated. BAF60C, a S-nitrosylated BAF complex protein, undergoes phosphorylation-dependent recruitment to the lipoBAF complex in insulin-treated liver cells (Wang et al., 2013). Although a similar phosphorylation event has not yet been described in neurons, it is possible that the interplay between various post-translational modifications may determine the fate and the composition of BAF complexes.

Indeed, an interplay between S-nitrosylation and other post-translational modifications has already been described, such as the mutually exclusive S-nitrosylation and S-palmitoylation of the synaptic scaffold protein PSD95 in hippocampal neurons (Ho et al., 2011a). Alternatively, S-nitrosylation may induce the disassembly of chromatin-modifying complexes, similar to stress-induced ubiquitylation of the protein SCF in *S. cerevisiae,* which causes dissociation of the multi-subunit SCF ligase complex (Yen et al., 2012).

CREB S-nitrosylation in cortical neurons

I discovered that the transcription factor CREB is S-nitrosylated in neurons upon both BDNF-treatment and depolarisation. CREB has been suggested to be S-nitrosylated in myoblast-derived cells overexpressing nNOS (Aquilano et al., 2014), however these experiments were not conclusive as input levels of CREB for the biotin switch experiments were not assessed. CREB is known to be subject to a number of posttranslational modifications in neurons. In unstimulated neurons, CREB is glycosylated at serine 40; this represses CREB transcriptional activity and inhibits dendritogenesis (Rexach et al., 2012). To date however, phosphorylation remains the only functionally characterised dynamic modification of CREB. Phosphorylation at serine 133 of CREB occurs in response to a wide variety of stimuli in neurons (Bonni et al., 1995; Gonzalez and Montminy, 1989b; Thompson et al., 1995) including neurotophins, neuronal activity and stressful stimuli (Deak et al., 1998; Kornhauser et al., 2002a; Riccio et al., 2006). Serine 133 phosphorylation mediates CREB interaction with the histone deacetylase CBP (Parker et al., 1996) and its recruitment to chromatin

(Cardinaux et al., 2000). Numerous studies have shown that CREB transcription positively correlates with phosphorylation of CREB at serine 133. A literature search by Mona Johannessen and colleagues uncovered 80 instances in which stimulus-induced CREB S133 phosphorylation correlated with CREB activation and only three reports in which there was no correlation (Johannessen et al., 2004). Phosphorylation has been shown to be critical for CREB-dependent transcription as mutation of serine 133 to alanine (S133A) suppresses CREB transcriptional activity in a number of model systems, including cortical neurons (Gonzalez et al., 1991; Gonzalez and Montminy, 1989b; Kornhauser et al., 2002b; Nakajima et al., 1997). In support of the physiological relevance of S133 phosphorylation, several reports show that the protective effect of wild type CREB is lost when phosphorylation at serine 133 is abolished (Gubbay et al., 2006; Ha et al., 2014; Larson et al., 2011; Lee and Lee, 2003). For example, expression of CREB S133A in the cingulate cortex of adult mice induces cell death in this region (Ao et al., 2006). A recent report suggests, however, that the requirement of S133 phosphorylation for CREB-dependent transcription may be context dependent. For example, in the hippocampus of CREB S133A knock-in mice, CREB-dependent transcription is unaffected and these mice do not exhibit behavioural defects when subjected to fear conditioning paradigms of learning and memory (Briand et al., 2015). Whether other post-translational modifications are important in this phosphoserine 133-independent context remains to be determined. In addition to S133, CREB is also phosphorylated on serines 142 and 143 in response to neuronal activity, although the

functional role of this phosphorylation is currently unknown (Kornhauser et al., 2002a).

How is S-nitrosylation affecting the function of CREB? Based on previous studies (**Table 1**, Introduction), it is possible that CREB S-nitrosylation regulates DNA binding, either by increasing or decreasing its affinity for DNA. This is plausible since, in this study, I found that CREB is S-nitrosylated on three cysteines (300,310,337) contained within the bZIP domain, a region that mediates CREB interaction with DNA and binding of cofactors such as CREB Regulated Transcription Coactivator 2 (CRTC2) (Landschulz et al., 1989; Luo et al., 2012; O'Shea et al., 1991). Since CREB is S-nitrosylated in response to BDNF and KCL, which are experimental conditions that induce activation of CREB-dependent gene expression (Finkbeiner et al., 1997; Ghosh et al., 1994b; Tao et al., 1998b), S-nitrosylation may increase the affinity of CREB for DNA. However, S-nitrosylation of CREB may also decrease the affinity of CREB for DNA. In support of this alternate hypothesis, reduction of CREB cysteines using DTT results in increased binding to DNA *in vitro* (Goren et al., 2001), suggesting that oxidative modification of CREB cysteines may inhibit DNA binding. Importantly, it is known that CREB binding to immediate-early gene promoters is transient. In cortical neurons, CREB binding to the c-Fos promoter peaks within 15 mins of BDNF treatment and is reduced to control levels after 45 mins (Riccio et al., 2006). The signalling mechanisms that regulate CREB dissociation from immediate-early gene promoters are unknown, however it is conceivable that S-nitrosylation of CREB could induce CREB dissociation

from DNA, thereby serving as an off-mechanism for transcription. In addition, it is now appreciated that individual transcription factors often interact with promoters in an oscillatory fashion, with residence times much shorter than the overall duration of transcription (McNally et al., 2000; Stenoien et al., 2001). Using FRAP (Flourescence Recovery After Photobleaching), it has been shown that CREB interacts with promoters in a dynamic manner, with an average promoter residence time of 100 seconds (Mayr et al., 2005). Ser133 phosphorylation of CREB is not involved in this process (Mayr et al., 2005), however S-nitrosylation may play a role.

Finally, CREB S-nitrosylation may modulate the interaction with transcriptional co-factors. In support of this hypothesis, cysteines 300/310/337 mediate the binding of CREB with the transcriptional cofactor CRTC2 and CREB-CRTC2 interaction is drastically reduced when C300/310/337 are mutated (Luo et al., 2012).

S-nitrosylation of RBBP7 in cortical neurons

RBBP7 is a core component of a number of nuclear complexes that regulate transcription in neurons, including the repressive Sin3a complex (Zhang et al., 1997) and the NuRD complex (Xue et al., 1998; Zhang et al., 1998a), which can have both repressive and activating functions (Miccio et al., 2010). In both complexes, the role(s) of RBBP7 and the closely related protein RBBP4 remains largely unknown, although it has been suggested that RBBP proteins may function as a scaffold due to the ability to bind histones (Murzina et al., 2008; Zhang et al., 2012) and other subunits within the complexes

(Zhang et al., 1997; 1999). Surprisingly however, RBBP7 only interacts with free histones *in vitro* and does not bind nucleosomal (DNA-bound) histones (Zhang et al., 1998b). Hence, if RBBP7 is participating in the binding of modifying complexes to chromatin, disruption of the contacts between DNA and histones may first be required. The NuRD complex contains intrinsic remodelling activity (Xue et al., 1998; Zhang et al., 1998a) which is provided by the CHD proteins (Tong et al., 1998), hence an initial binding event may induce a conformational change that promotes RBBP7 binding. There is also evidence suggesting that the epigenetic modifications of histones may affect RBBP7 binding. Pulldown assays on cellular extracts demonstrated that RBBP7 binding to histone H3 is inhibited by H3S10ph (phosphorylation at serine 10) (Klingberg et al., 2015) and H3R2me2 (dimethylation at arginine 2) (Migliori et al., 2012). The physiological relevance of these marks in neurons is as-of-yet unknown, however, in non-neuronal cell types, H3S10ph and H3R2me2 correlate with active transcription (Ivaldi et al., 2007; Migliori et al., 2012; Zippo et al., 2009). Furthermore, recent data suggest that RBBP proteins may readily dissociate from other members within each chromatin-remodelling complex. Using a subunit exchange assay *in vitro*, RBBP4 and 7 were found to be the most dynamic members of the NuRD complex (Kloet et al., 2015) and are the only proteins that dissociate when exposed to increasing detergent concentrations (Kloet et al., 2015). Hence, the binding of RBBP4/7 to other NuRD subunits may depend on post-translational modifications that alter the biochemical structure. Finally, several binding partners of RBBP7 in each complex have been identified; within the Sin3a complex, RBBP4/7 interact with HDAC1 and Sin3 (Zhang et al., 1997),

whereas in the NuRD complex RBBP4/7 interact with HDAC1 and 2 and MTA1,2,3 (Kloet et al., 2015). It is evident that RBBP proteins bind histones, readily dissociate from other subunits and can bind several components, including HDACs. Thus RBBP4/7 likely tethers HDACs at certain genomic locations, promoting deacetylation of the histone tails. S-nitrosylation of RBBP7 may induce the dissociation of NuRD and Sin3a complexes from chromatin in response to depolarisation, perhaps indirectly regulating the acetylation state of the chromatin.

S-nitrosylation of HDAC2 decreases the affinity of HDAC2 with chromatin (Nott et al., 2008). Since HDAC2 and RBBP7 are both S-nitrosylated, it is possible that SNO-HDAC2 transnitrosylates RBBP7, inducing conformational changes that prompt the dissociation of the complexes. Alternatively, within the NuRD complex, S-nitrosylation of RBBP7 may modulate the association with MTA2 through the known interaction at lysine 214, a residue that is located in close proximity to cysteine 166 (**Figure 22**). In this case, S-nitrosylation of RBBP7 may determine the stoichiometry of NuRD complexes by modulating subunit interactions. Finally, S-nitrosylation of RBBP7 could determine the specificity of the interacting proteins. For example, serum stimulation of MCF-7 cells induces cycles of methylation and demethylation of the NuRD member MTA1 (Nair et al., 2013). Once MTA1 is demethylated, it dissociates from the NuRD complex, promoting the interaction of MTA1 with histone H3 and the recruitment of the NuRF (nucleosome remodeling factor) coactivator complex. Since RBBP7 belongs

to several chromatin-modifying complexes in neurons, an S-nitrosylation based mechanism for selective complex recruitment may exist.

Direct detection of intact S-nitrosocysteines on neuronal proteins

My findings demonstrate, for the first time, that S-nitrosocysteines can be detected directly on endogenously S-nitrosylated neuronal proteins. Using direct detection by mass spectrometry, S-nitrosocysteines were detected in 42 out of 27835 peptides (0.19%) in CysNO-treated neurons, and 56/28554 peptides (0.20%) in BDNF-treated neurons. Although the number of peptides is significantly lower than the number of S-nitrosylated proteins identified using SNORAC, this is likely due to technical limitations of the methodology. Indeed, most proteins are expressed at high levels in neurons, such as the cytoskeletal components tubulin and actin, whereas some of the validated, but less abundant, S-nitrosylated proteins, including HDAC2, RBBP7 and CREB were not detected. Although we mostly identified cytoplasmic proteins, four zinc-finger transcription factors were also found, indicating that this technique is suitable to investigate endogenous nuclear S-nitrosylation. To date, only two studies have attempted to assess S-nitrosylation in whole cell lysates using mass spectrometry-based direct detection, both carried out on prokaryotes. In the bacterium *Leptospirillium*, S-nitrosocysteines were detected in 126 of the 78539 peptides (0.16%) (Li et al., 2014) and in a similar proportion of peptides from the bacterium *Synechococcus* (0.20%) (Yang et al., 2014). In these studies, the occurrence of S-nitrosylation relative to other post-translational modifications was 1.22% and 1.69% in *Leptospirillium* and *Synechococcus*, respectively. Although S-nitrosylation is detected far less

frequently than modifications such as methylation (29.7% in *Leptospirillium* and 26.94% in *Synechococcus,* respectively), this may be due to the relative lability of the S-nitrosocysteine moiety, when compared to other covalent modifications, that render their detection challenging.

Technical challenges facing researchers studying nitric oxide signaling in the cortex and beyond

There are several challenges associated with studying NO signalling and S-nitrosylation in neurons that are currently hampering progress in this field of research. Firstly, the nNOS knockout mouse most commonly used possess significant residual NOS activity (Eliasson et al., 1997; Huang et al., 1993), which may make the analysis of the phenotype problematic. In these KN1 mice, residual NOS activity is due to the expression of nNOSβ (Eliasson et al., 1997), an alternatively spliced isoform that is not affected by the deletion of the nNOSα-specific exon 2, which was used to generate these mice (Huang et al., 1993). Although this isoform only accounts for 5% of NO production in the adult brain (Eliasson et al., 1997), its contribution during development is unknown. To circumvent these issues, a complete nNOS knockout mouse named KN2, has been generated in which all isoforms of nNOS are knocked out through the deletion of exon 6, which encodes for the catalytic domain of all isoforms (Gyurko et al., 2002). Although only partially characterised, KN2 mice exhibit reproductive defects, such as hormonal abnormalities and lack of mating behaviour in males, that are not present in KN1 mice (Gyurko et al., 2002). These findings indicate that nNOSβ is capable of rescuing at least some phenotypic abnormalities in the KN1 mice.

Hence, KN2 mice represent a valuable tool to comprehensively assess the role of nNOS in cortical development *in vivo*. However, protein S-nitrosylation may still occur in these mice via nNOS-independent sources of NO, such as nitrite (Zweier et al., 1999), therefore knock-in mice expressing non-nitrosylatable forms of specific SNO-proteins may be more informative.

A second major factor limiting the progress of uncovering the role of S-nitrosylation in neuronal, or non-neuronal, cells is that detection of S-nitrosylation is technically challenging in several regards. To minimize signal loss and technical artifacts, experiments must be carried out under strictly controlled conditions (Forrester et al., 2009a), for example minimising the exposure of samples to light (Forrester et al., 2007). More importantly, biotin switch-based techniques have not yet been successfully adapted to study SNO-protein localization within intact cells. Localisation of total SNO-proteins has been reported using immunohistochemical analysis with pan-S-nitrosocysteine antibodies (Gow et al., 2002), however the specificity of these antibodies remains unclear. Therefore, the research field would greatly benefit from the development of more amenable approaches to detect S-nitrosylated proteins in both cell lysates and intact cells and tissues. An important technical advance would be to develop antibodies that target SNO-cysteines in the context of specific proteins and, in the longer term, to selectively modulate S-nitrosylation by targeting transnitrosylases that specifically transfer nitrosyl groups to proteins of interest.

A further important point concerns studying the biological consequences of S-nitrosylation. Currently, one of the only ways to discern the functional effect of S-nitrosylation of a particular protein is to mutate the cysteine(s) targeted by S-nitrosylation to a non-nitrosylatable amino acid, then to carry out experiments using the nitrosomutant to assess the effect of inhibiting S-nitrosylation of that protein. The choice of amino acid used as the substitute for cysteine is likely critical since certain amino acids may induce structural alterations that result in changes in protein function. If this occurs, then it may be difficult to separate out the effect of S-nitrosylation. To try to minimize the likelihood that protein structure is substantially changed, serine is often used to replace cysteine. This is because serine is the most structurally similar amino acid to cysteine, the only difference being that serine contains an -OH group in place of the -SH group of cysteine. Though this is currently regarded as the best option for cysteine replacement, this could still induce deleterious structural changes and, as serines are often modified by phosphorylation, this approach could also result in the spurious generation of new sites of phosphorylation of the protein. It is also important to note that mutation of a particular cysteine will also affect other cysteine modifications such S-glutathionylation. Therefore, cysteine mutants do not affect S-nitrosylation specifically and should be used as part of a wider experimental approach to uncover the role of protein S-nitrosylation. For example, the effect of S-nitrosylation of protein function may also be assessed by selective treatment of purified proteins with CysNO. In this way, following CysNO removal, the effect of S-nitrosylation of that protein on activity, interaction with other proteins, or interaction with DNA, may be assessed.

Remaining unanswered questions regarding S-nitrosylation of nuclear proteins

The development of new techniques is imperative if we are to accelerate the progress in a field in which so many open questions remain. For example, what is the intracellular range of stimulus-induced S-nitrosylation? This is an especially important question when nNOS-dependent S-nitrosylation of nuclear factors is considered. In embryonic cortical neurons, nNOS is detected in the cytoplasm (Bredt and Snyder, 1994), so it may be activated to release NO in close proximity to the nucleus. However, in most adult cortical and hippocampal neurons, nNOS is only detected at high levels in the postsynaptic densities of dendritic spines (Aoki et al., 1998; Burette et al., 2002). This is striking, given that S-nitrosylation of the nuclear protein HDAC2 occurs in response to synaptic activity in the adult hippocampus (Gräff et al., 2014). A possible explanation is that nuclear S-nitrosylation takes place in the small population of GABAergic cells that express nNOS in the cytoplasm. Alternatively, if taking place in non-GABAergic neurons, the S-nitrosylation signal must be transduced over a distance of hundreds of microns from the dendritic spines to the nucleus. In this case, two potential mechanisms may be considered: firstly, a long distance S-nitrosylation cascade may be taking place. Intriguingly, it is known that several synaptic proteins are S-nitrosylated (Dejanovic and Schwarz, 2014; Ho et al., 2011a) and SNO-GAPDH is capable of transferring SNO-signals from the cytoplasm to the nucleus (Kornberg et al., 2010). Hence, putative components of such a cascade have been identified, however a causal link between S-nitrosylation at the synapse and S-nitrosylation of GAPDH has not yet been demonstrated.

Secondly, upon certain stimuli, it is possible that nNOS may relocate from dendrites to a perinuclear position. Indeed, there is a precedent for involvement of long-range protein transport in the transduction of extracellular signals to the neuronal nucleus. Upon neurotrophin stimulation of sympathetic neurons, phosphorylated TrkA receptor is internalised at axon terminals and reaches the cell bodies, which are often located centimeters away, inducing CREB-dependent gene expression (Riccio et al., 1997). In addition, stimulus-induced transport of NOS has been demonstrated before. In endothelial cells, eNOS is redistributed from caveolae to intracellular membranes upon oxidative stress (Uittenbogaard et al., 2000).

A second important unanswered question regards the timing of nuclear protein S-nitrosylation in neurons, as it is not known for how long nuclear proteins remain S-nitrosylated. Proteins are likely to have specific kinetics of S-nitrosylation, however we only have information regarding HDAC2 S-nitrosylation in the hippocampus, in which SNO-HDAC2 is detected at 30 mins and 3 hours post memory recall and is lost after 5 hours (Gräff et al., 2014). It is possible that specific denitrosylases remove the NO group from S-nitrosylated nuclear proteins in neurons, given that stimulus-dependent denitrosylation has been detected in other systems, including cytokine-stimulated airway epithelia and Fas-stimulated lymphocytes (Benhar et al., 2008; Kelleher et al., 2014; Sun et al., 2013). In these model systems, denitrosylation is dependent on the thioredoxin system. Interestingly, several SNO-proteins identified in our screen, including the NuRD components HDAC1, RBBP4/7 and CHD4, have been shown to bind thioredoxin *in vitro*

(Ben-Lulu et al., 2014). Hence, upon nNOS activation in neurons, these proteins may be S-nitrosylated and subsequently subjected to thioredoxin-mediated denitrosylation.

S-nitrosylation: an evolutionary perspective

In this study, I laid out the groundwork for understanding the role of nuclear S-nitrosylation in mammalian neurons. Additional insights may be gained when the evolutionary history of S-nitrosylation is considered. There is now considerable evidence suggesting that S-nitrosylation represents an ancient mode of cellular signalling. For example, S-nitrosylation of the transcription factor OxyR has been detected in prokaryotes (Hausladen et al., 1996; Seth et al., 2012) as well as the denitrosylase system GSH/GSNOR (Liu et al., 2001). How did this highly reactive gas evolve to become a signalling molecule? A plausible hypothesis brought forward in 1995 by Martin Feelisch and John Martin suggests that roughly 2 billion years ago, in the oxygen rich atmosphere of the early earth, mutations taking place in bacteria may have resulted in NO release that conferred a selective advantage (Feelisch and Martin, 1995) due to the ability of NO to neutralise noxious oxygen species (Johnston, 1971; Malik and Tauler, 2015). Eukaryotic cells may have appropriated these mechanisms during an early symbiotic relationship with bacteria and used them to their advantage to generate signalling pathways (Yamasaki, 2004; 2005). Interestingly, we now know that NO signalling plays a key role during many cellular processes including the development of the cerebral cortex in mammals (Nott et al., 2008; 2013). Yet when did this role for NO emerge? Is nitric oxide signalling necessary for brain

development in all species? Birds and reptiles represent the oldest species in evolutionarily terms that contain a cortex (Northcutt, 1981). Modern-day turtles, for example, are morphologically almost identical to their Metozoic ancestors (Apesteguía and Novas, 2003). Strikingly, nitric oxide positive neurons are sparsely distributed in the cortex and hippocampus of turtle brains (Brüning et al., 1994), which is reminiscent of nNOS positive GABAergic cells in both rodents and humans (Garbossa et al., 2005; Kubota and Kawaguchi, 1994), suggesting an evolutionarily conserved role of nitric oxide in the cortex.

Closing remarks and perspectives

The main finding of my study is that hundreds of proteins are potentially S-nitrosylated in the nucleus of mammalian cortical neurons. However, the number of nuclear proteins S-nitrosylated in cortical neurons *in vivo* is unknown. Only nine nuclear proteins have so far been found to be S-nitrosylated *in vivo* in the brain (**Table S12**). Moreover, apart from for SNO-HDAC2 in the hippocampus (Gräff et al., 2014), endogenous S-nitrosylation of proteins in specific brain regions *in vivo* has not yet been defined. The data presented here suggests that our current knowledge of *in vivo* S-nitrosylation is anything but complete and that the current lack of information arises from methodological limitations. If methodologies to detect S-nitrosylated proteins continue to improve, researchers may hopefully be able to assess the prevalence and functional role of nuclear S-nitrosylation *in vivo.* It will be also of fundamental importance to understand the physiological role(s) of nuclear S-nitrosylation in neurons *in vivo.* Based upon my findings and previous

research, I suggest two key areas in which the role of nuclear S-nitrosylation should be further explored: during embryonic development and in the adult brain in response to learning and memory events. *In vitro* studies that address the functional consequences of nuclear S-nitrosylation with respect to transcriptional outcome and phenotypic response are an important first step along this path. The generation of knock-in mice expressing non-nitrosylatable forms of nuclear proteins in specific cell types, and at specific times, may represent powerful tools to understand the *in vivo* relevance of these findings.

5. References

Agranoff, B.W., Davis, R.E., Casola, L., and Lim, R. (1967). Actinomycin D blocks formation of memory of shock-avoidance in goldfish. Science *158*, 1600–1601.

Aiba, A., Kano, M., Chen, C., Stanton, M.E., Fox, G.D., Herrup, K., Zwingman, T.A., and Tonegawa, S. (1994). Deficient cerebellar long-term depression and impaired motor learning in mGluR1 mutant mice. Cell *79*, 377–388.

Akhtar, M.W., Sanz-Blasco, S., Dolatabadi, N., Parker, J., Chon, K., Lee, M.S., Soussou, W., McKercher, S.R., Ambasudhan, R., Nakamura, T., et al. (2016). Elevated glucose and oligomeric [beta]-amyloid disrupt synapses via a common pathway of aberrant protein S-nitrosylation. Nat Commun *7*, 10242.

Altaany, Z., Ju, Y., Yang, G., and Wang, R. (2014). The coordination of S-sulfhydration, S-nitrosylation, and phosphorylation of endothelial nitric oxide synthase by hydrogen sulfide. Sci Signal *7*, ra87–ra87.

Altarejos, J.Y., and Montminy, M. (2011). CREB and the CRTC co-activators: sensors for hormonal and metabolic signals. Nat. Rev. Mol. Cell Biol. *12*, 141–151.

Ao, H., Ko, S.W., and Zhuo, M. (2006). CREB activity maintains the survival of cingulate cortical pyramidal neurons in the adult mouse brain. Mol Pain.

Aoki, C., Bredt, D.S., Fenstemaker, S., and Lubin, M. (1998). The subcellular distribution of nitric oxide synthase relative to the NR1 subunit of NMDA receptors in the cerebral cortex. Prog. Brain Res. *118*, 83–97.

Apesteguía, S., and Novas, F.E. (2003). Large Cretaceous sphenodontian from Patagonia provides insight into lepidosaur evolution in Gondwana. Nature *425*, 609–612.

Aquilano, K., Baldelli, S., and Ciriolo, M.R. (2014). Nuclear recruitment of neuronal nitric-oxide synthase by α-syntrophin is crucial for the induction of mitochondrial biogenesis. J. Biol. Chem. *289*, 365–378.

Arancio, O., Kiebler, M., Lee, C.J., Lev-Ram, V., Tsien, R.Y., Kandel, E.R., and Hawkins, R.D. (1996). Nitric Oxide Acts Directly in the Presynaptic Neuron to Produce Long-Term Potentiationin Cultured Hippocampal Neurons. Cell *87*, 1025–1035.

Arnold, W.P., Mittal, C.K., Katsuki, S., and Murad, F. (1977). Nitric oxide activates guanylate cyclase and increases guanosine 3“:5-”cyclic monophosphate levels in various tissue preparations. Proc. Natl. Acad. Sci. U.S.a. *74*, 3203–3207.

Änggård, E. (1994). Nitric oxide: mediator, murderer, and medicine. The Lancet *343*, 1199–1206.

Barde, Y.A., Edgar, D., and Thoenen, H. (1982). Purification of a new neurotrophic factor from mammalian brain. Embo J. *1*, 549–553.

Barford, D., Hu, S.H., and Johnson, L.N. (1991). Structural mechanism for glycogen phosphorylase control by phosphorylation and AMP. J. Mol. Biol. *218*, 233–260.

Barrionuevo, G., Schottler, F., and Lynch, G. (1980). The effects of repetitive low frequency stimulation on control and “potentiated” synaptic responses in the hippocampus. Life Sciences *27*, 2385–2391.

Beckmann, J.S., Ye, Y.Z., Anderson, P.G., Chen, J., Accavitti, M.A., Tarpey, M.M., and White, C.R. (1994). Extensive nitration of protein tyrosines in human atherosclerosis detected

by immunohistochemistry. Biol. Chem. Hoppe-Seyler *375*, 81–88.

Ben-Lulu, S., Ziv, T., Admon, A., Weisman-Shomer, P., and Benhar, M. (2014). A substrate trapping approach identifies proteins regulated by reversible S-nitrosylation. Mol. Cell Proteomics *13*, 2573–2583.

Benhar, M., Forrester, M.T., Hess, D.T., and Stamler, J.S. (2008). Regulated protein denitrosylation by cytosolic and mitochondrial thioredoxins. Science *320*, 1050–1054.

Berendji, D., Kolb-Bachofen, V., Zipfel, P.F., Skerka, C., Carlberg, C., and Kröncke, K.D. (1999). Zinc finger transcription factors as molecular targets for nitric oxide-mediated immunosuppression: inhibition of IL-2 gene expression in murine lymphocytes. Mol. Med. *5*, 721–730.

Berger, S.L., Kouzarides, T., Shiekhattar, R., and Shilatifard, A. (2009). An operational definition of epigenetics. Genes Dev. *23*, 781–783.

Bernaudo, F., Monteleone, F., Mesuraca, M., Krishnan, S., Chiarella, E., Scicchitano, S., Cuda, G., Morrone, G., Bond, H.M., and Gaspari, M. (2015). Validation of a novel shotgun proteomic workflow for the discovery of protein-protein interactions: focus on ZNF521. J. Proteome Res. *14*, 1888–1899.

Blackshaw, S., Eliasson, M.J.L., Sawa, A., Watkins, C.C., Krug, D., Gupta, A., Arai, T., Ferrante, R.J., and Snyder, S.H. (2003). Species, strain and developmental variations in hippocampal neuronal and endothelial nitric oxide synthase clarify discrepancies in nitric oxide-dependent synaptic plasticity. Neuroscience *119*, 979–990.

Bliss, T.V., and Collingridge, G.L. (1993). A synaptic model of memory: long-term potentiation in the hippocampus. Nature *361*, 31–39.

Bliss, T.V.P., and Lomo, T. (1973). Long-lasting potentiation of synaptic transmission in the dentate area of the anaesthetized rabbit following stimulation of the perforant path. The Journal of Physiology *232*, 331–356.

Blough, N.V., and Zafiriou, O.C. (1985). Reaction of superoxide with nitric oxide to form peroxonitrite in alkaline aqueous solution. Inorg. Chem. *24*, 3502–3504.

Boersema, P.J., Raijmakers, R., Lemeer, S., Mohammed, S., and Heck, A.J.R. (2009). Multiplex peptide stable isotope dimethyl labeling for quantitative proteomics. Nat Protoc *4*, 484–494.

Bonasio, R., Tu, S., and Reinberg, D. (2010). Molecular signals of epigenetic states. Science *330*, 612–616.

Bonni, A., Brunet, A., West, A.E., Datta, S.R., Takasu, M.A., and Greenberg, M.E. (1999). Cell survival promoted by the Ras-MAPK signaling pathway by transcription-dependent and -independent mechanisms. Science *286*, 1358–1362.

Bonni, A., Ginty, D.D., Dudek, H., and Greenberg, M.E. (1995). Serine 133-Phosphorylated CREB Induces Transcription via a Cooperative Mechanism That May Confer Specificity to Neurotrophin Signals. Molecular and Cellular Neuroscience *6*, 168–183.

Böhme, G.A., Bon, C., Stutzmann, J.M., Doble, A., and Blanchard, J.C. (1991). Possible involvement of nitric oxide in long-term potentiation. Eur. J. Pharmacol. *199*, 379–381.

Bredt, D.S., and Snyder, S.H. (1990). Isolation of nitric oxide synthetase, a calmodulin-requiring enzyme. Proc. Natl. Acad. Sci. U.S.a. *87*, 682–685.

Bredt, D.S., and Snyder, S.H. (1994). Transient nitric oxide synthase neurons in embryonic

cerebral cortical plate, sensory ganglia, and olfactory epithelium. Neuron *13*, 301–313.

Bredt, D.S., Ferris, C.D., and Snyder, S.H. (1992). Nitric oxide synthase regulatory sites. Phosphorylation by cyclic AMP-dependent protein kinase, protein kinase C, and calcium/calmodulin protein kinase; identification of flavin and calmodulin binding sites. J. Biol. Chem. *267*, 10976–10981.

Brenman, J.E., Chao, D.S., Gee, S.H., McGee, A.W., Craven, S.E., Santillano, D.R., Wu, Z., Huang, F., Xia, H., Peters, M.F., et al. (1996a). Interaction of nitric oxide synthase with the postsynaptic density protein PSD-95 and alpha1-syntrophin mediated by PDZ domains. Cell *84*, 757–767.

Brenman, J.E., Christopherson, K.S., Craven, S.E., McGee, A.W., and Bredt, D.S. (1996b). Cloning and characterization of postsynaptic density 93, a nitric oxide synthase interacting protein. J. Neurosci. *16*, 7407–7415.

Briand, L.A., Lee, B.G., Lelay, J., Kaestner, K.H., and Blendy, J.A. (2015). Serine 133 phosphorylation is not required for hippocampal CREB-mediated transcription and behavior. Learn. Mem. *22*, 109–115.

Brüning, G., Wiese, S., and Mayer, B. (1994). Nitric oxide synthase in the brain of the turtle Pseudemys scripta elegans. J. Comp. Neurol. *348*, 183–206.

Burette, A., Zabel, U., Weinberg, R.J., Schmidt, H.H.H.W., and Valtschanoff, J.G. (2002). Synaptic localization of nitric oxide synthase and soluble guanylyl cyclase in the hippocampus. J. Neurosci. *22*, 8961–8970.

Buzas, B., Rosenberger, J., and Cox, B.M. (1998). Ca2+/calmodulin-dependent transcriptional activation of delta-opioid receptor gene expression induced by membrane depolarization in NG108-15 cells. J. Neurochem. *70*, 105–112.

Bystron, I., Blakemore, C., and Rakic, P. (2008). Development of the human cerebral cortex: Boulder Committee revisited. Nat. Rev. Neurosci. *9*, 110–122.

Cardinaux, J.R., Notis, J.C., Zhang, Q., Vo, N., Craig, J.C., Fass, D.M., Brennan, R.G., and Goodman, R.H. (2000). Recruitment of CREB binding protein is sufficient for CREB-mediated gene activation. Mol. Cell. Biol. *20*, 1546–1552.

Chen, Y.-J., Ku, W.-C., Lin, P.-Y., Chou, H.-C., Khoo, K.-H., and Chen, Y.-J. (2010). S-alkylating labeling strategy for site-specific identification of the s-nitrosoproteome. J. Proteome Res. *9*, 6417–6439.

Cho, D.-H., Nakamura, T., Fang, J., Cieplak, P., Godzik, A., Gu, Z., and Lipton, S.A. (2009). S-nitrosylation of Drp1 mediates beta-amyloid-related mitochondrial fission and neuronal injury. Science *324*, 102–105.

Chrivia, J.C., Kwok, R.P., Lamb, N., Hagiwara, M., Montminy, M.R., and Goodman, R.H. (1993). Phosphorylated CREB binds specifically to the nuclear protein CBP. Nature *365*, 855–859.

Collingridge, G.L., Peineau, S., Howland, J.G., and Wang, Y.T. (2010). Long-term depression in the CNS. Nat. Rev. Neurosci. *11*, 459–473.

Colussi, C., Mozzetta, C., Gurtner, A., Illi, B., Rosati, J., Straino, S., Ragone, G., Pescatori, M., Zaccagnini, G., Antonini, A., et al. (2008). HDAC2 blockade by nitric oxide and histone deacetylase inhibitors reveals a common target in Duchenne muscular dystrophy treatment. Proc. Natl. Acad. Sci. U.S.a. *105*, 19183–19187.

Cowley, S.M., Iritani, B.M., Mendrysa, S.M., Xu, T., Cheng, P.F., Yada, J., Liggitt, H.D., and Eisenman, R.N. (2005). The mSin3A chromatin-modifying complex is essential for

embryogenesis and T-cell development. Mol. Cell. Biol. *25*, 6990–7004.

Creekmore, A.L., Walt, K.A., Schultz-Norton, J.R., Ziegler, Y.S., McLeod, I.X., Yates, J.R., and Nardulli, A.M. (2008). The role of retinoblastoma-associated proteins 46 and 48 in estrogen receptor alpha mediated gene expression. Mol. Cell. Endocrinol. *291*, 79–86.

Crepaldi, L., Policarpi, C., Coatti, A., Sherlock, W.T., Jongbloets, B.C., Down, T.A., and Riccio, A. (2013). Binding of TFIIIC to sine elements controls the relocation of activity-dependent neuronal genes to transcription factories. PLoS Genet. *9*, e1003699.

Dailey, L., Caddle, M.S., Heintz, N., and Heintz, N.H. (1990). Purification of RIP60 and RIP100, mammalian proteins with origin-specific DNA-binding and ATP-dependent DNA helicase activities. Mol. Cell. Biol. *10*, 6225–6235.

Dannenberg, J.-H., David, G., Zhong, S., van der Torre, J., Wong, W.H., and Depinho, R.A. (2005). mSin3A corepressor regulates diverse transcriptional networks governing normal and neoplastic growth and survival. Genes Dev. *19*, 1581–1595.

Deak, M., Clifton, A.D., Lucocq, L.M., and Alessi, D.R. (1998). Mitogen- and stress-activated protein kinase-1 (MSK1) is directly activated by MAPK and SAPK2/p38, and may mediate activation of CREB. Embo J. *17*, 4426–4441.

Debril, M.-B., Gelman, L., Fayard, E., Annicotte, J.-S., Rocchi, S., and Auwerx, J. (2004). Transcription factors and nuclear receptors interact with the SWI/SNF complex through the BAF60c subunit. J. Biol. Chem. *279*, 16677–16686.

DeFelipe, J. (2011). The Evolution of the Brain, the Human Nature of Cortical Circuits, and Intellectual Creativity. Frontiers in Neuroanatomy *5*, 29.

Dehay, C., and Kennedy, H. (2007). Cell-cycle control and cortical development. Nat. Rev. Neurosci. *8*, 438–450.

Dejanovic, B., and Schwarz, G. (2014). Neuronal nitric oxide synthase-dependent S-nitrosylation of gephyrin regulates gephyrin clustering at GABAergic synapses. J. Neurosci. *34*, 7763–7768.

Doulias, P.-T., Greene, J.L., Greco, T.M., Tenopoulou, M., Seeholzer, S.H., Dunbrack, R.L., and Ischiropoulos, H. (2010). Structural profiling of endogenous S-nitrosocysteine residues reveals unique features that accommodate diverse mechanisms for protein S-nitrosylation. Proc. Natl. Acad. Sci. U.S.a. *107*, 16958–16963.

Doulias, P.-T., Tenopoulou, M., Raju, K., Spruce, L.A., Seeholzer, S.H., and Ischiropoulos, H. (2013). Site specific identification of endogenous S-nitrosocysteine proteomes. J Proteomics *92*, 195–203.

Doyle, C., Holscher, C., Rowan, M.J., and Anwyl, R. (1996). The selective neuronal NO synthase inhibitor 7-nitro-indazole blocks both long-term potentiation and depotentiation of field EPSPs in rat hippocampal CA1 in vivo. J. Neurosci. *16*, 418–424.

Drisaldi, B., Colnaghi, L., Fioriti, L., Rao, N., Myers, C., Snyder, A.M., Metzger, D.J., Tarasoff, J., Konstantinov, E., Fraser, P.E., et al. (2015). SUMOylation Is an Inhibitory Constraint that Regulates the Prion-like Aggregation and Activity of CPEB3. Cell Rep *11*, 1694–1702.

Dudek, S.M., and Bear, M.F. (1992). Homosynaptic long-term depression in area CA1 of hippocampus and effects of N-methyl-D-aspartate receptor blockade. Proc. Natl. Acad. Sci. U.S.a. *89*, 4363–4367.

Egan, C.M., Nyman, U., Skotte, J., Streubel, G., Turner, S., O'Connell, D.J., Rraklli, V., Dolan, M.J., Chadderton, N., Hansen, K., et al. (2013). CHD5 is required for neurogenesis and has a dual role in facilitating gene expression and polycomb gene repression. Dev. Cell *26*, 223–

236.

Ekerot, C.F., and Kano, M. (1985). Long-term depression of parallel fibre synapses following stimulation of climbing fibres. Brain Res. *342*, 357–360.

Eliasson, M.J., Blackshaw, S., Schell, M.J., and Snyder, S.H. (1997). Neuronal nitric oxide synthase alternatively spliced forms: prominent functional localizations in the brain. Proc. Natl. Acad. Sci. U.S.a. *94*, 3396–3401.

Eriksson, M., Taskinen, M., and Leppä, S. (2007). Mitogen activated protein kinase-dependent activation of c-Jun and c-Fos is required for neuronal differentiation but not for growth and stress response in PC12 cells. J. Cell. Physiol. *210*, 538–548.

Feelisch, M., and Martin, J.F. (1995). The early role of nitric oxide in evolution. Trends Ecol. Evol. (Amst.) *10*, 496–499.

Figueroa, X.F., Lillo, M.A., Gaete, P.S., Riquelme, M.A., and Sáez, J.C. (2013). Diffusion of nitric oxide across cell membranes of the vascular wall requires specific connexin-based channels. Neuropharmacology *75*, 471–478.

Filippakopoulos, P., and Knapp, S. (2014). Targeting bromodomains: epigenetic readers of lysine acetylation. Nat Rev Drug Discov *13*, 337–356.

Finkbeiner, S., Tavazoie, S.F., Maloratsky, A., Jacobs, K.M., Harris, K.M., and Greenberg, M.E. (1997). CREB: A Major Mediator of Neuronal Neurotrophin Responses. Neuron *19*, 1031–1047.

Finlay, B.L., and Darlington, R.B. (1995). Linked regularities in the development and evolution of mammalian brains. Science *268*, 1578–1584.

Fioriti, L., Myers, C., Huang, Y.-Y., Li, X., Stephan, J.S., Trifilieff, P., Colnaghi, L., Kosmidis, S., Drisaldi, B., Pavlopoulos, E., et al. (2015). The Persistence of Hippocampal-Based Memory Requires Protein Synthesis Mediated by the Prion-like Protein CPEB3. Neuron *86*, 1433–1448.

Fleming, I., and Busse, R. (2003). Molecular mechanisms involved in the regulation of the endothelial nitric oxide synthase. American Journal of Physiology - Regulatory, Integrative and Comparative Physiology *284*, R1–R12.

Flinker, A., Korzeniewska, A., Shestyuk, A.Y., Franaszczuk, P.J., Dronkers, N.F., Knight, R.T., and Crone, N.E. (2015). Redefining the role of Broca's area in speech. Proc. Natl. Acad. Sci. U.S.a. *112*, 2871–2875.

Florio, M., Albert, M., Taverna, E., Namba, T., Brandl, H., Lewitus, E., Haffner, C., Sykes, A., Wong, F.K., Peters, J., et al. (2015). Human-specific gene ARHGAP11B promotes basal progenitor amplification and neocortex expansion. Science *347*, 1465–1470.

Fong, H.K., Hurley, J.B., Hopkins, R.S., Miake-Lye, R., Johnson, M.S., Doolittle, R.F., and Simon, M.I. (1986). Repetitive segmental structure of the transducin beta subunit: homology with the CDC4 gene and identification of related mRNAs. Proc. Natl. Acad. Sci. U.S.a. *83*, 2162–2166.

Fontana, G., Fedele, E., Cossu, M., Munari, C., and Raiteri, M. (1997). Activation of brain nitric oxide synthase in depolarized human temporal cortex slices: differential role of voltage-sensitive calcium channels. Br. J. Pharmacol. *122*, 930–934.

Forrester, M.T., Foster, M.W., and Stamler, J.S. (2007). Assessment and application of the biotin switch technique for examining protein S-nitrosylation under conditions of pharmacologically induced oxidative stress. J. Biol. Chem. *282*, 13977–13983.

Forrester, M.T., Foster, M.W., Benhar, M., and Stamler, J.S. (2009a). Detection of protein S-nitrosylation with the biotin-switch technique. Free Radic. Biol. Med. *46*, 119–126.

Forrester, M.T., Thompson, J.W., Foster, M.W., Nogueira, L., Moseley, M.A., and Stamler, J.S. (2009b). Proteomic analysis of S-nitrosylation and denitrosylation by resin-assisted capture. Nat. Biotechnol. *27*, 557–559.

Foster, M.W. (2012). Methodologies for the characterization, identification and quantification of S-nitrosylated proteins. Biochim. Biophys. Acta *1820*, 675–683.

Foster, M.W., Forrester, M.T., and Stamler, J.S. (2009). A protein microarray-based analysis of S-nitrosylation. Proc. Natl. Acad. Sci. U.S.a. *106*, 18948–18953.

Förstermann, U., Pollock, J.S., Schmidt, H.H., Heller, M., and Murad, F. (1991). Calmodulin-dependent endothelium-derived relaxing factor/nitric oxide synthase activity is present in the particulate and cytosolic fractions of bovine aortic endothelial cells. Pnas *88*, 1788–1792.

Franco, M.C., Ye, Y., Refakis, C.A., Feldman, J.L., Stokes, A.L., Basso, M., Melero Fernández de Mera, R.M., Sparrow, N.A., Calingasan, N.Y., Kiaei, M., et al. (2013). Nitration of Hsp90 induces cell death. Proc. Natl. Acad. Sci. U.S.a. *110*, E1102–E1111.

Furchgott, R.F., Cherry, P.D., Zawadzki, J.V., and Jothianandan, D. (1984). Endothelial Cells as Mediators of Vasodilation of Arteries. Journal of Cardiovascular Pharmacology *6*, S336.

Garbossa, D., Fontanella, M., Tomasi, S., Ducati, A., and Vercelli, A. (2005). Differential distribution of NADPH-diaphorase histochemistry in human cerebral cortex. Brain Res. *1034*, 1–10.

Garcia-Higuera, I., Fenoglio, J., Li, Y., Lewis, C., Panchenko, M.P., Reiner, O., Smith, T.F., and Neer, E.J. (1996). Folding of Proteins with WD-Repeats: Comparison of Six Members of the WD-Repeat Superfamily to the G Protein β Subunit. Biochemistry *35*, 13985–13994.

Gareau, J.R., and Lima, C.D. (2010). The SUMO pathway: emerging mechanisms that shape specificity, conjugation and recognition. Nat. Rev. Mol. Cell Biol. *11*, 861–871.

Gautier, T., Bergès, T., Tollervey, D., and Hurt, E. (1997). Nucleolar KKE/D repeat proteins Nop56p and Nop58p interact with Nop1p and are required for ribosome biogenesis. Mol. Cell. Biol. *17*, 7088–7098.

Ghosh, A., Carnahan, J., and Greenberg, M.E. (1994a). Requirement for BDNF in activity-dependent survival of cortical neurons. Science *263*, 1618–1623.

Ghosh, A., Carnahan, J., and Greenberg, M.E. (1994b). Requirement for BDNF in activity-dependent survival of cortical neurons. Science *263*, 1618–1623.

Glass, D.J., Nye, S.H., Hantzopoulos, P., Macchi, M.J., Squinto, S.P., Goldfarb, M., and Yancopoulos, G.D. (1991). TrkB mediates BDNF/NT-3-dependent survival and proliferation in fibroblasts lacking the low affinity NGF receptor. Cell *66*, 405–413.

Gonzalez, G.A., and Montminy, M.R. (1989a). Cyclic AMP stimulates somatostatin gene transcription by phosphorylation of CREB at serine 133. Cell *59*, 675–680.

Gonzalez, G.A., Menzel, P., Leonard, J., Fischer, W.H., and Montminy, M.R. (1991). Characterization of motifs which are critical for activity of the cyclic AMP-responsive transcription factor CREB. Mol. Cell. Biol. *11*, 1306–1312.

Gonzalez, G.A., and Montminy, M.R. (1989b). Cyclic AMP stimulates somatostatin gene transcription by phosphorylation of CREB at serine 133. Cell *59*, 675–680.

Goren, I., Tavor, E., Goldblum, A., and Honigman, A. (2001). Two cysteine residues in the DNA-binding domain of CREB control binding to CRE and CREB-mediated gene expression. J. Mol. Biol. *313*, 695–709.

Gow, A.J., and Stamler, J.S. (1998). Reactions between nitric oxide and haemoglobin under physiological conditions. Nature *391*, 169–173.

Gow, A.J., Chen, Q., Hess, D.T., Day, B.J., Ischiropoulos, H., and Stamler, J.S. (2002). Basal and stimulated protein S-nitrosylation in multiple cell types and tissues. J. Biol. Chem. *277*, 9637–9640.

Gräff, J., Joseph, N.F., Horn, M.E., Samiei, A., Meng, J., Seo, J., Rei, D., Bero, A.W., Phan, T.X., Wagner, F., et al. (2014). Epigenetic priming of memory updating during reconsolidation to attenuate remote fear memories. Cell *156*, 261–276.

Greco, T.M., Hodara, R., Parastatidis, I., Heijnen, H.F.G., Dennehy, M.K., Liebler, D.C., and Ischiropoulos, H. (2006). Identification of S-nitrosylation motifs by site-specific mapping of the S-nitrosocysteine proteome in human vascular smooth muscle cells. Proc. Natl. Acad. Sci. U.S.a. *103*, 7420–7425.

Greenberg, M.E., Ziff, E.B., and Greene, L.A. (1986). Stimulation of neuronal acetylcholine receptors induces rapid gene transcription. Science *234*, 80–83.

Grunstein, M. (1990). Histone function in transcription. Annu. Rev. Cell Biol. *6*, 643–678.

Gu, Z., Kaul, M., Yan, B., Kridel, S.J., Cui, J., Strongin, A., Smith, J.W., Liddington, R.C., and Lipton, S.A. (2002). S-Nitrosylation of Matrix Metalloproteinases: Signaling Pathway to Neuronal Cell Death. Science *297*, 1186–1190.

Guan, L.S., Rauchman, M., and Wang, Z.Y. (1998). Induction of Rb-associated protein (RbAp46) by Wilms' tumor suppressor WT1 mediates growth inhibition. J. Biol. Chem. *273*, 27047–27050.

Gubbay, O., Rae, M.T., McNeilly, A.S., Donadeu, F.X., Zeleznik, A.J., and Hillier, S.G. (2006). cAMP response element-binding (CREB) signalling and ovarian surface epithelial cell survival. J. Endocrinol. *191*, 275–285.

Guo, J.U., Ma, D.K., Mo, H., Ball, M.P., Jang, M.-H., Bonaguidi, M.A., Balazer, J.A., Eaves, H.L., Xie, B., Ford, E., et al. (2011). Neuronal activity modifies the DNA methylation landscape in the adult brain. Nat. Neurosci. *14*, 1345–1351.

Gupta, A., Tsai, L.-H., and Wynshaw-Boris, A. (2002). Life is a journey: a genetic look at neocortical development. Nat. Rev. Genet. *3*, 342–355.

Gyurko, R., Leupen, S., and Huang, P.L. (2002). Deletion of exon 6 of the neuronal nitric oxide synthase gene in mice results in hypogonadism and infertility. Endocrinology *143*, 2767–2774.

Ha, J.H., Ward, J.D., Varadarajalu, L., Kim, S.G., and Dhanasekaran, D.N. (2014). The gep proto-oncogene Gα12 mediates LPA-stimulated activation of CREB in ovarian cancer cells. Cellular Signalling *26*, 122–132.

Haddad, I.Y., Pataki, G., Hu, P., Galliani, C., Beckman, J.S., and Matalon, S. (1994). Quantitation of nitrotyrosine levels in lung sections of patients and animals with acute lung injury. J. Clin. Invest. *94*, 2407–2413.

Hao, G., Derakhshan, B., Shi, L., Campagne, F., and Gross, S.S. (2006). SNOSID, a proteomic method for identification of cysteine S-nitrosylation sites in complex protein mixtures. Proc. Natl. Acad. Sci. U.S.a. *103*, 1012–1017.

Hara, M.R., Agrawal, N., Kim, S.F., Cascio, M.B., Fujimuro, M., Ozeki, Y., Takahashi, M., Cheah, J.H., Tankou, S.K., Hester, L.D., et al. (2005). S-nitrosylated GAPDH initiates apoptotic cell death by nuclear translocation following Siah1 binding. Nat. Cell Biol. *7*, 665–674.

Hasan, M.T., Hernández-González, S., Dogbevia, G., Treviño, M., Bertocchi, I., Gruart, A., and Delgado-García, J.M. (2013). Role of motor cortex NMDA receptors in learning-dependent synaptic plasticity of behaving mice. Nat Commun *4*.

Haun, F., Nakamura, T., Shiu, A.D., Cho, D.-H., Tsunemi, T., Holland, E.A., La Spada, A.R., and Lipton, S.A. (2013). S-nitrosylation of dynamin-related protein 1 mediates mutant huntingtin-induced mitochondrial fragmentation and neuronal injury in Huntington's disease. Antioxid. Redox Signal. *19*, 1173–1184.

Hausladen, A., Privalle, C.T., Keng, T., DeAngelo, J., and Stamler, J.S. (1996). Nitrosative stress: activation of the transcription factor OxyR. Cell *86*, 719–729.

Henriquez, B., Bustos, F.J., Aguilar, R., Becerra, A., Simon, F., Montecino, M., and van Zundert, B. (2013). Ezh1 and Ezh2 differentially regulate PSD-95 gene transcription in developing hippocampal neurons. Mol. Cell. Neurosci. *57*, 130–143.

Herrera, M., Hong, N.J., and Garvin, J.L. (2006). Aquaporin-1 transports NO across cell membranes. Hypertension *48*, 157–164.

Hess, D.T., Matsumoto, A., Kim, S.-O., Marshall, H.E., and Stamler, J.S. (2005). Protein S-nitrosylation: purview and parameters. Nat. Rev. Mol. Cell Biol. *6*, 150–166.

Ho, G.P.H., Selvakumar, B., Mukai, J., Hester, L.D., Wang, Y., Gogos, J.A., and Snyder, S.H. (2011a). S-nitrosylation and S-palmitoylation reciprocally regulate synaptic targeting of PSD-95. Neuron *71*, 131–141.

Ho, L., Jothi, R., Ronan, J.L., Cui, K., Zhao, K., and Crabtree, G.R. (2009). An embryonic stem cell chromatin remodeling complex, esBAF, is an essential component of the core pluripotency transcriptional network. Proc. Natl. Acad. Sci. U.S.a. *106*, 5187–5191.

Ho, L., Miller, E.L., Ronan, J.L., Ho, W.Q., Jothi, R., and Crabtree, G.R. (2011b). esBAF facilitates pluripotency by conditioning the genome for LIF/STAT3 signalling and by regulating polycomb function. Nat. Cell Biol. *13*, 903–913.

Hong, L., Schroth, G.P., Matthews, H.R., Yau, P., and Bradbury, E.M. (1993). Studies of the DNA binding properties of histone H4 amino terminus. Thermal denaturation studies reveal that acetylation markedly reduces the binding constant of the H4 “tail” to DNA. J. Biol. Chem. *268*, 305–314.

Huang, B., Liao, C.L., Lin, Y.P., Chen, S.C., and Wang, D.L. (2009). S-nitrosoproteome in endothelial cells revealed by a modified biotin switch approach coupled with Western blot-based two-dimensional gel electrophoresis. J. Proteome Res. *8*, 4835–4843.

Huang, E.J., and Reichardt, L.F. (2003). Trk receptors: roles in neuronal signal transduction. Annu. Rev. Biochem. *72*, 609–642.

Huang, P.L., Dawson, T.M., Bredt, D.S., Snyder, S.H., and Fishman, M.C. (1993). Targeted disruption of the neuronal nitric oxide synthase gene. Cell *75*, 1273–1286.

Huang, Z., Huang, P.L., Panahian, N., Dalkara, T., Fishman, M.C., and Moskowitz, M.A. (1994). Effects of cerebral ischemia in mice deficient in neuronal nitric oxide synthase. Science *265*, 1883–1885.

Hunot, S., Boissiere, F., Faucheux, B., Brugg, B., Mouatt-Prigent, A., Agid, Y., and Hirsch, E.C. (1996). Nitric oxide synthase and neuronal vulnerability in parkinson's disease.

Neuroscience *72*, 355–363.

Ignarro, L.J., Byrns, R.E., Buga, G.M., and Wood, K.S. (1987). Endothelium-derived relaxing factor from pulmonary artery and vein possesses pharmacologic and chemical properties identical to those of nitric oxide radical. Circ. Res. *61*, 866–879.

Ignarro, L.J., Edwards, J.C., Gruetter, D.Y., Barry, B.K., and Gruetter, C.A. (1979). Possible involvement of S-nitrosothiols in the activation of guanylate cyclase by nitroso compounds. FEBS Lett. *110*, 275–278.

Ihara, H., Kuwamura, M., Atsuta, M., Nihonmatsu, I., Okada, T., Mukamoto, M., and Kozaki, S. (2006). Expression of neuronal nitric oxide synthase variant, nNOS-mu, in rat brain. Nitric Oxide *15*, 13–19.

Ito, M. (2001). Cerebellar long-term depression: characterization, signal transduction, and functional roles. Physiol. Rev. *81*, 1143–1195.

Ivaldi, M.S., Karam, C.S., and Corces, V.G. (2007). Phosphorylation of histone H3 at Ser10 facilitates RNA polymerase II release from promoter-proximal pausing in Drosophila. Genes Dev. *21*, 2818–2831.

Jacobs, A.T., and Ignarro, L.J. (2001). Lipopolysaccharide-induced expression of interferon-beta mediates the timing of inducible nitric-oxide synthase induction in RAW 264.7 macrophages. J. Biol. Chem. *276*, 47950–47957.

Jia, J., Arif, A., Terenzi, F., Willard, B., Plow, E.F., Hazen, S.L., and Fox, P.L. (2014). Target-selective protein S-nitrosylation by sequence motif recognition. Cell *159*, 623–634.

Jinno, S., and Kosaka, T. (2002). Patterns of expression of calcium binding proteins and neuronal nitric oxide synthase in different populations of hippocampal GABAergic neurons in mice. J. Comp. Neurol. *449*, 1–25.

Johannessen, M., Delghandi, M.P., and Moens, U. (2004). What turns CREB on? Cellular Signalling *16*, 1211–1227.

Johnston, H. (1971). Reduction of stratospheric ozone by nitrogen oxide catalysts from supersonic transport exhaust. Science *173*, 517–522.

Jüch, M., Smalla, K.-H., Kähne, T., Lubec, G., Tischmeyer, W., Gundelfinger, E.D., and Engelmann, M. (2009). Congenital lack of nNOS impairs long-term social recognition memory and alters the olfactory bulb proteome. Neurobiol Learn Mem *92*, 469–484.

Kakiuchi, S., and Rall, T.W. (1968). The influence of chemical agents on the accumulation of adenosine 3“,5-”Phosphate in slices of rabbit cerebellum. Mol. Pharmacol. *4*, 367–378.

Kaneko, R., and Wada, Y. (2003). Decomposition of protein nitrosothiolsin matrix-assisted laser desorption/ionization and electrospray ionization mass spectrometry. J. Mass Spectrom. *38*, 526–530.

Katsuki, S., Arnold, W.P., and Murad, F. (1977a). Effects of sodium nitroprusside, nitroglycerin, and sodium azide on levels of cyclic nucleotides and mechanical activity of various tissues. J Cyclic Nucleotide Res *3*, 239–247.

Katsuki, S., Arnold, W., Mittal, C., and Murad, F. (1977b). Stimulation of guanylate cyclase by sodium nitroprusside, nitroglycerin and nitric oxide in various tissue preparations and comparison to the effects of sodium azide and hydroxylamine. J Cyclic Nucleotide Res *3*, 23–35.

Kaur, H., and Halliwell, B. (1994). Evidence for nitric oxide-mediated oxidative damage in chronic inflammation. Nitrotyrosine in serum and synovial fluid from rheumatoid patients.

FEBS Lett. *350*, 9–12.

Käll, L., Canterbury, J.D., Weston, J., Noble, W.S., and MacCoss, M.J. (2007). Semi-supervised learning for peptide identification from shotgun proteomics datasets. Nat. Methods *4*, 923–925.

Kehle, J., Beuchle, D., Treuheit, S., Christen, B., Kennison, J.A., Bienz, M., and Müller, J. (1998). dMi-2, a hunchback-interacting protein that functions in polycomb repression. Science *282*, 1897–1900.

Kelleher, Z.T., Potts, E.N., Brahmajothi, M.V., Foster, M.W., Auten, R.L., Foster, W.M., and Marshall, H.E. (2011). NOS2 regulation of LPS-induced airway inflammation via S-nitrosylation of NF-{kappa}B p65. Am. J. Physiol. Lung Cell Mol. Physiol. *301*, L327–L333.

Kelleher, Z.T., Sha, Y., Foster, M.W., Foster, W.M., Forrester, M.T., and Marshall, H.E. (2014). Thioredoxin-mediated denitrosylation regulates cytokine-induced nuclear factor κB (NF-κB) activation. J. Biol. Chem. *289*, 3066–3072.

Kelley, J.B., Balda, M.A., Anderson, K.L., and Itzhak, Y. (2009). Impairments in fear conditioning in mice lacking the nNOS gene. Learn. Mem. *16*, 371–378.

Kim, S.F., Huri, D.A., and Snyder, S.H. (2005). Inducible nitric oxide synthase binds, S-nitrosylates, and activates cyclooxygenase-2. Science *310*, 1966–1970.

Kim, T.-K., Hemberg, M., Gray, J.M., Costa, A.M., Bear, D.M., Wu, J., Harmin, D.A., Laptewicz, M., Barbara-Haley, K., Kuersten, S., et al. (2010). Widespread transcription at neuronal activity-regulated enhancers. Nature *465*, 182–187.

Kleinert, H., Pautz, A., Linker, K., and Schwarz, P.M. (2004). Regulation of the expression of inducible nitric oxide synthase. Eur. J. Pharmacol. *500*, 255–266.

Klingberg, R., Jost, J.O., Schümann, M., Gelato, K.A., Fischle, W., Krause, E., and Schwarzer, D. (2015). Analysis of phosphorylation-dependent protein-protein interactions of histone h3. ACS Chem. Biol. *10*, 138–145.

Kloet, S.L., Baymaz, H.I., Makowski, M., Groenewold, V., Jansen, P.W.T.C., Berendsen, M., Niazi, H., Kops, G.J., and Vermeulen, M. (2015). Towards elucidating the stability, dynamics and architecture of the nucleosome remodeling and deacetylase complex by using quantitative interaction proteomics. Febs J. *282*, 1774–1785.

Kneeshaw, S., Gelineau, S., Tada, Y., Loake, G.J., and Spoel, S.H. (2014). Selective Protein Denitrosylation Activity of Thioredoxin-h5 Modulates Plant Immunity. Mol. Cell *56*, 153–162.

Knock, E., Pereira, J., Lombard, P.D., Dimond, A., Leaford, D., Livesey, F.J., and Hendrich, B. (2015). The methyl binding domain 3/nucleosome remodelling and deacetylase complex regulates neural cell fate determination and terminal differentiation in the cerebral cortex. Neural Dev *10*, 1–20.

Kohr, M.J., Aponte, A.M., Sun, J., Wang, G., Murphy, E., Gucek, M., and Steenbergen, C. (2011). Characterization of potential S-nitrosylation sites in the myocardium. Am. J. Physiol. Heart Circ. Physiol. *300*, H1327–H1335.

Kohr, M.J., Aponte, A., Sun, J., Gucek, M., Steenbergen, C., and Murphy, E. (2012). Measurement of S-nitrosylation occupancy in the myocardium with cysteine-reactive tandem mass tags: short communication. Circ. Res. *111*, 1308–1312.

Kornberg, M.D., Sen, N., Hara, M.R., Juluri, K.R., Nguyen, J.V.K., Snowman, A.M., Law, L., Hester, L.D., and Snyder, S.H. (2010). GAPDH mediates nitrosylation of nuclear proteins. Nat. Cell Biol. *12*, 1094–1100.

Kornberg, R.D. (1974). Chromatin structure: a repeating unit of histones and DNA. Science *184*, 868–871.

Kornhauser, J.M., Cowan, C.W., Shaywitz, A.J., Dolmetsch, R.E., Griffith, E.C., Hu, L.S., Haddad, C., Xia, Z., and Greenberg, M.E. (2002a). CREB transcriptional activity in neurons is regulated by multiple, calcium-specific phosphorylation events. Neuron *34*, 221–233.

Kornhauser, J.M., Cowan, C.W., Shaywitz, A.J., Dolmetsch, R.E., Griffith, E.C., Hu, L.S., Haddad, C., Xia, Z., and Greenberg, M.E. (2002b). CREB Transcriptional Activity in Neurons Is Regulated by Multiple, Calcium-Specific Phosphorylation Events. Neuron *34*, 221–233.

Kouzarides, T. (2007). Chromatin modifications and their function. Cell *128*, 693–705.

Kriegsfeld, L.J., Eliasson, M.J., Demas, G.E., Blackshaw, S., Dawson, T.M., Nelson, R.J., and Snyder, S.H. (1999). Nocturnal motor coordination deficits in neuronal nitric oxide synthase knock-out mice. Neuroscience *89*, 311–315.

Kröncke, K.D. (2001). Zinc finger proteins as molecular targets for nitric oxide-mediated gene regulation. Antioxid. Redox Signal. *3*, 565–575.

Kubota, Y., and Kawaguchi, Y. (1994). Three classes of GABAergic interneurons in neocortex and neostriatum. Jpn J Physiol *44 Suppl 2*, S145–S148.

Kuncewicz, T., Sheta, E.A., Goldknopf, I.L., and Kone, B.C. (2003). Proteomic analysis of S-nitrosylated proteins in mesangial cells. Mol. Cell Proteomics *2*, 156–163.

Kwiecień, I., Sokołowska, M., Luchter-Wasylewska, E., and Włodek, L. (2003). Inhibition of the catalytic activity of rhodanese by S-nitrosylation using nitric oxide donors. Int. J. Biochem. Cell Biol. *35*, 1645–1657.

Kwon, M., Fernández, J.R., Zegarek, G.F., Lo, S.B., and Firestein, B.L. (2011). BDNF-promoted increases in proximal dendrites occur via CREB-dependent transcriptional regulation of cypin. J. Neurosci. *31*, 9735–9745.

Lam, Y.W., Yuan, Y., Isaac, J., Babu, C.V.S., Meller, J., and Ho, S.-M. (2010). Comprehensive Identification and Modified-Site Mapping of S- Nitrosylated Targets in Prostate Epithelial Cells. PLoS ONE *5*, e9075.

Lamas, S., Marsden, P.A., Li, G.K., Tempst, P., and Michel, T. (1992). Endothelial nitric oxide synthase: molecular cloning and characterization of a distinct constitutive enzyme isoform. Pnas *89*, 6348–6352.

Landschulz, W.H., Johnson, P.F., and McKnight, S.L. (1989). The DNA binding domain of the rat liver nuclear protein C/EBP is bipartite. Science *243*, 1681–1688.

Lange, M.D., Doengi, M., Lesting, J., Pape, H.C., and Jüngling, K. (2012). Heterosynaptic long-term potentiation at interneuron-principal neuron synapses in the amygdala requires nitric oxide signalling. The Journal of Physiology *590*, 131–143.

Lantin-Hermoso, R.L., Rosenfeld, C.R., Yuhanna, I.S., German, Z., Chen, Z., and Shaul, P.W. (1997). Estrogen acutely stimulates nitric oxide synthase activity in fetal pulmonary artery endothelium. Am. J. Physiol. *273*, L119–L126.

Larson, E.B., Graham, D.L., Arzaga, R.R., Buzin, N., Webb, J., Green, T.A., Bass, C.E., Neve, R.L., Terwilliger, E.F., Nestler, E.J., et al. (2011). Overexpression of CREB in the nucleus accumbens shell increases cocaine reinforcement in self-administering rats. J. Neurosci. *31*, 16447–16457.

Lee, P.-W., and Lee, Y.-M. (2003). Transcriptional regulation of mu opioid receptor gene by cAMP pathway. Mol. Pharmacol. *64*, 1410–1418.

Lee, S.B., Kim, C.K., Lee, K.-H., and Ahn, J.-Y. (2012). S-nitrosylation of B23/nucleophosmin by GAPDH protects cells from the SIAH1-GAPDH death cascade. J. Cell Biol. *199*, 65–76.

Lee, S.J., Lee, J.R., Kim, Y.H., Park, Y.S., Park, S.I., Park, H.S., and Kim, K.P. (2007). Investigation of tyrosine nitration and nitrosylation of angiotensin II and bovine serum albumin with electrospray ionization mass spectrometry. Rapid Commun. Mass Spectrom. *21*, 2797–2804.

Lee, T.-Y., Chen, Y.-J., Lu, T.-C., Huang, H.-D., and Chen, Y.-J. (2011). SNOSite: exploiting maximal dependence decomposition to identify cysteine S-nitrosylation with substrate site specificity. PLoS ONE *6*, e21849.

Leppä, S., Eriksson, M., Saffrich, R., Ansorge, W., and Bohmann, D. (2001). Complex functions of AP-1 transcription factors in differentiation and survival of PC12 cells. Mol. Cell. Biol. *21*, 4369–4378.

Lev-Ram, V., Nebyelul, Z., Ellisman, M.H., Huang, P.L., and Tsien, R.Y. (1997). Absence of cerebellar long-term depression in mice lacking neuronal nitric oxide synthase. Learn. Mem. *4*, 169–177.

Li, B.-Q., Hu, L.-L., Niu, S., Cai, Y.-D., and Chou, K.-C. (2012). Predict and analyze S-nitrosylation modification sites with the mRMR and IFS approaches. J Proteomics *75*, 1654–1665.

Li, H., Gu, X., Dawson, V.L., and Dawson, T.M. (2004). Identification of calcium- and nitric oxide-regulated genes by differential analysis of library expression (DAzLE). Proc. Natl. Acad. Sci. U.S.a. *101*, 647–652.

Li, Z., Wang, Y., Yao, Q., Justice, N.B., Ahn, T.-H., Xu, D., Hettich, R.L., Banfield, J.F., and Pan, C. (2014). Diverse and divergent protein post-translational modifications in two growth stages of a natural microbial community. Nat Commun *5*, 4405.

Liberatore, G.T., Jackson-Lewis, V., Vukosavic, S., Mandir, A.S., Vila, M., McAuliffe, W.G., Dawson, V.L., Dawson, T.M., and Przedborski, S. (1999). Inducible nitric oxide synthase stimulates dopaminergic neurodegeneration in the MPTP model of Parkinson disease. Nat. Med. *5*, 1403–1409.

Lipton, S.A., Choi, Y.B., Pan, Z.H., Lei, S.Z., Chen, H.S., Sucher, N.J., Loscalzo, J., Singel, D.J., and Stamler, J.S. (1993). A redox-based mechanism for the neuroprotective and neurodestructive effects of nitric oxide and related nitroso-compounds. Nature *364*, 626–632.

Liu, L., Hausladen, A., Zeng, M., Que, L., Heitman, J., and Stamler, J.S. (2001). A metabolic enzyme for S-nitrosothiol conserved from bacteria to humans. Nature *410*, 490–494.

Lomo, T. (1966). Frequency potentiation of excitatory synaptic activity in dentate area of hippocampal formation (Acta Physiologica Scandinavica).

Lonze, B.E., and Ginty, D.D. (2002). Function and regulation of CREB family transcription factors in the nervous system. Neuron *35*, 605–623.

Lorès, P., Visvikis, O., Luna, R., Lemichez, E., and Gacon, G. (2010). The SWI/SNF protein BAF60b is ubiquitinated through a signalling process involving Rac GTPase and the RING finger protein Unkempt. Febs J. *277*, 1453–1464.

Luchsinger, B.P., Rich, E.N., Gow, A.J., Williams, E.M., Stamler, J.S., and Singel, D.J. (2003). Routes to S-nitroso-hemoglobin formation with heme redox and preferential reactivity in the beta subunits. Pnas *100*, 461–466.

Luo, Q., Viste, K., Urday-Zaa, J.C., Senthil Kumar, G., Tsai, W.-W., Talai, A., Mayo, K.E., Montminy, M., and Radhakrishnan, I. (2012). Mechanism of CREB recognition and

coactivation by the CREB-regulated transcriptional coactivator CRTC2. Proc. Natl. Acad. Sci. U.S.a. *109*, 20865–20870.

Lynch, M.A. (2004). Long-Term Potentiation and Memory. Physiol. Rev. *84*, 87–136.

Malik, A., and Tauler, R. (2015). Exploring the interaction between O_3 and NOx pollution patterns in the atmosphere of Barcelona, Spain using the MCR-ALS method. Sci. Total Environ. *517*, 151–161.

Malik, A.N., Vierbuchen, T., Hemberg, M., Rubin, A.A., Ling, E., Couch, C.H., Stroud, H., Spiegel, I., Farh, K.K.-H., Harmin, D.A., et al. (2014). Genome-wide identification and characterization of functional neuronal activity-dependent enhancers. Nat. Neurosci. *17*, 1330–1339.

Mallis, R.J., Buss, J.E., and Thomas, J.A. (2001). Oxidative modification of H-ras: S-thiolation and S-nitrosylation of reactive cysteines. Biochem. J. *355*, 145–153.

Mannick, J.B., Hausladen, A., Liu, L., Hess, D.T., Zeng, M., Miao, Q.X., Kane, L.S., Gow, A.J., and Stamler, J.S. (1999). Fas-Induced Caspase Denitrosylation. Science *284*, 651–654.

Mantamadiotis, T., Lemberger, T., Bleckmann, S.C., Kern, H., Kretz, O., Martin Villalba, A., Tronche, F., Kellendonk, C., Gau, D., Kapfhammer, J., et al. (2002). Disruption of CREB function in brain leads to neurodegeneration. Nat. Genet. *31*, 47–54.

Marino, S.M., and Gladyshev, V.N. (2010). Structural analysis of cysteine S-nitrosylation: a modified acid-based motif and the emerging role of trans-nitrosylation. J. Mol. Biol. *395*, 844–859.

Marino, S.M., and Gladyshev, V.N. (2012). Analysis and functional prediction of reactive cysteine residues. J. Biol. Chem. *287*, 4419–4425.

Marshall, I.C., and Wilson, K.L. (1997). Nuclear envelope assembly after mitosis. Trends Cell Biol. *7*, 69–74.

Martínez-Balbás, M.A., Tsukiyama, T., Gdula, D., and Wu, C. (1998). Drosophila NURF-55, a WD repeat protein involved in histone metabolism. Proc. Natl. Acad. Sci. U.S.a. *95*, 132–137.

Martynoga, B., Drechsel, D., and Guillemot, F. (2012). Molecular control of neurogenesis: a view from the mammalian cerebral cortex. Cold Spring Harb Perspect Biol *4*, a008359–a008359.

Mayr, B.M., Guzman, E., and Montminy, M. (2005). Glutamine rich and basic region/leucine zipper (bZIP) domains stabilize cAMP-response element-binding protein (CREB) binding to chromatin. J. Biol. Chem. *280*, 15103–15110.

McDonel, P., Demmers, J., Tan, D.W.M., Watt, F., and Hendrich, B.D. (2012). Sin3a is essential for the genome integrity and viability of pluripotent cells. Dev. Biol. *363*, 62–73.

McNally, J.G., Müller, W.G., Walker, D., Wolford, R., and Hager, G.L. (2000). The glucocorticoid receptor: rapid exchange with regulatory sites in living cells. Science *287*, 1262–1265.

Miccio, A., Wang, Y., Hong, W., Gregory, G.D., Wang, H., Yu, X., Choi, J.K., Shelat, S., Tong, W., Poncz, M., et al. (2010). NuRD mediates activating and repressive functions of GATA-1 and FOG-1 during blood development. Embo J. *29*, 442–456.

Migliori, V., Müller, J., Phalke, S., Low, D., Bezzi, M., Mok, W.C., Sahu, S.K., Gunaratne, J., Capasso, P., Bassi, C., et al. (2012). Symmetric dimethylation of H3R2 is a newly identified histone mark that supports euchromatin maintenance. Nat. Struct. Mol. Biol. *19*, 136–144.

Mirza, U.A., Chait, B.T., and Lander, H.M. (1995). Monitoring Reactions of Nitric Oxide with Peptides and Proteins by Electrospray Ionization-Mass Spectrometry. J. Biol. Chem. *270*, 17185–17188.

Mohn, F., Weber, M., Rebhan, M., Roloff, T.C., Richter, J., Stadler, M.B., Bibel, M., and Schübeler, D. (2008). Lineage-specific polycomb targets and de novo DNA methylation define restriction and potential of neuronal progenitors. Mol. Cell *30*, 755–766.

Moncada, S., Palmer, R.M., and Higgs, E.A. (1991). Nitric oxide: physiology, pathophysiology, and pharmacology. Pharmacol Rev *43*, 109–142.

Morgan, J.I., and Curran, T. (1986). Role of ion flux in the control of c-fos expression. Nature *322*, 552–555.

Morse, R.H. (1989). Nucleosomes inhibit both transcriptional initiation and elongation by RNA polymerase III in vitro. Embo J. *8*, 2343–2351.

Murray, C.I., Uhrigshardt, H., O'Meally, R.N., Cole, R.N., and Van Eyk, J.E. (2012). Identification and quantification of S-nitrosylation by cysteine reactive tandem mass tag switch assay. Mol. Cell Proteomics *11*, M111.013441–M111.013441.

Murzina, N.V., Pei, X.-Y., Zhang, W., Sparkes, M., Vicente-Garcia, J., Pratap, J.V., McLaughlin, S.H., Ben-Shahar, T.R., Verreault, A., Luisi, B.F., et al. (2008). Structural Basis for the Recognition of Histone H4 by the Histone-Chaperone RbAp46. Structure *16*, 1077–1085.

Nabavi, S., Fox, R., Proulx, C.D., Lin, J.Y., Tsien, R.Y., and Malinow, R. (2014). Engineering a memory with LTD and LTP. Nature *511*, 348–352.

Nadarajah, B., and Parnavelas, J.G. (2002). Modes of neuronal migration in the developing cerebral cortex. Nat. Rev. Neurosci. *3*, 423–432.

Nair, S.S., Li, D.-Q., and Kumar, R. (2013). A Core Chromatin Remodeling Factor Instructs Global Chromatin Signaling through Multivalent Reading of Nucleosome Codes. Mol. Cell *49*, 704–718.

Nakajima, T., Uchida, C., Anderson, S.F., Parvin, J.D., and Montminy, M. (1997). Analysis of a cAMP-responsive activator reveals a two-component mechanism for transcriptional induction via signal-dependent factors. Genes Dev. *11*, 738–747.

Nakamura, T., and Lipton, S.A. (2013). Emerging role of protein-protein transnitrosylation in cell signaling pathways. Antioxid. Redox Signal. *18*, 239–249.

Narlikar, G.J., Sundaramoorthy, R., and Owen-Hughes, T. (2013). Mechanisms and functions of ATP-dependent chromatin-remodeling enzymes. Cell *154*, 490–503.

Nascimento, E.M., Cox, C.L., MacArthur, S., Hussain, S., Trotter, M., Blanco, S., Suraj, M., Nichols, J., Kübler, B., Benitah, S.A., et al. (2011). The opposing transcriptional functions of Sin3a and c-Myc are required to maintain tissue homeostasis. Nat. Cell Biol. *13*, 1395–1405.

Nedospasov, A., Rafikov, R., Beda, N., and Nudler, E. (2000). An autocatalytic mechanism of protein nitrosylation. Proc. Natl. Acad. Sci. U.S.a. *97*, 13543–13548.

Nikitovic, D., Holmgren, A., and Spyrou, G. (1998). Inhibition of AP-1 DNA binding by nitric oxide involving conserved cysteine residues in Jun and Fos. Biochem. Biophys. Res. Commun. *242*, 109–112.

Northcutt, R.G. (1981). Evolution of the telencephalon in nonmammals. Annu. Rev. Neurosci. *4*, 301–350.

Norton, V.G., Imai, B.S., Yau, P., and Bradbury, E.M. (1989). Histone acetylation reduces nucleosome core particle linking number change. Cell *57*, 449–457.

Nott, A., Nitarska, J., Veenvliet, J.V., Schacke, S., Derijck, A.A.H.A., Sirko, P., Muchardt, C., Pasterkamp, R.J., Smidt, M.P., and Riccio, A. (2013). S-nitrosylation of HDAC2 regulates the expression of the chromatin-remodeling factor Brm during radial neuron migration. Proc. Natl. Acad. Sci. U.S.a. *110*, 3113–3118.

Nott, A., Watson, P.M., Robinson, J.D., Crepaldi, L., and Riccio, A. (2008). S-Nitrosylation of histone deacetylase 2 induces chromatin remodelling in neurons. Nature *455*, 411–415.

O'Shea, E.K., Klemm, J.D., Kim, P.S., and Alber, T. (1991). X-ray structure of the GCN4 leucine zipper, a two-stranded, parallel coiled coil. Science *254*, 539–544.

Oae, S., Kim, Y.H., Fukushima, D., and Shinhama, K. (1978). New syntheses of thionitrites and their chemical reactivites. Journal of the Chemical Society, Perkin Transactions 1 *0*, 913–917.

Okamoto, S.-I., Nakamura, T., Cieplak, P., Chan, S.F., Kalashnikova, E., Liao, L., Saleem, S., Han, X., Clemente, A., Nutter, A., et al. (2014). S-nitrosylation-mediated redox transcriptional switch modulates neurogenesis and neuronal cell death. Cell Rep *8*, 217–228.

Olave, I., Wang, W., Xue, Y., Kuo, A., and Crabtree, G.R. (2002). Identification of a polymorphic, neuron-specific chromatin remodeling complex. Genes Dev. *16*, 2509–2517.

Palmer, R.M.J., Ashton, D.S., and Moncada, S. (1988). Vascular endothelial cells synthesize nitric oxide from L-arginine. , Published Online: 16 June 1988; | Doi:10.1038/333664a0 *333*, 664–666.

Palmer, R.M.J., Ferrige, A.G., and Moncada, S. (1987). Nitric oxide release accounts for the biological activity of endothelium-derived relaxing factor. , Published Online: 11 June 1987; | Doi:10.1038/327524a0 *327*, 524–526.

Park, H., and Poo, M.-M. (2013). Neurotrophin regulation of neural circuit development and function. Nat. Rev. Neurosci. *14*, 7–23.

Park, S.Y., Kim, J.B., and Han, Y.-M. (2007). REST is a key regulator in brain-specific homeobox gene expression during neuronal differentiation. J. Neurochem. *103*, 2565–2574.

Parker, D., Ferreri, K., Nakajima, T., LaMorte, V.J., Evans, R., Koerber, S.C., Hoeger, C., and Montminy, M.R. (1996). Phosphorylation of CREB at Ser-133 induces complex formation with CREB-binding protein via a direct mechanism. Mol. Cell. Biol. *16*, 694–703.

Pavesi, E., Heldt, S.A., and Fletcher, M.L. (2013). Neuronal nitric-oxide synthase deficiency impairs the long-term memory of olfactory fear learning and increases odor generalization. Learn. Mem. *20*, 482–490.

Pengelly, A.R., Copur, Ö., Jäckle, H., Herzig, A., and Müller, J. (2013). A histone mutant reproduces the phenotype caused by loss of histone-modifying factor Polycomb. Science *339*, 698–699.

Pereira, J.D., Sansom, S.N., Smith, J., Dobenecker, M.-W., Tarakhovsky, A., and Livesey, F.J. (2010). Ezh2, the histone methyltransferase of PRC2, regulates the balance between self-renewal and differentiation in the cerebral cortex. Proc. Natl. Acad. Sci. U.S.a. *107*, 15957–15962.

Potts, R.C., Zhang, P., Wurster, A.L., Precht, P., Mughal, M.R., Wood, W.H., Zhang, Y., Becker, K.G., Mattson, M.P., and Pazin, M.J. (2011). CHD5, a brain-specific paralog of Mi2 chromatin remodeling enzymes, regulates expression of neuronal genes. PLoS ONE *6*, e24515.

Qian, Y.W., and Lee, E.Y. (1995). Dual retinoblastoma-binding proteins with properties related to a negative regulator of ras in yeast. J. Biol. Chem. *270*, 25507–25513.

Qu, Z., Meng, F., Bomgarden, R.D., Viner, R.I., Li, J., Rogers, J.C., Cheng, J., Greenlief, C.M., Cui, J., Lubahn, D.B., et al. (2014). Proteomic quantification and site-mapping of S-nitrosylated proteins using isobaric iodoTMT reagents. J. Proteome Res. *13*, 3200–3211.

Raju, K., Doulias, P.-T., Evans, P., Krizman, E.N., Jackson, J.G., Horyn, O., Daikhin, Y., Nissim, I., Yudkoff, M., Nissim, I., et al. (2015). Regulation of brain glutamate metabolism by nitric oxide and S-nitrosylation. *8*, ra68–ra68.

Rameau, G.A., Chiu, L.-Y., and Ziff, E.B. (2003). NMDA receptor regulation of nNOS phosphorylation and induction of neuron death. Neurobiol. Aging *24*, 1123–1133.

Rameau, G.A., Tukey, D.S., Garcin-Hosfield, E.D., Titcombe, R.F., Misra, C., Khatri, L., Getzoff, E.D., and Ziff, E.B. (2007). Biphasic coupling of neuronal nitric oxide synthase phosphorylation to the NMDA receptor regulates AMPA receptor trafficking and neuronal cell death. J. Neurosci. *27*, 3445–3455.

Rappsilber, J., Mann, M., and Ishihama, Y. (2007). Protocol for micro-purification, enrichment, pre-fractionation and storage of peptides for proteomics using StageTips. Nat Protoc *2*, 1896–1906.

Rexach, J.E., Clark, P.M., Mason, D.E., Neve, R.L., Peters, E.C., and Hsieh-Wilson, L.C. (2012). Dynamic O-GlcNAc modification regulates CREB-mediated gene expression and memory formation. Nat. Chem. Biol. *8*, 253–261.

Ribet, D., and Cossart, P. (2010). Post-translational modifications in host cells during bacterial infection. FEBS Lett. *584*, 2748–2758.

Riccio, A., Ahn, S., Davenport, C.M., Blendy, J.A., and Ginty, D.D. (1999). Mediation by a CREB family transcription factor of NGF-dependent survival of sympathetic neurons. Science *286*, 2358–2361.

Riccio, A., Pierchala, B.A., Ciarallo, C.L., and Ginty, D.D. (1997). An NGF-TrkA-mediated retrograde signal to transcription factor CREB in sympathetic neurons. Science *277*, 1097–1100.

Riccio, A. (2010). Dynamic epigenetic regulation in neurons: enzymes, stimuli and signaling pathways. Nat. Neurosci. *13*, 1330–1337.

Riccio, A., Alvania, R.S., Lonze, B.E., Ramanan, N., Kim, T., Huang, Y., Dawson, T.M., Snyder, S.H., and Ginty, D.D. (2006). A nitric oxide signaling pathway controls CREB-mediated gene expression in neurons. Mol. Cell *21*, 283–294.

Roopra, A., Sharling, L., Wood, I.C., Briggs, T., Bachfischer, U., Paquette, A.J., and Buckley, N.J. (2000). Transcriptional repression by neuron-restrictive silencer factor is mediated via the Sin3-histone deacetylase complex. Mol. Cell. Biol. *20*, 2147–2157.

Rudolph, D., Tafuri, A., Gass, P., Hämmerling, G.J., Arnold, B., and Schütz, G. (1998). Impaired fetal T cell development and perinatal lethality in mice lacking the cAMP response element binding protein. Proc. Natl. Acad. Sci. U.S.a. *95*, 4481–4486.

Ryan, S.D., Dolatabadi, N., Chan, S.F., Zhang, X., Akhtar, M.W., Parker, J., Soldner, F., Sunico, C.R., Nagar, S., Talantova, M., et al. (2013). Isogenic human iPSC Parkinson's model shows nitrosative stress-induced dysfunction in MEF2-PGC1α transcription. Cell *155*, 1351–1364.

Saini, R., Patel, S., Saluja, R., Sahasrabuddhe, A.A., Singh, M.P., Habib, S., Bajpai, V.K., and Dikshit, M. (2006). Nitric oxide synthase localization in the rat neutrophils:

immunocytochemical, molecular, and biochemical studies. J. Leukoc. Biol. *79*, 519–528.

Sampedro, M.N., Bussineau, C.M., and Cotman, C.W. (1981). Postsynaptic density antigens: preparation and characterization of an antiserum against postsynaptic densities. J. Cell Biol. *90*, 675–686.

Santhanam, L., Lim, H.K., Lim, H.K., Lim, H.K., Miriel, V., Brown, T., Patel, M., Balanson, S., Ryoo, S., Anderson, M., et al. (2007). Inducible NO synthase dependent S-nitrosylation and activation of arginase1 contribute to age-related endothelial dysfunction. Circ. Res. *101*, 692–702.

Sasaki, M., Gonzalez-Zulueta, M., Huang, H., Herring, W.J., Ahn, S., Ginty, D.D., Dawson, V.L., and Dawson, T.M. (2000). Dynamic regulation of neuronal NO synthase transcription by calcium influx through a CREB family transcription factor-dependent mechanism. Proc. Natl. Acad. Sci. U.S.a. *97*, 8617–8622.

Scharfstein, J.S., Keaney, J.F., Jr, Slivka, A., Welch, G.N., Vita, J.A., Stamler, J.S., and Loscalzo, J. (1994). In vivo transfer of nitric oxide between a plasma protein-bound reservoir and low molecular weight thiols. Journal of Clinical Investigation *94*, 1432–1439.

Scheving, R., Wittig, I., Heide, H., Albuquerque, B., Steger, M., Brandt, U., and Tegeder, I. (2012). Protein S-nitrosylation and denitrosylation in the mouse spinal cord upon injury of the sciatic nerve. J Proteomics *75*, 3987–4004.

Schumacher, M.A., Goodman, R.H., and Brennan, R.G. (2000). The structure of a CREB bZIP.somatostatin CRE complex reveals the basis for selective dimerization and divalent cation-enhanced DNA binding. J. Biol. Chem. *275*, 35242–35247.

Schuman, E.M., and Madison, D.V. (1991). A requirement for the intercellular messenger nitric oxide in long-term potentiation. Science *254*, 1503–1506.

Scoville, W.B., and Milner, B. (1957). Loss of recent memory after bilateral hippocampal lesions. J. Neurol. Neurosurg. Psychiatr. *20*, 11–21.

Seamon, K.B., and Daly, J.W. (1981). Forskolin: a unique diterpene activator of cyclic AMP-generating systems. J Cyclic Nucleotide Res *7*, 201–224.

Selvakumar, B., Huganir, R.L., and Snyder, S.H. (2009). S-nitrosylation of stargazin regulates surface expression of AMPA-glutamate neurotransmitter receptors. Proc. Natl. Acad. Sci. U.S.a. *106*, 16440–16445.

Sen, N., and Snyder, S.H. (2011). Neurotrophin-mediated degradation of histone methyltransferase by S-nitrosylation cascade regulates neuronal differentiation. Proc. Natl. Acad. Sci. U.S.a. *108*, 20178–20183.

Seneviratne, U., Godoy, L.C., Wishnok, J.S., Wogan, G.N., and Tannenbaum, S.R. (2013). Mechanism-Based Triarylphosphine-Ester Probes for Capture of Endogenous RSNOs. J. Am. Chem. Soc. *135*, 7693–7704.

Seneviratne, U., Nott, A., Bhat, V.B., Ravindra, K.C., Wishnok, J.S., Tsai, L.-H., and Tannenbaum, S.R. (2016). S-nitrosation of proteins relevant to Alzheimer's disease during early stages of neurodegeneration. Proc. Natl. Acad. Sci. U.S.a. *113*, 4152–4157.

Seth, D., Hausladen, A., Wang, Y.-J., and Stamler, J.S. (2012). Endogenous protein S-Nitrosylation in E. coli: regulation by OxyR. Science *336*, 470–473.

Sherman, T.S., Chen, Z., Yuhanna, I.S., Lau, K.S., Margraf, L.R., and Shaul, P.W. (1999). Nitric oxide synthase isoform expression in the developing lung epithelium. Am. J. Physiol. Lung Cell Mol. Physiol. *276*, L383–L390.

Shi, Q., Feng, J., Qu, H., and Cheng, Y.-Y. (2008). A proteomic study of S-nitrosylation in the rat cardiac proteins in vitro. Biol. Pharm. Bull. *31*, 1536–1540.

Shibuki, K., and Okada, D. (1991). Endogenous nitric oxide release required for long-term synaptic depression in the cerebellum. , Published Online: 24 January 1991; | Doi:10.1038/349326a0 *349*, 326–328.

Shogren-Knaak, M., Ishii, H., Sun, J.-M., Pazin, M.J., Davie, J.R., and Peterson, C.L. (2006). Histone H4-K16 acetylation controls chromatin structure and protein interactions. Science *311*, 844–847.

Smith, M.A., Richey Harris, P.L., Sayre, L.M., Beckman, J.S., and Perry, G. (1997). Widespread peroxynitrite-mediated damage in Alzheimer's disease. J. Neurosci. *17*, 2653–2657.

Smits, A.H., Jansen, P.W.T.C., Poser, I., Hyman, A.A., and Vermeulen, M. (2012). Stoichiometry of chromatin-associated protein complexes revealed by label-free quantitative mass spectrometry-based proteomics. Nucleic Acids Res. *41*, gks941–e28.

Son, E.Y., and Crabtree, G.R. (2014a). The role of BAF (mSWI/SNF) complexes in mammalian neural development. Am J Med Genet C Semin Med Genet *166C*, 333–349.

Son, E.Y., and Crabtree, G.R. (2014b). The role of BAF (mSWI/SNF) complexes in mammalian neural development. Am J Med Genet C Semin Med Genet *166C*, 333–349.

Spratt, D.E., Taiakina, V., Palmer, M., and Guillemette, J.G. (2007). Differential binding of calmodulin domains to constitutive and inducible nitric oxide synthase enzymes. Biochemistry *46*, 8288–8300.

Stahl, R., Walcher, T., De Juan Romero, C., Pilz, G.A., Cappello, S., Irmler, M., Sanz-Aquela, J.M., Beckers, J., Blum, R., Borrell, V., et al. (2013). Trnp1 regulates expansion and folding of the mammalian cerebral cortex by control of radial glial fate. Cell *153*, 535–549.

Stamler, J.S., Jaraki, O., Osborne, J., Simon, D.I., Keaney, J., Vita, J., Singel, D., Valeri, C.R., and Loscalzo, J. (1992a). Nitric oxide circulates in mammalian plasma primarily as an S-nitroso adduct of serum albumin. Proc. Natl. Acad. Sci. U.S.a. *89*, 7674–7677.

Stamler, J.S., Simon, D.I., Osborne, J.A., Mullins, M.E., Jaraki, O., Michel, T., Singel, D.J., and Loscalzo, J. (1992b). S-nitrosylation of proteins with nitric oxide: synthesis and characterization of biologically active compounds. Proc. Natl. Acad. Sci. U.S.a. *89*, 444–448.

Stamler, J.S., Toone, E.J., Lipton, S.A., and Sucher, N.J. (1997). (S)NO signals: translocation, regulation, and a consensus motif. Neuron *18*, 691–696.

Stanton, P.K., Winterer, J., Bailey, C.P., Kyrozis, A., Raginov, I., Laube, G., Veh, R.W., Nguyen, C.Q., and Müller, W. (2003). Long-term depression of presynaptic release from the readily releasable vesicle pool induced by NMDA receptor-dependent retrograde nitric oxide. J. Neurosci. *23*, 5936–5944.

Stanton, P.K., Winterer, J., Zhang, X.-L., and Müller, W. (2005). Imaging LTP of presynaptic release of FM1-43 from the rapidly recycling vesicle pool of Schaffer collateral-CA1 synapses in rat hippocampal slices. Eur. J. Neurosci. *22*, 2451–2461.

Stenoien, D.L., Patel, K., Mancini, M.G., Dutertre, M., Smith, C.L., O'Malley, B.W., and Mancini, M.A. (2001). FRAP reveals that mobility of oestrogen receptor-alpha is ligand- and proteasome-dependent. Nat. Cell Biol. *3*, 15–23.

Stirnimann, C.U., Petsalaki, E., Russell, R.B., and Müller, C.W. (2010). WD40 proteins propel cellular networks. Trends in Biochemical Sciences *35*, 565–574.

Stryker, M.P., and Harris, W.A. (1986). Binocular impulse blockade prevents the formation of ocular dominance columns in cat visual cortex. J. Neurosci. *6*, 2117–2133.

Stubauer, G. (1999). Mechanism of S-Nitrosothiol Formation and Degradation Mediated by Copper Ions. J. Biol. Chem. *274*, 28128–28133.

Sun, N., Hao, J.R., Li, X.Y., Yin, X.H., Zong, Y.Y., Zhang, G.Y., and Gao, C. (2013). GluR6-FasL-Trx2 mediates denitrosylation and activation of procaspase-3 in cerebral ischemia/reperfusion in rats. Cell Death Dis *4*, e771.

Sun, T., and Hevner, R.F. (2014). Growth and folding of the mammalian cerebral cortex: from molecules to malformations. Nat. Rev. Neurosci. *15*, 217–232.

Sutherland, E.W., Robison, G.A., and Butcher, R.W. (1968). Some Aspects of the Biological Role of Adenosine 3“,5-”monophosphate (Cyclic AMP). Circulation *37*, 279–306.

Szabó, C., Ischiropoulos, H., and Radi, R. (2007). Peroxynitrite: biochemistry, pathophysiology and development of therapeutics. Nat Rev Drug Discov *6*, 662–680.

Tao, X., Finkbeiner, S., Arnold, D.B., Shaywitz, A.J., and Greenberg, M.E. (1998a). Ca2+ influx regulates BDNF transcription by a CREB family transcription factor-dependent mechanism. Neuron *20*, 709–726.

Tao, X., Finkbeiner, S., Arnold, D.B., Shaywitz, A.J., and Greenberg, M.E. (1998b). Ca2+ Influx Regulates BDNF Transcription by a CREB Family Transcription Factor-Dependent Mechanism. Neuron *20*, 709–726.

Thompson, M.A., Ginty, D.D., Bonni, A., and Greenberg, M.E. (1995). L-type voltage-sensitive Ca2+ channel activation regulates c-fos transcription at multiple levels. J. Biol. Chem. *270*, 4224–4235.

Tong, J.K., Hassig, C.A., Schnitzler, G.R., Kingston, R.E., and Schreiber, S.L. (1998). Chromatin deacetylation by an ATP-dependent nucleosome remodelling complex. Nature *395*, 917–921.

Trainor, B.C., Workman, J.L., Jessen, R., and Nelson, R.J. (2007). Impaired nitric oxide synthase signaling dissociates social investigation and aggression. Behav. Neurosci. *121*, 362–369.

Uittenbogaard, A., Shaul, P.W., Yuhanna, I.S., Blair, A., and Smart, E.J. (2000). High density lipoprotein prevents oxidized low density lipoprotein-induced inhibition of endothelial nitric-oxide synthase localization and activation in caveolae. J. Biol. Chem. *275*, 11278–11283.

van der Voorn, L., and Ploegh, H.L. (1992). The WD-40 repeat. FEBS Lett. *307*, 131–134.

Vaquerizas, J.M., Kummerfeld, S.K., Teichmann, S.A., and Luscombe, N.M. (2009). A census of human transcription factors: function, expression and evolution. Nat. Rev. Genet. *10*, 252–263.

Vettese-Dadey, M., Grant, P.A., Hebbes, T.R., Crane- Robinson, C., Allis, C.D., and Workman, J.L. (1996). Acetylation of histone H4 plays a primary role in enhancing transcription factor binding to nucleosomal DNA in vitro. Embo J. *15*, 2508–2518.

Viré, E., Brenner, C., Deplus, R., Blanchon, L., Fraga, M., Didelot, C., Morey, L., Van Eynde, A., Bernard, D., Vanderwinden, J.-M., et al. (2006). The Polycomb group protein EZH2 directly controls DNA methylation. Nature *439*, 871–874.

Vodovotz, Y., Lucia, M.S., Flanders, K.C., Chesler, L., Xie, Q.W., Smith, T.W., Weidner, J., Mumford, R., Webber, R., Nathan, C., et al. (1996). Inducible nitric oxide synthase in tangle-bearing neurons of patients with Alzheimer's disease. J. Exp. Med. *184*, 1425–1433.

Volman, I., Roelofs, K., Koch, S., Verhagen, L., and Toni, I. (2011). Anterior Prefrontal Cortex Inhibition Impairs Control over Social Emotional Actions. Current Biology *21*, 1766–1770.

Wall, M.A., Coleman, D.E., Lee, E., and Iñiguez-Lluhi, J.A. (1995). The structure of the G protein heterotrimer G iα1 β 1 γ 2. Cell.

Walton, J.C., Selvakumar, B., Weil, Z.M., Snyder, S.H., and Nelson, R.J. (2013). Neuronal nitric oxide synthase and NADPH oxidase interact to affect cognitive, affective, and social behaviors in mice. Behav. Brain Res. *256*, 320–327.

Walton, M., Woodgate, A.M., Muravlev, A., Xu, R., During, M.J., and Dragunow, M. (1999). CREB phosphorylation promotes nerve cell survival. J. Neurochem. *73*, 1836–1842.

Wang, H., and Storm, D.R. (2003). Calmodulin-regulated adenylyl cyclases: cross-talk and plasticity in the central nervous system. Mol. Pharmacol. *63*, 463–468.

Wang, W., Côté, J., Xue, Y., Zhou, S., Khavari, P.A., Biggar, S.R., Muchardt, C., Kalpana, G.V., Goff, S.P., Yaniv, M., et al. (1996). Purification and biochemical heterogeneity of the mammalian SWI-SNF complex. Embo J. *15*, 5370–5382.

Wang, Y., Liu, T., Wu, C., and Li, H. (2008). A strategy for direct identification of protein S-nitrosylation sites by quadrupole time-of-flight mass spectrometry. J. Am. Soc. Mass Spectrom. *19*, 1353–1360.

Wang, Y.-C., Peterson, S.E., and Loring, J.F. (2014). Protein post-translational modifications and regulation of pluripotency in human stem cells. Cell Res. *24*, 143–160.

Wang, Y., Wong, R.H.F., Tang, T., Hudak, C.S., Yang, D., Duncan, R.E., and Sul, H.S. (2013). Phosphorylation and recruitment of BAF60c in chromatin remodeling for lipogenesis in response to insulin. Mol. Cell *49*, 283–297.

Wei, W., Li, B., Hanes, M.A., Kakar, S., Chen, X., and Liu, L. (2010). S-nitrosylation from GSNOR deficiency impairs DNA repair and promotes hepatocarcinogenesis. Sci Transl Med *2*, 19ra13–19ra13.

Weitzdoerfer, R., Hoeger, H., Engidawork, E., Engelmann, M., Singewald, N., Lubec, G., and Lubec, B. (2004). Neuronal nitric oxide synthase knock-out mice show impaired cognitive performance. Nitric Oxide *10*, 130–140.

Wu, J.I., Lessard, J., Olave, I.A., Qiu, Z., Ghosh, A., Graef, I.A., and Crabtree, G.R. (2007). Regulation of Dendritic Development by Neuron-Specific Chromatin Remodeling Complexes. Neuron *56*, 94–108.

Xiang, G., Pan, L., Xing, W., Zhang, L., Huang, L., Yu, J., Zhang, R., Wu, J., Cheng, J., and Zhou, Y. (2007). Identification of activity-dependent gene expression profiles reveals specific subsets of genes induced by different routes of Ca(2+) entry in cultured rat cortical neurons. J. Cell. Physiol. *212*, 126–136.

Xie, Q.W., Cho, H.J., Calaycay, J., Mumford, R.A., Swiderek, K.M., Lee, T.D., Ding, A., Troso, T., and Nathan, C. (1992). Cloning and characterization of inducible nitric oxide synthase from mouse macrophages. Science *256*, 225–228.

Xin, F., and Radivojac, P. (2012). Post-translational modifications induce significant yet not extreme changes to protein structure. Bioinformatics *28*, 2905–2913.

Xu, R., Serritella, A.V., Sen, T., Farook, J.M., Sedlak, T.W., Baraban, J., Snyder, S.H., and Sen, N. (2013). Behavioral Effects of Cocaine Mediated by Nitric Oxide-GAPDH Transcriptional Signaling. Neuron *78*, 623–630.

Xue, Y., Wong, J., Moreno, G.T., Young, M.K., Côté, J., and Wang, W. (1998). NURD, a

Novel Complex with Both ATP-Dependent Chromatin-Remodeling and Histone Deacetylase Activities. Mol. Cell *2*, 851–861.

Yamada, T., Yang, Y., Hemberg, M., Yoshida, T., Cho, H.Y., Murphy, J.P., Fioravante, D., Regehr, W.G., Gygi, S.P., Georgopoulos, K., et al. (2014). Promoter decommissioning by the NuRD chromatin remodeling complex triggers synaptic connectivity in the mammalian brain. Neuron *83*, 122–134.

Yamasaki, H. (2004). Nitric oxide research in plant biology: its past and future (nitric oxide signaling in higher …).

Yamasaki, H. (2005). The NO world for plants: achieving balance in an open system. Plant, Cell &Amp; Environment *28*, 78–84.

Yang, M.-K., Yang, Y.-H., Chen, Z., Zhang, J., Lin, Y., Wang, Y., Xiong, Q., Li, T., Ge, F., Bryant, D.A., et al. (2014). Proteogenomic analysis and global discovery of posttranslational modifications in prokaryotes. Proc. Natl. Acad. Sci. U.S.a. *111*, E5633–E5642.

Yang, Q., Chen, S.R., Li, D.P., and Pan, H.L. (2007). Kv1.1/1.2 channels are downstream effectors of nitric oxide on synaptic GABA release to preautonomic neurons in the paraventricular nucleus. Neuroscience *149*, 315–327.

Yang, Y., and Loscalzo, J. (2005). S-nitrosoprotein formation and localization in endothelial cells. Proc. Natl. Acad. Sci. U.S.a. *102*, 117–122.

Yen, J.L., Flick, K., Papagiannis, C.V., Mathur, R., Tyrrell, A., Ouni, I., Kaake, R.M., Huang, L., and Kaiser, P. (2012). Signal-induced disassembly of the SCF ubiquitin ligase complex by Cdc48/p97. Mol. Cell *48*, 288–297.

Yui, Y., Hattori, R., Kosuga, K., Eizawa, H., Hiki, K., and Kawai, C. (1991). Purification of nitric oxide synthase from rat macrophages. J. Biol. Chem. *266*, 12544–12547.

Zaręba-Kozioł, M., Szwajda, A., Dadlez, M., Wysłouch-Cieszyńska, A., and Lalowski, M. (2014). Global analysis of S-nitrosylation sites in the wild type (APP) transgenic mouse brain-clues for synaptic pathology. Mol. Cell Proteomics *13*, 2288–2305.

Zhang, T.-F., Yu, S.-Q., and Wang, Z.-Y. (2007). RbAp46 inhibits estrogen-stimulated progression of neoplastigenic breast epithelial cells. Anticancer Res. *27*, 3205–3209.

Zhang, W., Tyl, M., Ward, R., Sobott, F., Maman, J., Murthy, A.S., Watson, A.A., Fedorov, O., Bowman, A., Owen-Hughes, T., et al. (2012). Structural plasticity of histones H3–H4 facilitates their allosteric exchange between RbAp48 and ASF1. Nat. Struct. Mol. Biol. *20*, 29–35.

Zhang, Y., Iratni, R., Erdjument-Bromage, H., Tempst, P., and Reinberg, D. (1997). Histone deacetylases and SAP18, a novel polypeptide, are components of a human Sin3 complex. Cell *89*, 357–364.

Zhang, Y., LeRoy, G., Seelig, H.P., Lane, W.S., and Reinberg, D. (1998a). The dermatomyositis-specific autoantigen Mi2 is a component of a complex containing histone deacetylase and nucleosome remodeling activities. Cell *95*, 279–289.

Zhang, Y., Ng, H.H., Erdjument-Bromage, H., Tempst, P., Bird, A., and Reinberg, D. (1999). Analysis of the NuRD subunits reveals a histone deacetylase core complex and a connection with DNA methylation. Genes Dev. *13*, 1924–1935.

Zhang, Y., Sun, Z.-W., Iratni, R., Erdjument-Bromage, H., Tempst, P., Hampsey, M., and Reinberg, D. (1998b). SAP30, a Novel Protein Conserved between Human and Yeast, Is a Component of a Histone Deacetylase Complex. Mol. Cell *1*, 1021–1031.

Zhou, L., and Zhu, D.-Y. (2009). Neuronal nitric oxide synthase: Structure, subcellular localization, regulation, and clinical implications. Nitric Oxide *20*, 223–230.

Zippo, A., Serafini, R., Rocchigiani, M., Pennacchini, S., Krepelova, A., and Oliviero, S. (2009). Histone crosstalk between H3S10ph and H4K16ac generates a histone code that mediates transcription elongation. Cell *138*, 1122–1136.

Zoubovsky, S.P., Pogorelov, V.M., Taniguchi, Y., Kim, S.-H., Yoon, P., Nwulia, E., Sawa, A., Pletnikov, M.V., and Kamiya, A. (2011). Working memory deficits in neuronal nitric oxide synthase knockout mice: potential impairments in prefrontal cortex mediated cognitive function. Biochem. Biophys. Res. Commun. *408*, 707–712.

Zweier, J.L., Samouilov, A., and Kuppusamy, P. (1999). Non-enzymatic nitric oxide synthesis in biological systems. Biochim. Biophys. Acta *1411*, 250–262.

(1988). Phosphorylation-induced binding and transcriptional efficacy of nuclear factor CREB. Nature *334*, 494–498.

Table S1

Nuclear S-nitrosylated proteins in CysNO-treated HEK293T nuclear extracts

27 proteins (★=novel target in any system)

Hit Number	Uniprot ID	Description	Molecular Function	Biological Process	Protein Class
1	NOP56_HUMAN ★	Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4	RNA binding(GO:0005488)	nitrogen compound metabolic process(GO:0008152);rRNA metabolic process(GO:0006807);cellular process(GO:0044238);cellular component biogenesis(GO:0006139)	ribonucleoprotein(PC00171)
2	REPI1_HUMAN ★	Replication initiator 1 OS=Homo sapiens GN=REPIN1 PE=1 SV=1			
3	SUMO2_HUMAN ★	Small ubiquitin-related modifier 2 OS=Homo sapiens GN=SUMO2 PE=1 SV=1		cellular protein modification process(GO:0008152);cell cycle(GO:0044238)	
4	SMRD2_HUMAN ★	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2 OS=Homo sapiens GN=SMARCD2 PE=1 SV=2	nucleic acid binding(GO:0005488);chromatin binding(GO:0003676)	nucleobase-containing compound metabolic process(GO:0008152);cellular process(GO:0044238);chromatin organization(GO:0006139)	chromatin/chromatin-binding protein(PC00171)
5	RS14_HUMAN	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	structural constituent of ribosome(GO:0005198);nucleic acid binding(GO:0003735)	translation(GO:0008152)	ribosomal protein(PC00171)
6	RS27_HUMAN	40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3	structural constituent of ribosome(GO:0005198);nucleic acid binding(GO:0003735)	translation(GO:0008152)	ribosomal protein(PC00171)
7	BRD4_HUMAN	Bromodomain-containing protein 4 OS=Homo sapiens GN=BRD4 PE=1 SV=2	acetyltransferase activity(GO:0003824);nucleic acid binding(GO:0016740);chromatin binding(GO:0016746)	transcription from RNA polymerase II promoter(GO:0008152);cellular process(GO:0044238);chromatin organization(GO:0006139)	acetyltransferase(PC00220);chromatin/chromatin-binding protein(PC00038)
8	DNMT1_HUMAN	DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens GN=DNMT1 PE=1 SV=2			
9	MCM3_HUMAN	DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3	DNA helicase activity(GO:0003824);hydrolase activity(GO:0004386);nucleic acid binding(GO:0003678)	DNA replication(GO:0008152);cell cycle(GO:0044238)	DNA helicase(PC00171);helicase(PC00009);hydrolase(PC00011)
10	TOP1_HUMAN	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2	DNA topoisomerase activity(GO:0003824);DNA topoisomerase activity(GO:0016853)	nitrogen compound metabolic process(GO:0008152);biosynthetic process(GO:0006807);DNA metabolic process(GO:0009058);cellular process(GO:0044238);chromatin organization(GO:0006139)	DNA topoisomerase(PC00171)
11	FLNA_HUMAN	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	structural constituent of cytoskeleton(GO:0005198);actin binding(GO:0005200)	cellular component movement(GO:0009987);cellular component morphogenesis(GO:0006928);cellular component organization(GO:0032502)	non-motor actin binding protein(PC00085)

12	GTF2I_HUMAN	General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2	sequence-specific DNA binding transcription factor activity(GO:0001071);sequence-specific DNA binding transcription factor activity(GO:0003700)	transcription from RNA polymerase II promoter(GO:0008152)	transcription factor(PC00218)
13	ROA0_HUMAN	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1			
14	HNRPM_HUMAN	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	RNA binding(GO:0005488)	mRNA splicing, via spliceosome(GO:0008152)	ribonucleoprotein(PC00171)
15	HDAC1_HUMAN	Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=1 SV=1	oxidoreductase activity(GO:0003824);deacetylase activity(GO:0016491);nucleic acid binding(GO:0016787)	apoptotic process(GO:0006915);transcription from RNA polymerase II promoter(GO:0008152);cell cycle(GO:0044238);apoptotic process(GO:0006139);regulation of transcription from RNA polymerase II promoter(GO:0016070);negative regulation of apoptotic process(GO:0006351);chromatin organization(GO:0006366)	reductase(PC00176);nucleic acid binding(PC00198);deacetylase(PC00171)
16	IMB1_HUMAN	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	transmembrane transporter activity(GO:0005215)	protein targeting(GO:0051179);nuclear transport(GO:0006810)	transporter(PC00227);transfer/carrier protein(PC00219)
17	ILF2_HUMAN	Interleukin enhancer-binding factor 2 OS=Homo sapiens GN=ILF2 PE=1 SV=2	transcription cofactor activity(GO:0000988);sequence-specific DNA binding transcription factor activity(GO:0000989);sequence-specific DNA binding transcription factor activity(GO:0003712);protein binding(GO:0001071)	spermatogenesis(GO:0000003);response to interferon-gamma(GO:0007276);apoptotic process(GO:0007283);neurological system process(GO:0002376);anterior/posterior axis specification(GO:0006955);anterior/posterior axis specification(GO:0034341);apoptotic process(GO:0006915);response to stimulus(GO:0032501);RNA localization(GO:0044707)	transcription cofactor(PC00218)
18	MAPK2_HUMAN	MAP kinase-activated protein kinase 2 OS=Homo sapiens GN=MAPKAPK2 PE=1 SV=1	protein kinase activity(GO:0003824);protein binding(GO:0016740)	phosphate-containing compound metabolic process(GO:0008152);protein phosphorylation(GO:0006796);cell communication(GO:0044238);response to stress(GO:0019538);regulation of biological process(GO:0006464)	non-receptor serine/threonine protein kinase(PC00220);non-receptor serine/threonine protein kinase(PC00137);non-motor microtubule binding protein(PC00193)
19	MATR3_HUMAN	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2	DNA binding(GO:0005488);RNA binding(GO:0003676)		DNA binding protein(PC00171);RNA binding protein(PC00009)
20	NDKA_HUMAN	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	kinase activity(GO:0003824)	apoptotic process(GO:0006915);phosphate-containing compound metabolic process(GO:0008152);nitrogen compound metabolic process(GO:0006796);biosynthetic process(GO:0006807);nucleobase-containing compound metabolic process(GO:0009058);cellular process(GO:0044238);apoptotic process(GO:0006139);regulation of biological process(GO:0009987)	
21	PCBP1_HUMAN	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	catalytic activity(GO:0003824);mRNA binding(GO:0005488);protein binding(GO:0003676)	induction of apoptosis(GO:0006915);RNA splicing, via transesterification reactions(GO:0006917);transcription from RNA polymerase II promoter(GO:0008152);mRNA splicing, via spliceosome(GO:0044238);RNA splicing, via transesterification reactions(GO:0006139);protein metabolic process(GO:0016070);cell cycle(GO:0000375);cell communication(GO:0006351);neurological system process(GO:0006366);induction of apoptosis(GO:0006397);intracellular protein transport(GO:0000398);nuclear transport(GO:0008380)	mRNA splicing factor(PC00171);ribonucleoprotein(PC00031);enzyme modulator(PC00147)

22	PCBP2_HUMAN	Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1	catalytic activity(GO:0003824);mRNA binding(GO:0005488);protein binding(GO:0003676)	induction of apoptosis(GO:0006915);RNA splicing, via transesterification reactions(GO:0006917);transcription from RNA polymerase II promoter(GO:0008152);mRNA splicing, via spliceosome(GO:0044238);RNA splicing, via transesterification reactions(GO:0006139);protein metabolic process(GO:0016070);cell cycle(GO:0000375);cell communication(GO:0006351);neurological system process(GO:0006366);induction of apoptosis(GO:0006397);intracellular protein transport(GO:0000398);nuclear transport(GO:0008380)	mRNA splicing factor(PC00171);ribonucleoprotein(PC00031);enzyme modulator(PC00147)
23	DEK_HUMAN	Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1			
24	DHX15_HUMAN	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	RNA helicase activity(GO:0003824);pyrophosphatase activity(GO:0004386)	phosphate-containing compound metabolic process(GO:0008152);nitrogen compound metabolic process(GO:0006796);catabolic process(GO:0006807);RNA splicing, via transesterification reactions(GO:0009056);mRNA processing(GO:0044238);RNA splicing, via transesterification reactions(GO:0006139);cellular process(GO:0016070)	RNA helicase(PC00171);helicase(PC00031)
25	RAVR1_HUMAN	Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1	catalytic activity(GO:0003824);mRNA binding(GO:0005488)	RNA splicing, via transesterification reactions(GO:0008152);transcription from RNA polymerase II promoter(GO:0044238);mRNA splicing, via spliceosome(GO:0006139);RNA splicing, via transesterification reactions(GO:0016070);regulation of transcription from RNA polymerase II promoter(GO:0000375)	mRNA splicing factor(PC00171)
26	SF3A1_HUMAN	Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1	nucleic acid binding(GO:0005488)	nitrogen compound metabolic process(GO:0008152);RNA splicing, via transesterification reactions(GO:0006807);mRNA splicing, via spliceosome(GO:0044238);RNA splicing, via transesterification reactions(GO:0006139);cellular process(GO:0016070);regulation of nucleobase-containing compound metabolic process(GO:0000375);cellular component organization(GO:0006397);cellular component biogenesis(GO:0000398)	mRNA splicing factor(PC00171)
27	ZN207_HUMAN	Zinc finger protein 207 OS=Homo sapiens GN=ZNF207 PE=1 SV=1	DNA binding(GO:0005488)	nucleobase-containing compound metabolic process(GO:0008152)	DNA binding protein(PC00171)

Table S2

Collated hits: CysNO-treated neuronal nuclear extracts

614 proteins (★=novel target in any system)

Hit number	Uniprot ID	Description	Molecular Function	Cellular Component	Biological Process	1mM CysNO/Cys (Exp A)	1mM CysNO/CysNO-asc (Exp A)	1mM CysNO/Cys (Exp B)	1mM CysNO/CysNO -asc (Exp B)	100uM CysNO/ Cys (Exp C)	100uM CysNO/CysNO -asc (Exp C)	100uM CysNO/Cys (Exp E)	100uM CysNO/CysNO-asc (Exp E)	100uM CysNO/cys (Exp F)	average
1	P10687	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1 OS=Rattus norvegicus GN=Plcb1 PE=1 SV=1 - [PLCB1_RAT]	catalytic activity; signal transducer activity; enzyme regulator activity; metal ion binding; protein binding	nucleus; cytoplasm; cytosol; membrane	metabolic process; regulation of biological process; response to stimulus; cell differentiation	0.8	4.4	11.5	0.7	2.2	3.5		100.0	10.4	14.8
2	P35213	14-3-3 protein beta/alpha OS=Rattus norvegicus GN=Ywhab PE=1 SV=3 - [1433B_RAT]	protein binding	nucleus; cytoplasm; cytosol; membrane	transport; regulation of biological process; cell organization and biogenesis	2.8	4.1	8.7	1.6					5.0	3.7
3	P62260	14-3-3 protein epsilon OS=Rattus norvegicus GN=Ywhae PE=1 SV=1 - [1433E_RAT]	protein binding; enzyme regulator activity; RNA binding	cytoplasm; mitochondrion; membrane	cellular component movement; transport; regulation of biological process; response to stimulus	2.8	5.2	8.0	1.0					14.7	5.3
4	P68511	14-3-3 protein eta OS=Rattus norvegicus GN=Ywhah PE=1 SV=2 - [1433F_RAT]	protein binding	cytoplasm; membrane	regulation of biological process; metabolic process; transport; response to stimulus	2.8	13.2	9.3	3.1					13.4	7.0
5	P61983	14-3-3 protein gamma OS=Rattus norvegicus GN=Ywhag PE=1 SV=2 - [1433G_RAT]	protein binding; enzyme regulator activity; RNA binding	cytoplasm; membrane	transport; regulation of biological process; response to stimulus	5.5	8.1	11.5	3.2	2.7	1.8			5.2	4.8
6	P68255	14-3-3 protein theta OS=Rattus norvegicus GN=Ywhaq PE=1 SV=1 - [1433T_RAT]	protein binding	cytoplasm; membrane	transport; regulation of biological process; response to stimulus	2.8	4.9	9.0	2.4					6.8	4.3
7	P63102	14-3-3 protein zeta/delta OS=Rattus norvegicus GN=Ywhaz PE=1 SV=1 - [1433Z_RAT]	protein binding; RNA binding	nucleus; cytoplasm; mitochondrion; vacuole	transport; regulation of biological process; response to stimulus; cell organization and biogenesis	2.7	4.6	7.9	1.7					7.5	4.1
8	B0BMW2	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Rattus norvegicus GN=Hsd17b10 PE=2 SV=1 - [B0BMW2_RAT]	nucleotide binding; catalytic activity; protein binding; RNA binding	mitochondrion; membrane; endoplasmic reticulum	metabolic process; cell differentiation; cell organization and biogenesis	5.3	3.5	5.9	4.5					61.2	13.4
9	P13471	40S ribosomal protein S14 OS=Rattus norvegicus GN=Rps14 PE=2 SV=3 - [RS14_RAT]	RNA binding; structural molecule activity; translation regulator activity	cytoplasm; mitochondrion; ribosome; membrane	cell organization and biogenesis; regulation of biological process; metabolic process; cell differentiation	3.4	2.0	7.4	4.3					2.2	3.2
10	P62853	40S ribosomal protein S25 OS=Rattus norvegicus GN=Rps25 PE=2 SV=1 - [RS25_RAT]	structural molecule activity; RNA binding	nucleus; cytoplasm; ribosome	cell organization and biogenesis	2.7	5.1	12.6						2.4	4.6
11	P62856	40S ribosomal protein S26 OS=Rattus norvegicus GN=Rps26 PE=3 SV=3 - [RS26_RAT]	RNA binding; structural molecule activity	cytoplasm; ribosome; membrane	metabolic process; regulation of biological process		25.1	2.0						3.3	7.6
12	P62859	40S ribosomal protein S28 OS=Rattus norvegicus GN=Rps28 PE=1 SV=1 - [RS28_RAT]	RNA binding; structural molecule activity	cytoplasm; ribosome	metabolic process; transport	6.6	5.6	23.7	2.3					6.7	7.5
13	P62909	40S ribosomal protein S3 OS=Rattus norvegicus GN=Rps3 PE=1 SV=1 - [RS3_RAT]	DNA binding; RNA binding; structural molecule activity; catalytic activity; protein binding	nucleus; cytoplasm; membrane; cytosol; ribosome	metabolic process; response to stimulus; regulation of biological process; cell death; cell organization and biogenesis; cell division	2.2	3.6	3.0	2.0	1.7	15.0		1.9	3.9	3.7

14	M0R6L4	40S ribosomal protein S3a OS=Rattus norvegicus GN=LOC100365839 PE=3 SV=1 - [M0R6L4_RAT]	structural molecule activity	nucleus; cytoplasm; cytosol; ribosome	metabolic process; cell differentiation	2.3	5.2	3.4	2.9					2.6	2.7
15	B0BN81	40S ribosomal protein S5 OS=Rattus norvegicus GN=Rps5 PE=2 SV=1 - [B0BN81_RAT]	RNA binding; structural molecule activity	ribosome; membrane	metabolic process; regulation of biological process		2.7	3.4			3.6			2.9	2.5
16	P62243	40S ribosomal protein S8 OS=Rattus norvegicus GN=Rps8 PE=1 SV=2 - [RS8_RAT]	structural molecule activity; RNA binding	nucleus; cytoplasm; ribosome; membrane	metabolic process	1.8	4.0	2.8	2.5					2.3	2.2
17	P29314	40S ribosomal protein S9 OS=Rattus norvegicus GN=Rps9 PE=1 SV=4 - [RS9_RAT]	RNA binding; structural molecule activity; translation regulator activity	nucleus; cytoplasm; ribosome; membrane	metabolic process; regulation of biological process	1.3	21.4	1.6	2.5					12.2	6.5
18	D4A914	5'-3' exoribonuclease 2 (Predicted), isoform CRA_c OS=Rattus norvegicus GN=Xrn2 PE=4 SV=2 - [D4A914_RAT]	DNA binding; catalytic activity; metal ion binding; RNA binding	nucleus; membrane	metabolic process; cell growth	1.6	23.8	2.9	2.9					3.5	5.8
19	P63039	60 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspd1 PE=1 SV=1 - [CH60_RAT]	nucleotide binding; protein binding; RNA binding	cytoplasm; mitochondrion; membrane; organelle lumen; endosome; endoplasmic reticulum; Golgi; cytosol; cell surface	response to stimulus; regulation of biological process; metabolic process; cell proliferation	4.0	4.7	8.2	7.0					13.8	6.3
20	P19945	60S acidic ribosomal protein P0 OS=Rattus norvegicus GN=Rplp0 PE=1 SV=2 - [RLA0_RAT]	structural molecule activity; RNA binding	nucleus; cytoplasm; ribosome; membrane	metabolic process; response to stimulus	4.7	10.8	17.6	6.0					9.7	8.1
21	Q6PDV7	60S ribosomal protein L10 OS=Rattus norvegicus GN=Rpl10 PE=1 SV=3 - [RL10_RAT]	structural molecule activity; RNA binding	cytoplasm; endoplasmic reticulum; ribosome; membrane	metabolic process	2.0	3.4		2.7					3.1	2.2
22	P62914	60S ribosomal protein L11 OS=Rattus norvegicus GN=Rpl11 PE=1 SV=2 - [RL11_RAT]	RNA binding; structural molecule activity	nucleus; ribosome; membrane	metabolic process; transport	4.1	4.2	6.2	6.4	4.3	2.8		100.0	12.9	15.7
23	F1LSW7	60S ribosomal protein L14 OS=Rattus norvegicus GN=Rpl14 PE=4 SV=1 - [F1LSW7_RAT]	structural molecule activity	ribosome	metabolic process	1.3	3.3	2.4	1.8					2.3	1.9
24	P24049	60S ribosomal protein L17 OS=Rattus norvegicus GN=Rpl17 PE=2 SV=3 - [RL17_RAT]	structural molecule activity; RNA binding	nucleus; ribosome	metabolic process	1.8	15.8	100.0	0.7					2.3	20.1
25	P62718	60S ribosomal protein L18a OS=Rattus norvegicus GN=Rpl18a PE=2 SV=1 - [RL18A_RAT]	structural molecule activity; RNA binding	ribosome; membrane	metabolic process	1.4	3.2	2.6	1.8					3.2	2.0
26	P62832	60S ribosomal protein L23 OS=Rattus norvegicus GN=Rpl23 PE=2 SV=1 - [RL23_RAT]	structural molecule activity; RNA binding	cytoplasm; ribosome; membrane	metabolic process	1.9	3.2	5.1	2.4					51.3	10.6
27	P17077	60S ribosomal protein L9 OS=Rattus norvegicus GN=Rpl9 PE=1 SV=1 - [RL9_RAT]	structural molecule activity; RNA binding	nucleus; cytoplasm; ribosome; membrane	metabolic process	10.7	5.1	1.5	5.1					100.0	20.4
28	P06761	78 kDa glucose-regulated protein OS=Rattus norvegicus GN=Hspa5 PE=1 SV=1 - [GRP78_RAT]	nucleotide binding; protein binding; catalytic activity; enzyme regulator activity	nucleus; cytoplasm; mitochondrion; endoplasmic reticulum; organelle lumen; membrane; cell surface	cell organization and biogenesis; regulation of biological process; response to stimulus; cell communication; metabolic process; transport	1.0	1.5	2.6	3.4	2.2	2.0		1.8	3.2	2.0
29	Q7TMC7	Ab2-417 OS=Rattus norvegicus GN=Tf PE=2 SV=1 - [Q7TMC7_RAT]	nucleotide binding; metal ion binding; protein binding	extracellular; cytoplasm; mitochondrion; endosome; membrane; cell surface	transport; cellular homeostasis; regulation of biological process; response to stimulus	2.5	4.3				13.7			9.7	6.0
30	Q7TQ86	Ac1158 OS=Rattus norvegicus GN=Rsl1d1 PE=2 SV=1 - [Q7TQ86_RAT]	RNA binding; structural molecule activity	membrane	cell differentiation; metabolic process; regulation of biological process		100.0	3.6						100.0	50.9
31	P17764	Acetyl-CoA acetyltransferase, mitochondrial OS=Rattus norvegicus GN=Acat1 PE=1 SV=1 - [THIL_RAT]	catalytic activity; protein binding; metal ion binding	mitochondrion; membrane; organelle lumen	metabolic process; response to stimulus; cell organization and biogenesis	3.6	5.0	100.0	6.1	3.7	1.8		29.1	100.0	27.7
32	M0RAP9	Acetyltransferase component of pyruvate dehydrogenase complex OS=Rattus norvegicus PE=3 SV=1 - [M0RAP9_RAT]	catalytic activity	organelle lumen	metabolic process		3.2	5.4						4.6	3.3
33	Q9ER34	Aconitate hydratase, mitochondrial OS=Rattus norvegicus GN=Aco2 PE=1 SV=2 - [ACON_RAT]	catalytic activity; metal ion binding; protein binding	nucleus; mitochondrion	metabolic process	1.3	2.1	1.9	1.1	4.0	26.1		100.0	2.6	15.5

34	G3V6Z3	Actin filament-associated protein 1 OS=Rattus norvegicus GN=Afap1 PE=4 SV=1 - [G3V6Z3_RAT]	protein binding	cytoplasm; cytoskeleton	regulation of biological process; response to stimulus	1.4	3.0	5.2	5.4					7.0	3.7
35	Q4KM87 ★	Actin-like 6A OS=Rattus norvegicus GN=Actl6a PE=2 SV=1 - [Q4KM87_RAT]	DNA binding; nucleotide binding; protein binding	nucleus; membrane	cell organization and biogenesis; metabolic process	2.7	4.6	10.5	2.7	3.7	2.6	4.0	5.0	9.3	4.5
36	P86173 ★	Actin-like protein 6B OS=Rattus norvegicus GN=Actl6b PE=1 SV=2 - [ACL6B_RAT]	nucleotide binding	nucleus	cell organization and biogenesis; metabolic process; regulation of biological process	3.9	6.0	4.2	17.1	3.7	2.6	4.0	5.2	10.5	5.7
37	Q4V7C7	Actin-related protein 3 OS=Rattus norvegicus GN=Actr3 PE=1 SV=1 - [ARP3_RAT]	nucleotide binding; protein binding; structural molecule activity	membrane; cytoplasm; cytoskeleton	cell division; response to stimulus; regulation of biological process; cellular component movement; cell organization and biogenesis					100.0	3.9		100.0	2.9	51.7
38	P62738	Actin, aortic smooth muscle OS=Rattus norvegicus GN=Acta2 PE=2 SV=1 - [ACTA_RAT]	nucleotide binding; catalytic activity; protein binding	cytoplasm; cytoskeleton	cell death; response to stimulus; cell organization and biogenesis; cellular component movement	3.1	4.0	5.7	3.6	2.9	2.5	2.7	3.2	5.1	3.3
39	V9GZ85	Actin, cytoplasmic 2 (Fragment) OS=Rattus norvegicus GN=LOC100361457 PE=3 SV=1 - [V9GZ85_RAT]				3.3	3.8	5.7	3.5	2.9	2.7	2.9	2.8	5.6	3.3
40	Q9WVP7	Activity and neurotransmitter-induced early gene protein 4 OS=Rattus norvegicus GN=Dclk1 PE=2 SV=1 - [Q9WVP7_RAT]	catalytic activity; nucleotide binding		cellular component movement; metabolic process; cell organization and biogenesis; response to stimulus; cell differentiation; cell growth	5.1	2.8	5.4	6.4					4.4	4.0
41	D3ZUY8	Adaptor protein complex AP-2, alpha 1 subunit (Predicted) OS=Rattus norvegicus GN=Ap2a1 PE=4 SV=1 - [D3ZUY8_RAT]	protein binding; transporter activity	membrane	transport; regulation of biological process	1.7	3.5	2.9	1.1	2.2	18.6		100.0	3.2	14.8
42	Q05962	ADP/ATP translocase 1 OS=Rattus norvegicus GN=Slc25a4 PE=1 SV=3 - [ADT1_RAT]	transporter activity; protein binding	nucleus; mitochondrion; membrane	transport; cell organization and biogenesis; regulation of biological process; response to stimulus	1.6	3.1	2.1	1.8	1.8	2.9	1.7	2.8	2.3	2.0
43	Q09073	ADP/ATP translocase 2 OS=Rattus norvegicus GN=Slc25a5 PE=1 SV=3 - [ADT2_RAT]	transporter activity; protein binding; RNA binding	nucleus; mitochondrion; membrane	transport; regulation of biological process	1.5	3.0	2.3	1.5	2.0	3.4	1.7	2.2	2.4	2.0
44	Q9EQR2	Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Rattus norvegicus GN=Agps PE=2 SV=1 - [ADAS_RAT]	catalytic activity; nucleotide binding	mitochondrion; membrane	metabolic process; response to stimulus	5.5	3.5	3.4	2.9					51.9	11.2
45	D3ZZ99	Alpha-adducin OS=Rattus norvegicus GN=Add1 PE=4 SV=2 - [D3ZZ99_RAT]	structural molecule activity; protein binding; RNA binding	nucleus; cytoskeleton; membrane	cell organization and biogenesis; transport; cellular homeostasis; metabolic process; cell differentiation; regulation of biological process; response to stimulus	2.8	5.1	3.8	2.2			3.5	10.2	7.0	4.3
46	Q6MG11	Alpha-tubulin N-acetyltransferase 1 OS=Rattus norvegicus GN=Atat1 PE=3 SV=1 - [ATAT_RAT]	catalytic activity	cytoplasm; cytoskeleton; membrane	regulation of biological process; metabolic process	3.0	4.3	3.5	1.4	2.5	2.6	100.0	4.5	2.4	12.4
47	O70511	Ankyrin-3 OS=Rattus norvegicus GN=Ank3 PE=1 SV=3 - [ANK3_RAT]	structural molecule activity; protein binding	cytoplasm; vacuole; cytoskeleton; membrane; cell surface; endoplasmic reticulum	cell organization and biogenesis; regulation of biological process; response to stimulus; cellular component movement; transport	1.1	3.1	2.7	1.0	8.8	100.0		100.0	4.8	24.6
48	F1LNM3	Ankyrin-3 OS=Rattus norvegicus GN=Ank3 PE=4 SV=2 - [F1LNM3_RAT]	structural molecule activity; protein binding	membrane; endoplasmic reticulum	cell organization and biogenesis; regulation of biological process; response to stimulus; cellular component movement; transport	1.2	3.3	2.7	1.0	8.8	100.0		100.0	4.9	24.7
49	P18484	AP-2 complex subunit alpha-2 OS=Rattus norvegicus GN=Ap2a2 PE=1 SV=3 - [AP2A2_RAT]	protein binding; transporter activity	membrane	transport	2.0	5.8	3.3	1.3	2.2	4.4		100.0	3.7	13.6
50	P62944	AP-2 complex subunit beta OS=Rattus norvegicus GN=Ap2b1 PE=1 SV=1 - [AP2B1_RAT]	protein binding; transporter activity	membrane	transport; cell organization and biogenesis	1.8	2.7	1.8	1.6	2.8	4.7		20.2	3.2	4.3
51	P84092	AP-2 complex subunit mu OS=Rattus norvegicus GN=Ap2m1 PE=1 SV=1 - [AP2M1_RAT]	protein binding	mitochondrion; membrane	transport; regulation of biological process; response to stimulus	1.6	3.4	1.5	0.6	1.8	4.1		5.2	1.7	2.2
52	B1WC49 ★	Api5 protein OS=Rattus norvegicus GN=Api5 PE=2 SV=1 - [B1WC49_RAT]	protein binding; RNA binding	nucleus; spliceosomal complex; membrane	regulation of biological process	1.8	2.4	3.5	1.7	4.3	9.2	1.3	100.0	5.4	13.0
53	P15178	Aspartate--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Dars PE=2 SV=1 - [SYDC_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	metabolic process		6.8	7.6						8.0	5.6

54	F1LP05	ATP synthase subunit alpha OS=Rattus norvegicus GN=Atp5a1 PE=3 SV=1 - [F1LP05_RAT]	nucleotide binding; catalytic activity; transporter activity	mitochondrion; membrane	metabolic process; transport	1.5	3.9	3.9	2.1	2.1	2.0	100.0	3.9	2.7	12.2
55	Q641Y8	ATP-dependent RNA helicase DDX1 OS=Rattus norvegicus GN=Ddx1 PE=2 SV=1 - [DDX1_RAT]	nucleotide binding; DNA binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; membrane	metabolic process; response to stimulus; regulation of biological process; development	2.0	8.6	10.4	3.9	4.4	11.9	3.1	10.8	52.0	10.7
56	Q5U216	ATP-dependent RNA helicase DDX39A OS=Rattus norvegicus GN=Ddx39a PE=2 SV=1 - [DX39A_RAT]	nucleotide binding; catalytic activity; RNA binding	nucleus; cytoplasm; membrane	metabolic process; transport	2.4	3.7	4.1	2.4	2.1	2.0	1.5	6.3	5.6	3.0
57	D4A0W4 ★	B-cell leukemia/lymphoma 11B (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Bcl11b PE=4 SV=1 - [D4A0W4_RAT]	DNA binding; metal ion binding	nucleus	cell organization and biogenesis; metabolic process; regulation of biological process; cell differentiation; cellular component movement	1.1	4.1	2.1	1.4		1.9		100.0	4.3	14.4
58	B1H235	Banp protein OS=Rattus norvegicus GN=Banp PE=2 SV=1 - [B1H235_RAT]	protein binding	nucleus	regulation of biological process		100.0		3.1					53.4	39.1
59	F8WFS9	Beta-adducin OS=Rattus norvegicus GN=Add2 PE=4 SV=1 - [F8WFS9_RAT]	protein binding; structural molecule activity; metal ion binding	cytoplasm; cytoskeleton; membrane	cell organization and biogenesis; transport; regulation of biological process	2.6	4.2	4.0	2.4					4.9	3.0
60	B5DFM8 ★	Breast carcinoma amplified sequence 2 OS=Rattus norvegicus GN=Bcas2 PE=2 SV=1 - [B5DFM8_RAT]		nucleus; spliceosomal complex	metabolic process	5.2	15.7	27.1	2.5					17.0	11.2
61	D3ZWU1	Bromodomain containing 3 (Predicted), isoform CRA_b OS=Rattus norvegicus GN=Brd3 PE=4 SV=2 - [D3ZWU1_RAT]	protein binding		regulation of biological process	1.4	1.7	4.1	2.2			2.3		4.5	2.3
62	D3ZXX7 ★	Bromodomain containing 7 (Predicted) OS=Rattus norvegicus GN=Brd7 PE=4 SV=1 - [D3ZXX7_RAT]	protein binding; DNA binding	nucleus	regulation of biological process	1.2	3.3		3.1					3.3	2.2
63	Q9EQH5	C-terminal-binding protein 2 OS=Rattus norvegicus GN=Ctbp2 PE=1 SV=2 - [CTBP2_RAT]	catalytic activity; protein binding; nucleotide binding	nucleus	metabolic process; regulation of biological process; cell differentiation		31.7	52.0						51.7	33.8
64	Q91XJ0 ★	Calcium-responsive transcription coactivator OS=Rattus norvegicus GN=Ss18l1 PE=1 SV=1 - [CREST_RAT]	protein binding	chromosome; nucleus	metabolic process; regulation of biological process; cell organization and biogenesis		3.3	2.3						2.8	2.1
65	G3V9G3	Calcium/calmodulin-dependent protein kinase II, beta, isoform CRA_a OS=Rattus norvegicus GN=Camk2b PE=4 SV=1 - [G3V9G3_RAT]	nucleotide binding; catalytic activity; protein binding	cytosol; membrane	metabolic process; transport; regulation of biological process; response to stimulus; cell organization and biogenesis	1.9	4.1	2.6	1.8	3.1	3.4	3.0	21.4	3.2	4.5
66	P11275	Calcium/calmodulin-dependent protein kinase type II subunit alpha OS=Rattus norvegicus GN=Camk2a PE=1 SV=1 - [KCC2A_RAT]	nucleotide binding; catalytic activity; protein binding	nucleus; mitochondrion; membrane	response to stimulus; metabolic process; transport; regulation of biological process; cell organization and biogenesis	2.1	2.6	2.3	1.8	20.0	100.0			3.1	16.5
67	P15791	Calcium/calmodulin-dependent protein kinase type II subunit delta OS=Rattus norvegicus GN=Camk2d PE=1 SV=1 - [KCC2D_RAT]	nucleotide binding; catalytic activity; protein binding	nucleus; cytoplasm; cytosol; membrane; endoplasmic reticulum	response to stimulus; regulation of biological process; metabolic process; transport; cellular homeostasis; cell organization and biogenesis; cell growth; cellular component movement	2.1	2.6	2.3	1.8	20.0	100.0			3.1	16.5
68	P11730	Calcium/calmodulin-dependent protein kinase type II subunit gamma OS=Rattus norvegicus GN=Camk2g PE=2 SV=1 - [KCC2G_RAT]	nucleotide binding; catalytic activity; protein binding	membrane; endoplasmic reticulum	response to stimulus; metabolic process; transport; development; cell differentiation; regulation of biological process; cell organization and biogenesis	2.0	3.5	2.5	1.9	20.0	100.0		100.0	3.2	25.9
69	G3V9E3	Caldesmon 1, isoform CRA_b OS=Rattus norvegicus GN=Cald1 PE=4 SV=1 - [G3V9E3_RAT]	protein binding	membrane; cytoskeleton	cell organization and biogenesis; response to stimulus	1.2	2.8	21.1	1.5					18.5	7.5
70	P37397	Calponin-3 OS=Rattus norvegicus GN=Cnn3 PE=1 SV=1 - [CNN3_RAT]	protein binding	cytoplasm; cytoskeleton	cell differentiation; cell organization and biogenesis; regulation of biological process		8.4	100.0						100.0	52.1
71	P12369	cAMP-dependent protein kinase type II-beta regulatory subunit OS=Rattus norvegicus GN=Prkar2b PE=1 SV=3 - [KAP3_RAT]	nucleotide binding; enzyme regulator activity; protein binding; catalytic activity	cytoplasm; membrane	regulation of biological process; metabolic process; response to stimulus		100.0	100.0	7.8					50.8	51.7
72	Q5M9G3	Caprin-1 OS=Rattus norvegicus GN=Caprin1 PE=1 SV=2 - [CAPR1_RAT]	RNA binding	cytoplasm; cytosol; membrane	regulation of biological process; cell differentiation	1.9	3.6	100.0	1.9					12.3	19.9
73	Q9QX80	CArG-binding factor A OS=Rattus norvegicus GN=Hnrnpab PE=2 SV=1 - [Q9QX80_RAT]	nucleotide binding; DNA binding; RNA binding	nucleus; cytoplasm	regulation of biological process; cell organization and biogenesis	2.8	8.6	5.2	3.6	2.4	1.7	1.7	3.5	8.1	3.8

74	Q704S8	Carnitine O-acetyltransferase OS=Rattus norvegicus GN=Crat PE=1 SV=1 - [CACP_RAT]	catalytic activity; protein binding	mitochondrion; membrane; endoplasmic reticulum	metabolic process; transport	2.9	5.5	3.5	2.5	100.0	100.0			2.9	27.2
75	Q9JJ76 ★	Casein kinase 1 epsilon OS=Rattus norvegicus GN=Csnk1e PE=2 SV=1 - [Q9JJ76_RAT]	nucleotide binding; catalytic activity; RNA binding	nucleus; cytoplasm	metabolic process; transport; regulation of biological process; response to stimulus	3.3	3.7	2.7	2.6	2.0	2.9	2.1	100.0	4.9	12.4
76	Q06486 ★	Casein kinase I isoform delta OS=Rattus norvegicus GN=Csnk1d PE=1 SV=2 - [KC1D_RAT]	nucleotide binding; protein binding; catalytic activity	nucleus; cytoplasm; Golgi; cytoskeleton; membrane	regulation of biological process; metabolic process; transport; response to stimulus; cell organization and biogenesis	3.9	3.2	3.8	1.7	1.9	3.5		2.3	3.0	2.6
77	P04762	Catalase OS=Rattus norvegicus GN=Cat PE=1 SV=3 - [CATA_RAT]	catalytic activity; antioxidant activity; protein binding; metal ion binding; nucleotide binding	mitochondrion; vacuole; membrane; endoplasmic reticulum; Golgi; cytosol	response to stimulus; cell differentiation; metabolic process; regulation of biological process; cell organization and biogenesis	2.2	2.8	2.8	2.1					6.5	2.7
78	B4F786	CD2 antigen (Cytoplasmic tail) binding protein 2 (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Cd2bp2 PE=2 SV=1 - [B4F786_RAT]	protein binding	nucleus; cytoplasm	regulation of biological process	1.8	3.3	4.0						2.8	2.4
79	Q5U2X0	CDKN2A-interacting protein OS=Rattus norvegicus GN=Cdkn2aip PE=1 SV=1 - [CARF_RAT]	protein binding; RNA binding	nucleus; cytoplasm	response to stimulus; regulation of biological process	5.3	6.8	100.0	5.6					16.1	22.3
80	O08837	Cell division cycle 5-like protein OS=Rattus norvegicus GN=Cdc5l PE=1 SV=2 - [CDC5L_RAT]	DNA binding; RNA binding; protein binding	nucleus; spliceosomal complex; cytoplasm; membrane	metabolic process; response to stimulus; regulation of biological process; cell division	2.8	5.2	7.1	3.3	1.9	1.8	2.0	4.5	5.9	3.4
81	Q6AYK5 ★	Cell growth-regulating nucleolar protein OS=Rattus norvegicus GN=Lyar PE=2 SV=1 - [LYAR_RAT]	RNA binding; metal ion binding	nucleus		62.6	23.2	43.6	3.9					15.2	24.8
82	G3V9Z5	Centaurin, gamma 3 (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Agap3 PE=4 SV=1 - [G3V9Z5_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; cytoplasm	transport; metabolic process; response to stimulus; regulation of biological process		2.6	4.3	0.6					5.4	2.6
83	Q3MHS9	Chaperonin containing Tcp1, subunit 6A (Zeta 1) OS=Rattus norvegicus GN=Cct6a PE=2 SV=1 - [Q3MHS9_RAT]	nucleotide binding; RNA binding; protein binding	cytoplasm	metabolic process; transport	4.0	3.7	9.3	4.3					15.8	6.2
84	D4ACB8	Chaperonin subunit 8 (Theta) (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Cct8 PE=3 SV=1 - [D4ACB8_RAT]	nucleotide binding; protein binding	cytoplasm; cytosol; cytoskeleton	metabolic process; cell organization and biogenesis; transport	3.7	4.7	10.1	1.8		9.0		100.0	13.4	17.8
85	A0JPQ9 ★	Chitinase domain-containing protein 1 OS=Rattus norvegicus GN=Chid1 PE=2 SV=2 - [CHID1_RAT]	catalytic activity	extracellular; nucleus; vacuole; endosome; membrane	metabolic process; defense response; response to stimulus; regulation of biological process	3.6	4.1	100.0	1.4					14.5	20.6
86	Q5RJK5 ★	Chromobox homolog 3 (HP1 gamma homolog, Drosophila) OS=Rattus norvegicus GN=LOC100360260 PE=2 SV=1 - [Q5RJK5_RAT]	DNA binding; protein binding	chromosome; nucleus	regulation of biological process; response to stimulus	3.4	4.6	8.9	2.1					11.7	5.1
87	D3ZR50 ★	Chromodomain-helicase-DNA-binding protein 5 OS=Rattus norvegicus GN=Chd5 PE=4 SV=1 - [D3ZR50_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding; metal ion binding	nucleus	metabolic process; regulation of biological process	0.6	1.9	1.4		1.5	4.8		8.7	3.3	2.8
88	G3V936	Citrate synthase OS=Rattus norvegicus GN=Cs PE=3 SV=1 - [G3V936_RAT]	catalytic activity	mitochondrion; organelle lumen	metabolic process	1.4	2.2	2.0	1.2	2.0	3.1	2.3	3.5	2.5	2.0
89	P08082	Clathrin light chain B OS=Rattus norvegicus GN=Cltb PE=1 SV=1 - [CLCB_RAT]	structural molecule activity; transporter activity	cytoplasm; membrane	transport; cell organization and biogenesis	13.3			11.3					100.0	31.2
90	D4A0H5 ★	Cleavage and polyadenylation specific factor 1, 160kDa (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Cpsf1 PE=4 SV=1 - [D4A0H5_RAT]	RNA binding	nucleus	metabolic process	1.3	3.6	1.4	0.7	1.7	100.0	1.8	7.7	2.1	12.0
91	D3ZPL1	Cleavage and polyadenylation specific factor 6, 68kDa (Predicted), isoform CRA_b OS=Rattus norvegicus GN=Cpsf6 PE=4 SV=2 - [D3ZPL1_RAT]	nucleotide binding; RNA binding	nucleus; membrane	metabolic process; cell organization and biogenesis	2.1	3.2	5.1	1.6	2.5	1.4		18.6	6.2	4.5
92	Q5XI29	Cleavage and polyadenylation specificity factor subunit 7 OS=Rattus norvegicus GN=Cpsf7 PE=2 SV=1 - [CPSF7_RAT]	nucleotide binding; RNA binding	nucleus; membrane	metabolic process; cell organization and biogenesis	2.6	5.2	100.0	0.9					100.0	34.8
93	Q5BJQ6 ★	Cleavage stimulation factor subunit 1 OS=Rattus norvegicus GN=Cstf1 PE=2 SV=1 - [CSTF1_RAT]	protein binding; RNA binding	nucleus; cytoplasm	metabolic process	2.9	6.0	3.5	1.6					3.7	2.9

94	Q99JD4	CLIP-associating protein 2 OS=Rattus norvegicus GN=Clasp2 PE=2 SV=1 - [CLAP2_RAT]	protein binding	chromosome; cytoplasm; Golgi; cytoskeleton; membrane	cell organization and biogenesis; regulation of biological process; cellular component movement; cell division	2.1	17.9	2.6	0.6	3.4	3.0		6.6	6.2	4.7
95	P45592	Cofilin-1 OS=Rattus norvegicus GN=Cfl1 PE=1 SV=3 - [COF1_RAT]	protein binding	nucleus; cytoplasm; cytoskeleton; membrane	cellular component movement; metabolic process; transport; cell organization and biogenesis; response to stimulus; regulation of biological process	20.0	8.1	7.0	1.4				3.6	15.6	8.0
96	F1LMV9	Coronin (Fragment) OS=Rattus norvegicus GN=Coro2b PE=3 SV=2 - [F1LMV9_RAT]	protein binding	membrane	cell organization and biogenesis	2.3		2.2						10.7	3.8
97	G3V624	Coronin OS=Rattus norvegicus GN=Coro1c PE=3 SV=1 - [G3V624_RAT]	protein binding	cytoskeleton	cell organization and biogenesis	3.3	5.2	4.9	2.8	6.2	6.3	4.3	24.9	4.5	6.2
98	Q91ZN1	Coronin-1A OS=Rattus norvegicus GN=Coro1a PE=1 SV=3 - [COR1A_RAT]	protein binding; RNA binding	nucleus; cytoplasm; endosome; cytoskeleton; membrane	cell organization and biogenesis; transport; regulation of biological process; cellular component movement; cell differentiation; response to stimulus	4.9	5.0	12.8	7.0	100.0	100.0		100.0	4.4	37.1
99	O09018 ★	COUP transcription factor 2 OS=Rattus norvegicus GN=Nr2f2 PE=1 SV=1 - [COT2_RAT]	DNA binding; receptor activity; signal transducer activity; metal ion binding; protein binding	nucleus	regulation of biological process; cellular component movement; metabolic process; response to stimulus; cell differentiation	2.4	4.1	2.6	3.5	2.8	4.4			3.6	2.9
100	P63155 ★	Crooked neck-like protein 1 OS=Rattus norvegicus GN=Crnkl1 PE=2 SV=1 - [CRNL1_RAT]	RNA binding; protein binding	nucleus; spliceosomal complex	cell organization and biogenesis; metabolic process	4.2	4.5	3.8						33.1	9.1
101	Q4QQT3	CUGBP Elav-like family member 1 OS=Rattus norvegicus GN=Celf1 PE=2 SV=1 - [CELF1_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; membrane	cell organization and biogenesis; metabolic process; regulation of biological process	2.2	6.1	6.1	2.4	5.7				4.6	3.9
102	Z4YNP1	CUGBP Elav-like family member 2 OS=Rattus norvegicus GN=Celf2 PE=4 SV=1 - [Z4YNP1_RAT]	nucleotide binding; RNA binding			2.1	14.1	7.7	3.5	3.7	3.3	20.6	3.1	4.5	6.3
103	B1WBY1	Cul1 protein OS=Rattus norvegicus GN=Cul1 PE=2 SV=1 - [B1WBY1_RAT]	protein binding		metabolic process; cell death; cell proliferation		24.2		2.4					3.3	7.5
104	P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	protein binding	nucleus; cytoplasm; membrane	metabolic process; regulation of biological process; transport; cell organization and biogenesis; cell differentiation		3.9	2.5	1.1	1.8	15.1		4.9	3.5	4.1
105	P15337 ★	Cyclic AMP-responsive element-binding protein 1 OS=Rattus norvegicus GN=Creb1 PE=1 SV=1 - [CREB1_RAT]	DNA binding; protein binding	chromosome; nucleus; mitochondrion	metabolic process; regulation of biological process; response to stimulus; cell organization and biogenesis; transport; cell differentiation		6.8	2.7						7.5	4.2
106	Q5M963	Cytidine monophosphate N-acetylneuraminic acid synthetase OS=Rattus norvegicus GN=Cmas PE=2 SV=1 - [Q5M963_RAT]	catalytic activity	nucleus; membrane	metabolic process	1.6	3.3	2.5	1.1	4.2	9.5	23.6	100.0	2.8	14.9
107	Q68FY0	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Rattus norvegicus GN=Uqcrc1 PE=1 SV=1 - [QCR1_RAT]	catalytic activity; metal ion binding; protein binding	mitochondrion; membrane	metabolic process; transport; response to stimulus	2.5	3.3	4.2	1.1					52.4	10.6
108	P00406	Cytochrome c oxidase subunit 2 OS=Rattus norvegicus GN=Mtco2 PE=2 SV=2 - [COX2_RAT]	catalytic activity; transporter activity; metal ion binding	mitochondrion; membrane	transport; response to stimulus; metabolic process		100.0	12.1						8.8	30.2
109	P38650	Cytoplasmic dynein 1 heavy chain 1 OS=Rattus norvegicus GN=Dync1h1 PE=1 SV=1 - [DYHC1_RAT]	nucleotide binding; catalytic activity; motor activity; protein binding; RNA binding	cytoplasm; Golgi; cytoskeleton; membrane	metabolic process; transport; cellular component movement; cell organization and biogenesis	1.0	2.5	1.4	0.7	1.7	12.2	2.5	14.9	2.1	3.9
110	F1LRT9	Cytoplasmic dynein 1 heavy chain 1 OS=Rattus norvegicus GN=Dync1h1 PE=4 SV=2 - [F1LRT9_RAT]	nucleotide binding; catalytic activity; motor activity		metabolic process; cellular component movement	1.1	2.5	1.3	0.7	1.6	10.8	2.8	13.0	2.1	3.6
111	G3V792	Cytoplasmic dynein 1 intermediate chain 1 OS=Rattus norvegicus GN=Dync1i1 PE=4 SV=2 - [G3V792_RAT]	protein binding	chromosome	cellular component movement	14.3	6.6	5.1	2.3					6.1	5.7
112	D3ZU74	Cytoplasmic dynein 1 intermediate chain 2 OS=Rattus norvegicus GN=Dync1i2 PE=4 SV=1 - [D3ZU74_RAT]	catalytic activity; motor activity; protein binding		transport; cellular component movement; metabolic process	2.5	5.2	3.8	1.7	2.2	2.0			5.0	2.8
113	Q5D023	Cytoplasmic dynein 1 light intermediate chain 2 OS=Rattus norvegicus GN=Dync1li2 PE=2 SV=1 - [Q5D023_RAT]	catalytic activity; motor activity; nucleotide binding	membrane	cell organization and biogenesis; cellular component movement; transport; metabolic process	3.3	6.5	4.5	2.6					5.8	3.8

114	D4A8H8	Cytoplasmic FMR1 interacting protein 1 (Predicted) OS=Rattus norvegicus GN=Cyfip1 PE=4 SV=1 - [D4A8H8_RAT]	protein binding	cytoplasm	regulation of biological process; response to stimulus; cell organization and biogenesis; cell growth	1.2	3.4	2.0	1.1	2.5	6.6	1.4	4.9	3.0	2.6
115	D3ZX82	Cytoplasmic FMR1 interacting protein 2 (Predicted) OS=Rattus norvegicus GN=Cyfip2 PE=4 SV=2 - [D3ZX82_RAT]	nucleotide binding	cytoplasm; membrane	cell death; regulation of biological process; metabolic process	1.4	3.0	1.6	1.5	2.6	11.3		9.9	2.6	3.8
116	Q4KLZ3	DAZ associated protein 1 OS=Rattus norvegicus GN=Dazap1 PE=2 SV=1 - [Q4KLZ3_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm	cell proliferation; regulation of biological process	2.4	3.5	2.2	0.5				6.3	4.9	2.8
117	A0A096MIX2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a OS=Rattus norvegicus GN=Ddx17 PE=4 SV=1 - [A0A096MIX2_RAT]	catalytic activity; nucleotide binding; protein binding; RNA binding	nucleus; membrane	metabolic process; regulation of biological process	2.1	3.2	2.9	1.5	3.5	3.6	2.9	7.1	2.9	3.0
118	G3V9M1 ★	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23 (Predicted), isoform CRA_b OS=Rattus norvegicus GN=Ddx23 PE=3 SV=1 - [G3V9M1_RAT]	nucleotide binding; DNA binding; catalytic activity; RNA binding	nucleus; mitochondrion; membrane; spliceosomal complex	metabolic process	2.2	2.7	13.5	1.9	1.4	3.0		100.0	50.2	19.4
119	Q6AYI1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 OS=Rattus norvegicus GN=Ddx5 PE=1 SV=1 - [Q6AYI1_RAT]	nucleotide binding; catalytic activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	regulation of biological process; metabolic process; response to stimulus	2.0	3.0	2.7	1.6	2.7	3.5	2.9	5.4	2.8	2.7
120	D4ADE8	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked OS=Rattus norvegicus GN=Ddx3x PE=4 SV=2 - [D4ADE8_RAT]	DNA binding; RNA binding; catalytic activity; nucleotide binding; protein binding	nucleus; cytoplasm	metabolic process; regulation of biological process; response to stimulus; cell organization and biogenesis; defense response	2.3	2.9	2.7	1.4	2.9	3.5	9.6	1.3	3.0	3.0
121	D3ZD97	DEAH (Asp-Glu-Ala-His) box polypeptide 15 (Predicted), isoform CRA_b OS=Rattus norvegicus GN=Dhx15 PE=4 SV=1 - [D3ZD97_RAT]	nucleotide binding; RNA binding; catalytic activity	nucleus; spliceosomal complex; cytoplasm	metabolic process	1.4	3.1	2.0	1.1	2.9	6.9	4.4	10.4	2.5	3.5
122	D4A9D6	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (Predicted) OS=Rattus norvegicus GN=Dhx9 PE=4 SV=1 - [D4A9D6_RAT]	nucleotide binding; protein binding; RNA binding; catalytic activity	nucleus; cytoplasm; membrane	cell differentiation; metabolic process; response to stimulus; regulation of biological process	1.4	3.3	1.7	0.7	2.6	6.6	3.5	8.7	2.0	3.1
123	Q7M0E3	Destrin OS=Rattus norvegicus GN=Dstn PE=1 SV=3 - [DEST_RAT]	protein binding	cytoplasm; cytoskeleton	cellular component movement; cell organization and biogenesis; regulation of biological process		100.0	12.5	7.1					100.0	43.9
124	G3V9K8 ★	Developmentally regulated RNA-binding protein 1 OS=Rattus norvegicus GN=Rbm45 PE=4 SV=1 - [G3V9K8_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm	cell differentiation	100.0	3.1		4.6					75.9	36.7
125	B2GV15	Dihydrolipoamide branched chain transacylase E2 OS=Rattus norvegicus GN=Dbt PE=2 SV=1 - [B2GV15_RAT]	catalytic activity	cytoplasm; mitochondrion; cytoskeleton	metabolic process		20.0	2.8	100.0					100.0	44.5
126	Q62950	Dihydropyrimidinase-related protein 1 OS=Rattus norvegicus GN=Crmp1 PE=1 SV=1 - [DPYL1_RAT]	catalytic activity; protein binding	cytoplasm; cytoskeleton	metabolic process	2.0	3.3	3.3	2.1	2.7	2.4	16.1	11.2	4.0	4.7
127	P47942	Dihydropyrimidinase-related protein 2 OS=Rattus norvegicus GN=Dpysl2 PE=1 SV=1 - [DPYL2_RAT]	protein binding; catalytic activity	cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	response to stimulus; metabolic process; transport; cell organization and biogenesis; development; regulation of biological process; cell differentiation	2.6	3.5	4.1	3.8	4.1	2.7	5.0	6.6	4.5	3.7
128	Q62952	Dihydropyrimidinase-related protein 3 OS=Rattus norvegicus GN=Dpysl3 PE=1 SV=2 - [DPYL3_RAT]	catalytic activity; protein binding	cytoplasm; cytosol	metabolic process; regulation of biological process; response to stimulus; cell organization and biogenesis	2.3	3.2	3.2	2.4	3.9	3.9	15.3	26.1	3.7	6.4
129	Q62951	Dihydropyrimidinase-related protein 4 (Fragment) OS=Rattus norvegicus GN=Dpysl4 PE=1 SV=1 - [DPYL4_RAT]	catalytic activity; protein binding	cytoplasm	metabolic process		83.6		2.8					20.8	26.8
130	Q9JHU0	Dihydropyrimidinase-related protein 5 OS=Rattus norvegicus GN=Dpysl5 PE=1 SV=1 - [DPYL5_RAT]	protein binding; catalytic activity	cytoplasm	metabolic process; cell differentiation	3.9	4.8	4.3	2.6	3.7	4.1	100.0	41.7	6.8	17.2
131	Q6P730	Disabled homolog 2-interacting protein OS=Rattus norvegicus GN=Dab2ip PE=1 SV=1 - [DAB2P_RAT]	enzyme regulator activity; protein binding	cytoplasm; membrane	regulation of biological process; cell death; response to stimulus; metabolic process; development; cellular component movement; cell organization and biogenesis	2.6		80.3		14.8	4.7			3.1	17.6

132	D4ABM3	Dishevelled associated activator of morphogenesis 1 (Predicted) OS=Rattus norvegicus GN=Daam1 PE=4 SV=1 - [D4ABM3_RAT]	protein binding	cytoplasm; membrane	cell organization and biogenesis		100.0	100.0						9.3	52.3
133	Q568Y6 ★	DNA methyltransferase 1-associated protein 1 OS=Rattus norvegicus GN=Dmap1 PE=2 SV=1 - [Q568Y6_RAT]	protein binding; catalytic activity	nucleus; cytoplasm	regulation of biological process; metabolic process; response to stimulus; cell organization and biogenesis	3.3		13.1	3.3					12.5	6.4
134	Q9WUL0	DNA topoisomerase 1 OS=Rattus norvegicus GN=Top1 PE=2 SV=1 - [TOP1_RAT]	DNA binding; catalytic activity; nucleotide binding; protein binding; RNA binding	chromosome; nucleus; cytoplasm	metabolic process; cell organization and biogenesis; response to stimulus; regulation of biological process; cell division	1.5	3.1	2.6	1.6	3.5	5.7	3.3	6.6	2.5	3.0
135	F1M7A0	DNA topoisomerase 2 (Fragment) OS=Rattus norvegicus GN=Top2a PE=3 SV=2 - [F1M7A0_RAT]	nucleotide binding; metal ion binding; DNA binding; catalytic activity; protein binding	chromosome; nucleus	metabolic process; response to stimulus; cell organization and biogenesis; cell division; regulation of biological process	1.9	6.3	3.8	1.4	2.5	16.9	2.2	14.3	7.0	5.6
136	P43138	DNA-(apurinic or apyrimidinic site) lyase OS=Rattus norvegicus GN=Apex1 PE=1 SV=2 - [APEX1_RAT]	DNA binding; RNA binding; catalytic activity; protein binding; metal ion binding	nucleus; cytoplasm; mitochondrion; endoplasmic reticulum	metabolic process; response to stimulus; regulation of biological process; cellular homeostasis	1.6	5.4	4.9	0.5	5.0	3.2			100.0	15.1
137	P07153	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Rattus norvegicus GN=Rpn1 PE=2 SV=1 - [RPN1_RAT]	catalytic activity; RNA binding	endoplasmic reticulum; membrane	metabolic process; transport	1.0	2.4	2.1	1.3	1.7	2.5	1.7	14.1	2.7	2.9
138	Q07266	Drebrin OS=Rattus norvegicus GN=Dbn1 PE=1 SV=3 - [DREB_RAT]	protein binding	cytoplasm; membrane; cytoskeleton	cell organization and biogenesis; development; cell communication; cell differentiation; cell proliferation	4.3	7.2	7.3	4.1	4.2	5.0	4.2	10.9	10.4	5.7
139	D4A8U7	Dynactin 1, isoform CRA_a OS=Rattus norvegicus GN=Dctn1 PE=4 SV=2 - [D4A8U7_RAT]	catalytic activity; motor activity; protein binding	chromosome; cytoplasm; cytoskeleton; membrane	cell organization and biogenesis; transport; metabolic process; cellular component movement; regulation of biological process	1.0	6.4	2.3	1.2	2.8	12.2	2.3	30.5	3.8	6.2
140	P28023	Dynactin subunit 1 OS=Rattus norvegicus GN=Dctn1 PE=1 SV=2 - [DCTN1_RAT]	catalytic activity; motor activity; protein binding	chromosome; cytoplasm; cytoskeleton; membrane	cell organization and biogenesis; transport; metabolic process; cellular component movement; regulation of biological process	1.0	4.7	2.5	1.1	2.8	12.2	2.3	30.5	3.6	6.1
141	Q6AYH5	Dynactin subunit 2 OS=Rattus norvegicus GN=Dctn2 PE=1 SV=1 - [DCTN2_RAT]	catalytic activity; motor activity; protein binding	chromosome; cytoplasm; cytoskeleton; membrane	cell organization and biogenesis; metabolic process; cell proliferation; transport		2.6	66.7						53.0	30.6
142	D3ZQQ5	Dynamin-1 OS=Rattus norvegicus GN=Dnm1 PE=3 SV=2 - [D3ZQQ5_RAT]	nucleotide binding; catalytic activity		metabolic process	6.4	5.1	6.6	3.7	3.1	4.7		100.0	52.0	20.2
143	P39052	Dynamin-2 OS=Rattus norvegicus GN=Dnm2 PE=1 SV=1 - [DYN2_RAT]	nucleotide binding; catalytic activity; protein binding	membrane; nucleus; cytoplasm; endosome; Golgi; cytosol; cytoskeleton	metabolic process; transport; response to stimulus; regulation of biological process; cell organization and biogenesis	5.5	4.2	5.5	4.0	3.0	4.5		39.8	21.3	9.8
144	A0A0A0MY48	Dynamin-2 OS=Rattus norvegicus GN=Dnm2 PE=4 SV=1 - [A0A0A0MY48_RAT]				5.5	4.2	5.4	4.0	3.0	4.5		39.8	21.3	9.7
145	D4A0D1	Dynamin-3 OS=Rattus norvegicus GN=Dnm3 PE=3 SV=2 - [D4A0D1_RAT]	nucleotide binding; catalytic activity		metabolic process	2.7	4.6	6.0	3.1	3.0	1.7		39.8	52.0	12.5
146	D4AAL9	Dynamin-3 OS=Rattus norvegicus GN=Dnm3 PE=3 SV=2 - [D4AAL9_RAT]	nucleotide binding; catalytic activity		metabolic process	2.8	4.2	6.0	2.1					14.4	4.9
147	D4A8U5	Dynamin-like 120 kDa protein, mitochondrial OS=Rattus norvegicus GN=Opa1 PE=4 SV=2 - [D4A8U5_RAT]	nucleotide binding; catalytic activity	mitochondrion; membrane	metabolic process; cell organization and biogenesis; regulation of biological process; response to stimulus		100.0	4.2	2.0					45.1	30.3
148	P63170	Dynein light chain 1, cytoplasmic OS=Rattus norvegicus GN=Dynll1 PE=1 SV=1 - [DYL1_RAT]	catalytic activity; motor activity; enzyme regulator activity; protein binding	chromosome; nucleus; cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	metabolic process; regulation of biological process; transport; cell death	4.6	10.1	3.9	2.7					2.8	4.0
149	Q78P75	Dynein light chain 2, cytoplasmic OS=Rattus norvegicus GN=Dynll2 PE=1 SV=1 - [DYL2_RAT]	catalytic activity; motor activity; protein binding	nucleus; cytoplasm; cytoskeleton; membrane	transport; metabolic process	2.2			2.7					2.9	2.0

150	Q9Z336	Dynein light chain Tctex-type 1 OS=Rattus norvegicus GN=Dynlt1 PE=1 SV=1 - [DYLT1_RAT]	catalytic activity; motor activity; protein binding	cytoplasm; Golgi; cytoskeleton	cell organization and biogenesis; transport; metabolic process; regulation of biological process; cell division		6.2	5.2						4.0	3.9
151	Q4KLY4	E3 ubiquitin-protein ligase RING2 OS=Rattus norvegicus GN=Rnf2 PE=2 SV=1 - [RING2_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; chromosome	regulation of biological process; metabolic process; cell organization and biogenesis; response to stimulus	3.2	3.2	100.0	2.9					23.0	22.0
152	F1LP64	E3 ubiquitin-protein ligase TRIP12 OS=Rattus norvegicus GN=Trip12 PE=2 SV=1 - [TRIPC_RAT]	catalytic activity; protein binding	nucleus; cytoplasm	metabolic process; response to stimulus; regulation of biological process	1.1	4.2	2.8	2.6	4.2	8.7	3.3	100.0	3.8	13.0
153	O09032 ★	ELAV-like protein 4 OS=Rattus norvegicus GN=Elavl4 PE=1 SV=1 - [ELAV4_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; cytosol; cytoskeleton; membrane; ribosome	response to stimulus; cell differentiation; regulation of biological process; cell organization and biogenesis	3.4	6.1	4.0	2.4					3.7	3.3
154	B5DF91	ELAV-like protein OS=Rattus norvegicus GN=Elavl1 PE=2 SV=1 - [B5DF91_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; membrane	regulation of biological process	4.2	7.4	7.0	1.5	2.7	1.6	1.2	2.6	5.5	3.4
155	G3V6U4	ELAV-like protein OS=Rattus norvegicus GN=Elavl2 PE=3 SV=2 - [G3V6U4_RAT]	nucleotide binding; RNA binding			3.4	4.8	4.7	3.5					3.9	3.4
156	Q76IJ9	ELAV-like protein OS=Rattus norvegicus GN=Elavl3 PE=2 SV=1 - [Q76IJ9_RAT]	nucleotide binding; RNA binding			2.7	3.7	3.9	2.7					3.2	2.7
157	F1LPE9	ELKS/Rab6-interacting/CAST family member 1 OS=Rattus norvegicus GN=Erc1 PE=4 SV=1 - [F1LPE9_RAT]	protein binding	cytoplasm	metabolic process; transport	2.9		1.5	1.2	2.3	2.8		100.0	4.5	14.4
158	M0R757	Elongation factor 1-alpha OS=Rattus norvegicus GN=LOC100360413 PE=3 SV=1 - [M0R757_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; membrane	metabolic process; response to stimulus	3.2	5.7	7.0	5.3	2.2	2.2	1.8	2.8	5.7	3.6
159	Q68FR9	Elongation factor 1-delta OS=Rattus norvegicus GN=Eef1d PE=1 SV=2 - [EF1D_RAT]	DNA binding; RNA binding; signal transducer activity	nucleus; cytoplasm	metabolic process; regulation of biological process; response to stimulus	57.2	3.9	15.7	4.4	16.5	1.3			12.0	13.9
160	Q68FR6	Elongation factor 1-gamma OS=Rattus norvegicus GN=Eef1g PE=1 SV=3 - [EF1G_RAT]	RNA binding; protein binding	nucleus; membrane	metabolic process; response to stimulus	3.5	4.5	4.7	1.8	3.0	9.7		2.5	5.9	4.0
161	P05197	Elongation factor 2 OS=Rattus norvegicus GN=Eef2 PE=1 SV=4 - [EF2_RAT]	nucleotide binding; RNA binding; catalytic activity; translation regulator activity; protein binding	nucleus; cytoplasm; membrane	cell differentiation; metabolic process; regulation of biological process	2.4	4.6	5.4	2.2	3.1	4.2	3.5	6.3	52.7	8.4
162	P85834	Elongation factor Tu, mitochondrial OS=Rattus norvegicus GN=Tufm PE=1 SV=1 - [EFTU_RAT]	nucleotide binding; RNA binding; catalytic activity	mitochondrion; membrane	metabolic process	2.6	18.5	100.0	4.4					4.3	21.6
163	F1M8I7	Ena/VASP-like protein (Fragment) OS=Rattus norvegicus GN=Evl PE=4 SV=1 - [F1M8I7_RAT]	protein binding	cytoplasm; cytoskeleton	cell organization and biogenesis		17.2	27.8	34.7					100.0	35.9
164	A0A0A0MY09	Endoplasmin OS=Rattus norvegicus GN=Hsp90b1 PE=4 SV=1 - [A0A0A0MY09_RAT]				1.2	2.8	4.2	1.3					4.3	2.3
165	Q5XIC0	Enoyl-CoA delta isomerase 2, mitochondrial OS=Rattus norvegicus GN=Eci2 PE=1 SV=1 - [ECI2_RAT]	catalytic activity; protein binding	nucleus; mitochondrion; organelle lumen; membrane	metabolic process	21.2	4.5		2.6					100.0	25.7
166	Q66HT2	Epidermal Langerhans cell protein LCP1 OS=Rattus norvegicus GN=Tox4 PE=2 SV=1 - [Q66HT2_RAT]	DNA binding; protein binding	chromosome; nucleus	cell organization and biogenesis; regulation of biological process	3.6	20.5	7.5	5.5					100.0	22.8
167	P56571	ES1 protein homolog, mitochondrial OS=Rattus norvegicus PE=1 SV=2 - [ES1_RAT]		mitochondrion		6.5	6.8	7.2	6.2					6.5	5.5
168	Q5RKI1	Eukaryotic initiation factor 4A-II OS=Rattus norvegicus GN=Eif4a2 PE=1 SV=1 - [IF4A2_RAT]	nucleotide binding; RNA binding; catalytic activity		metabolic process; regulation of biological process		3.6	22.9	2.3		100.0			3.6	22.1
169	Q3B8Q2 ★	Eukaryotic initiation factor 4A-III OS=Rattus norvegicus GN=Eif4a3 PE=1 SV=1 - [IF4A3_RAT]	nucleotide binding; RNA binding; catalytic activity	nucleus; spliceosomal complex; cytoplasm; membrane	metabolic process; regulation of biological process; transport	2.4	4.7	5.1	1.6	3.5	3.6	3.0	100.0	3.8	12.8
170	B5DEN5	Eukaryotic translation elongation factor 1 beta 2 OS=Rattus norvegicus GN=Eef1b2 PE=2 SV=1 - [B5DEN5_RAT]	RNA binding		metabolic process	6.2	6.6	87.7	12.3					52.4	27.5
171	P81795	Eukaryotic translation initiation factor 2 subunit 3 OS=Rattus norvegicus GN=Eif2s3 PE=1 SV=2 - [IF2G_RAT]	nucleotide binding; RNA binding; catalytic activity		metabolic process		2.4			100.0	4.6			53.7	32.1

172	Q6P685	Eukaryotic translation initiation factor 2, subunit 2 (Beta) OS=Rattus norvegicus GN=Eif2s2 PE=2 SV=1 - [Q6P685_RAT]	RNA binding; protein binding		cell proliferation; metabolic process	3.2	39.8	3.9	3.2	2.5	3.8		6.6	12.2	8.3
173	B5DFC8	Eukaryotic translation initiation factor 3 subunit C OS=Rattus norvegicus GN=Eif3c PE=2 SV=1 - [EIF3C_RAT]	RNA binding; protein binding	cytoplasm	cell organization and biogenesis; metabolic process; regulation of biological process	1.4	3.5	2.0						10.5	3.5
174	Q5RK09	Eukaryotic translation initiation factor 3 subunit G OS=Rattus norvegicus GN=Eif3g PE=2 SV=1 - [EIF3G_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm	cell organization and biogenesis; metabolic process; regulation of biological process		100.0	100.0						54.9	63.7
175	Q6P3V8	Eukaryotic translation initiation factor 4A1 OS=Rattus norvegicus GN=Eif4a1 PE=2 SV=1 - [Q6P3V8_RAT]	nucleotide binding; RNA binding; catalytic activity	cytoplasm; membrane	metabolic process	3.3	6.0	4.8	2.5	3.1	100.0			12.4	16.5
176	Q5RKG9	Eukaryotic translation initiation factor 4B OS=Rattus norvegicus GN=Eif4b PE=2 SV=1 - [Q5RKG9_RAT]	nucleotide binding; RNA binding		metabolic process		4.1	3.0	3.7					100.0	22.2
177	Q3T1J1	Eukaryotic translation initiation factor 5A-1 OS=Rattus norvegicus GN=Eif5a PE=1 SV=3 - [IF5A1_RAT]	RNA binding; protein binding	nucleus; cytoplasm; endoplasmic reticulum; membrane	transport; metabolic process; cell death; regulation of biological process	7.7	21.8	24.3	11.5					57.6	20.5
178	B1WC50	Ewsr1 protein OS=Rattus norvegicus GN=Ewsr1 PE=2 SV=1 - [B1WC50_RAT]	nucleotide binding; metal ion binding; protein binding; RNA binding	nucleus; cytoplasm		1.0	1.7	1.1	100.0	3.4	1.9	1.4	4.3	1.7	11.6
179	Q5XI32	F-actin-capping protein subunit beta OS=Rattus norvegicus GN=Capzb PE=1 SV=1 - [CAPZB_RAT]	protein binding	cytoplasm; cytoskeleton; membrane	cell organization and biogenesis; regulation of biological process	3.8	5.0	15.6	2.9					6.3	5.6
180	B5DF95	Family with sequence similarity 164, member A OS=Rattus norvegicus GN=Zc2hc1a PE=2 SV=1 - [B5DF95_RAT]			metabolic process; response to stimulus	100.0	1.1	7.2	2.7					3.6	19.1
181	M0R961	Far upstream element-binding protein 2 OS=Rattus norvegicus GN=Khsrp PE=4 SV=1 - [M0R961_RAT]	DNA binding; RNA binding; protein binding	nucleus; cytoplasm; membrane	metabolic process; regulation of biological process; transport	2.1	3.3	2.4	1.6	2.1	3.1	100.0	5.9	3.8	12.4
182	P85845	Fascin OS=Rattus norvegicus GN=Fscn1 PE=1 SV=2 - [FSCN1_RAT]	protein binding; RNA binding	cytoplasm; cytosol; cytoskeleton; membrane	cellular component movement; cell organization and biogenesis; cell communication; response to stimulus	3.1	7.7	3.5	2.0					3.4	3.3
183	C0JPT7	Filamin alpha OS=Rattus norvegicus GN=Flna PE=2 SV=1 - [C0JPT7_RAT]	protein binding; signal transducer activity; RNA binding	nucleus; cytoplasm; cytosol; membrane; cytoskeleton	cell organization and biogenesis; regulation of biological process; response to stimulus; metabolic process; transport	1.5	4.6	3.1	1.3					4.6	2.5
184	Q5RKI5	Flightless I homolog (Drosophila) OS=Rattus norvegicus GN=Flii PE=2 SV=1 - [Q5RKI5_RAT]	protein binding	nucleus; cytoplasm	development; cell organization and biogenesis	0.5	32.2	3.3	1.3					12.0	8.2
185	F1M742	Formin-binding protein 1-like (Fragment) OS=Rattus norvegicus GN=Fnbp1l PE=4 SV=1 - [F1M742_RAT]	protein binding			17.5	10.7	5.2	2.6					3.9	6.6
186	Q80WE1	Fragile X mental retardation protein 1 homolog OS=Rattus norvegicus GN=Fmr1 PE=1 SV=2 - [FMR1_RAT]	RNA binding; protein binding	nucleus; cytoplasm; membrane	regulation of biological process; transport		2.1	100.0						4.1	26.6
187	P05065	Fructose-bisphosphate aldolase A OS=Rattus norvegicus GN=Aldoa PE=1 SV=2 - [ALDOA_RAT]	protein binding; catalytic activity; RNA binding	nucleus; cytoplasm; mitochondrion; cytoskeleton; membrane	response to stimulus; metabolic process; regulation of biological process; cellular homeostasis; cell organization and biogenesis	1.8	5.2	7.2	3.1	4.3	4.5		1.1	7.0	3.8
188	P09117	Fructose-bisphosphate aldolase C OS=Rattus norvegicus GN=Aldoc PE=1 SV=3 - [ALDOC_RAT]	catalytic activity; protein binding	cytoplasm; mitochondrion	response to stimulus; metabolic process; cell death; cell differentiation; cell organization and biogenesis	1.4	11.7	6.7	3.8					5.3	4.8
189	Q4KM38	FUS interacting protein (Serine-arginine rich) 1 OS=Rattus norvegicus GN=Srsf10 PE=2 SV=1 - [Q4KM38_RAT]	nucleotide binding; RNA binding		metabolic process; cell organization and biogenesis; transport; regulation of biological process	6.0	5.3	4.3	3.1					51.4	11.7
190	F1LNV7 ★	General transcription factor 3C polypeptide 1 OS=Rattus norvegicus GN=Gtf3c1 PE=4 SV=1 - [F1LNV7_RAT]		nucleus			3.0				100.0		100.0	3.3	41.3
191	Q5U2Y1	General transcription factor II-I OS=Rattus norvegicus GN=Gtf2i PE=2 SV=2 - [GTF2I_RAT]	DNA binding; protein binding	nucleus; cytoplasm; membrane	metabolic process; regulation of biological process; cellular homeostasis	6.6	5.9	6.5	4.9					12.0	6.0
192	D4A7Q9	General transcription factor IIIC, polypeptide 3, 102kDa (Predicted) OS=Rattus norvegicus GN=Gtf3c3 PE=4 SV=1 - [D4A7Q9_RAT]	protein binding			2.7		32.2						6.5	10.3

193	M0R590	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus GN=LOC685186 PE=3 SV=1 - [M0R590_RAT]	catalytic activity; nucleotide binding		metabolic process	2.9	6.0	6.0	5.9					4.4	4.2
194	M0R660	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus GN=RGD1565368 PE=3 SV=1 - [M0R660_RAT]	catalytic activity; nucleotide binding	cytoplasm; membrane	metabolic process; regulation of biological process; response to stimulus	2.5	24.5	4.1	5.9					4.4	6.9
195	Q0VGK4	Glycerophosphodiester phosphodiesterase domain-containing protein 1 OS=Rattus norvegicus GN=Gdpd1 PE=2 SV=1 - [GDPD1_RAT]	catalytic activity; metal ion binding	membrane	metabolic process	2.3	24.8	68.3						5.4	20.2
196	F1LP91	Glycogen synthase kinase-3 alpha OS=Rattus norvegicus GN=Gsk3a PE=4 SV=2 - [F1LP91_RAT]	nucleotide binding; catalytic activity		metabolic process; regulation of biological process; response to stimulus; cellular component movement		7.8	8.0	2.8	24.5	26.8			51.6	17.4
197	P18266	Glycogen synthase kinase-3 beta OS=Rattus norvegicus GN=Gsk3b PE=1 SV=1 - [GSK3B_RAT]	nucleotide binding; protein binding; catalytic activity	nucleus; cytoplasm; cytosol; membrane	cell organization and biogenesis; regulation of biological process; metabolic process; transport; response to stimulus; development; cell differentiation; cellular component movement		9.9	5.1	3.4	100.0	100.0			7.8	32.3
198	M0R4R4	Growth arrest-specific protein 7 (Fragment) OS=Rattus norvegicus GN=Gas7 PE=4 SV=1 - [M0R4R4_RAT]	protein binding		regulation of biological process; cell organization and biogenesis; cell differentiation	1.1	16.3	100.0	3.6					100.0	36.8
199	P62828	GTP-binding nuclear protein Ran OS=Rattus norvegicus GN=Ran PE=1 SV=3 - [RAN_RAT]	nucleotide binding; catalytic activity; protein binding; RNA binding	chromosome; nucleus; cytoplasm; membrane; endosome	transport; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; cell division	2.5	5.2	2.6	1.9	2.1	2.4			2.8	2.4
200	D4AE68	Guanine nucleotide binding protein, alpha q polypeptide, isoform CRA_a OS=Rattus norvegicus GN=Gnaq PE=4 SV=2 - [D4AE68_RAT]	nucleotide binding; protein binding; catalytic activity; signal transducer activity; enzyme regulator activity; metal ion binding	membrane; cytosol	metabolic process; regulation of biological process; response to stimulus		16.9	2.7						2.8	5.6
201	P10824	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Rattus norvegicus GN=Gnai1 PE=1 SV=3 - [GNAI1_RAT]	nucleotide binding; protein binding; catalytic activity; signal transducer activity; enzyme regulator activity; metal ion binding	nucleus; cytoplasm; membrane; Golgi; cytoskeleton	metabolic process; regulation of biological process; response to stimulus; cell division	18.4	25.5	4.4	2.7	4.0	8.8		7.5	15.2	9.6
202	P04897	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Rattus norvegicus GN=Gnai2 PE=1 SV=3 - [GNAI2_RAT]	nucleotide binding; protein binding; catalytic activity; signal transducer activity; metal ion binding	nucleus; cytoplasm; cytosol; cytoskeleton; membrane	regulation of biological process; response to stimulus; metabolic process; cell proliferation; cell division	5.3	3.3	6.7	2.4	4.0	8.8		7.5	4.8	4.7
203	P54311	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Rattus norvegicus GN=Gnb1 PE=1 SV=4 - [GBB1_RAT]	protein binding; catalytic activity; signal transducer activity	membrane	metabolic process; regulation of biological process; response to stimulus; cellular homeostasis; cell proliferation; cell death	3.1	13.8	6.2	2.1	0.8				8.8	5.0
204	P54313	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Rattus norvegicus GN=Gnb2 PE=1 SV=4 - [GBB2_RAT]	signal transducer activity; protein binding	cytoplasm; membrane	regulation of biological process; response to stimulus	3.1	13.8	8.2	2.4	100.0	34.9		2.2	51.0	23.9
205	P08753	Guanine nucleotide-binding protein G(k) subunit alpha OS=Rattus norvegicus GN=Gnai3 PE=1 SV=3 - [GNAI3_RAT]	nucleotide binding; catalytic activity; signal transducer activity; protein binding; metal ion binding	membrane; cytoplasm; Golgi; cytoskeleton	metabolic process; cell organization and biogenesis; regulation of biological process; response to stimulus; cell division	3.0	50.5	5.4	3.4		8.8			7.1	11.2
206	D4ABT0	Guanine nucleotide-binding protein G(o) subunit alpha OS=Rattus norvegicus GN=Gnao1 PE=4 SV=2 - [D4ABT0_RAT]	nucleotide binding; catalytic activity; signal transducer activity; protein binding; metal ion binding	membrane	metabolic process; regulation of biological process; response to stimulus; cell organization and biogenesis	3.3	13.2	5.8	2.3	4.0	5.7		15.5	8.5	6.5
207	P63095	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Rattus norvegicus GN=Gnas PE=1 SV=1 - [GNAS2_RAT]	nucleotide binding; protein binding; catalytic activity; signal transducer activity; metal ion binding	extracellular; nucleus; cytoplasm; endosome; cytosol; membrane	regulation of biological process; metabolic process; response to stimulus	3.4	100.0	4.4	3.8	4.0	8.8		7.5	3.7	15.1

208	Q63210	Guanine nucleotide-binding protein subunit alpha-12 OS=Rattus norvegicus GN=Gna12 PE=1 SV=3 - [GNA12_RAT]	nucleotide binding; protein binding; catalytic activity; signal transducer activity; metal ion binding	membrane	metabolic process; regulation of biological process; response to stimulus; cell differentiation		5.5				4.1			5.3	3.7
209	P63245	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Rattus norvegicus GN=Gnb2l1 PE=1 SV=3 - [GBLP_RAT]	protein binding; enzyme regulator activity; RNA binding	nucleus; cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	cell differentiation; regulation of biological process; cell death; metabolic process; response to stimulus; development	6.0	7.1	5.4	2.7					4.1	4.2
210	Q811S9 ★	Guanine nucleotide-binding protein-like 3 OS=Rattus norvegicus GN=Gnl3 PE=1 SV=1 - [GNL3_RAT]	nucleotide binding; catalytic activity; protein binding; RNA binding	nucleus; membrane	metabolic process; cell proliferation; regulation of biological process		3.5		3.5					13.9	5.2
211	P40615	H/ACA ribonucleoprotein complex subunit 4 OS=Rattus norvegicus GN=Dkc1 PE=1 SV=4 - [DKC1_RAT]	catalytic activity; RNA binding; protein binding	nucleus	metabolic process; cell proliferation	4.5	4.4	6.1	4.1	2.8	4.0	3.0	24.7	13.8	6.7
212	F1LRV4	Heat shock 70 kDa protein 4 OS=Rattus norvegicus GN=Hspa4 PE=3 SV=1 - [F1LRV4_RAT]	nucleotide binding	nucleus; mitochondrion	cell organization and biogenesis; transport	100.0	24.4	7.7						68.4	40.1
213	D3ZC55	Heat shock 70kDa protein 12A (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Hspa12a PE=4 SV=1 - [D3ZC55_RAT]			response to stimulus	13.3	47.0	7.6	3.6					8.8	13.4
214	P63018	Heat shock cognate 71 kDa protein OS=Rattus norvegicus GN=Hspa8 PE=1 SV=1 - [HSP7C_RAT]	nucleotide binding; protein binding; catalytic activity; RNA binding	nucleus; spliceosomal complex; cytoplasm; cytosol; membrane; cell surface	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	1.0	1.6	2.6	2.2	2.0	2.0	2.3	2.2	4.4	2.0
215	P82995	Heat shock protein HSP 90-alpha OS=Rattus norvegicus GN=Hsp90aa1 PE=1 SV=3 - [HS90A_RAT]	nucleotide binding; RNA binding; protein binding; catalytic activity; enzyme regulator activity	nucleus; cytoplasm; mitochondrion; cytosol; membrane; cell surface	cellular component movement; metabolic process; response to stimulus; regulation of biological process; cell death; cell organization and biogenesis; transport	2.7	4.1	100.0	4.0					6.4	19.5
216	P34058	Heat shock protein HSP 90-beta OS=Rattus norvegicus GN=Hsp90ab1 PE=1 SV=4 - [HS90B_RAT]	nucleotide binding; RNA binding; protein binding	cytoplasm; mitochondrion; cytosol; cell surface; membrane	metabolic process; response to stimulus; regulation of biological process; cell organization and biogenesis	2.6	3.3	12.4	3.5					6.1	4.7
217	Q925G1 ★	Hepatoma-derived growth factor-related protein 2 OS=Rattus norvegicus GN=Hdgfrp2 PE=2 SV=2 - [HDGR2_RAT]	DNA binding	nucleus; mitochondrion	metabolic process		2.4				2.1			100.0	26.1
218	Q923W4 ★	Hepatoma-derived growth factor-related protein 3 OS=Rattus norvegicus GN=Hdgfrp3 PE=2 SV=1 - [HDGR3_RAT]	protein binding	nucleus; cytoplasm		6.2	14.9	15.3	9.8					44.2	15.1
219	Q6P747 ★	Heterochromatin protein 1-binding protein 3 OS=Rattus norvegicus GN=Hp1bp3 PE=2 SV=1 - [HP1B3_RAT]	DNA binding; protein binding	chromosome; nucleus	cell organization and biogenesis; regulation of biological process; response to stimulus	1.9	4.6	3.3	2.3	2.2	4.5	1.8	4.2	2.2	2.7
220	Q6URK4	Heterogeneous nuclear ribonucleoprotein A3 OS=Rattus norvegicus GN=Hnrnpa3 PE=1 SV=1 - [ROA3_RAT]	nucleotide binding; RNA binding; transporter activity	nucleus; spliceosomal complex; cytoplasm	metabolic process; transport	2.7	7.3	3.6	1.5	3.1	2.2	2.6	4.3	3.8	3.1
221	G3V9R8	Heterogeneous nuclear ribonucleoprotein C OS=Rattus norvegicus GN=Hnrnpc PE=1 SV=2 - [HNRPC_RAT]	nucleotide binding; DNA binding; RNA binding; protein binding	nucleus; spliceosomal complex; cytosol; membrane	cell differentiation; metabolic process; cell organization and biogenesis; regulation of biological process	3.4	6.9	4.1	2.1		0.6	1.2	2.0	2.2	2.5
222	Q3SWU3	Heterogeneous nuclear ribonucleoprotein D-like OS=Rattus norvegicus GN=Hnrnpdl PE=2 SV=1 - [HNRDL_RAT]	nucleotide binding; DNA binding; RNA binding	nucleus; cytoplasm	metabolic process; regulation of biological process	3.1	15.0	7.0	1.1	2.5	2.6	2.5	3.6	10.9	4.8
223	G3V6A4	Heterogeneous nuclear ribonucleoprotein D, isoform CRA_b OS=Rattus norvegicus GN=Hnrpd PE=4 SV=1 - [G3V6A4_RAT]	nucleotide binding; RNA binding; DNA binding	nucleus; cytosol	metabolic process; transport; regulation of biological process	5.6	9.4	5.3	2.4	2.7	2.5	3.7	4.9	3.6	4.0
224	Q794E4	Heterogeneous nuclear ribonucleoprotein F OS=Rattus norvegicus GN=Hnrnpf PE=1 SV=3 - [HNRPF_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex; cytoplasm; membrane	metabolic process; regulation of biological process	2.2	3.5	3.4	2.1	2.2	2.0		4.2	2.4	2.4
225	G3V9Q3	Heterogeneous nuclear ribonucleoprotein H OS=Rattus norvegicus GN=Hnrnph1 PE=4 SV=1 - [G3V9Q3_RAT]	nucleotide binding; RNA binding	nucleus; spliceosomal complex; cytoplasm; cytoskeleton; membrane	metabolic process; regulation of biological process	2.8	3.8	3.4	2.2	2.3	2.1	100.0	4.7	2.6	12.4
226	Q6AY09	Heterogeneous nuclear ribonucleoprotein H2 OS=Rattus norvegicus GN=Hnrnph2 PE=1 SV=1 - [HNRH2_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm; cytoskeleton; membrane		2.8	3.8	3.4	2.1	2.3	2.2	100.0	4.5	2.7	12.4

227	P61980	Heterogeneous nuclear ribonucleoprotein K OS=Rattus norvegicus GN=Hnrnpk PE=1 SV=1 - [HNRPK_RAT]	DNA binding; RNA binding	nucleus; spliceosomal complex; cytoplasm; membrane	metabolic process; regulation of biological process	3.5	5.4	5.5	2.7	2.7	1.8	3.4	4.8	6.2	3.6
228	F1LV13	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus GN=Hnrnpm PE=4 SV=1 - [F1LV13_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex; membrane	metabolic process	2.7	5.2	5.8	1.0	2.3	1.2		4.1	7.4	3.3
229	R9PXZ2	Heterogeneous nuclear ribonucleoprotein Q (Fragment) OS=Rattus norvegicus GN=Syncrip PE=4 SV=1 - [R9PXZ2_RAT]	nucleotide binding			1.7	2.9	2.6	1.0	2.2	2.1	1.7	3.4	2.6	2.0
230	Q566E4	Heterogeneous nuclear ribonucleoprotein R OS=Rattus norvegicus GN=Hnrnpr PE=2 SV=1 - [Q566E4_RAT]	nucleotide binding; RNA binding	nucleus; spliceosomal complex		1.5	2.8	2.4	1.1	2.9	2.3	2.1	3.7	2.2	2.1
231	Q6IMY8	Heterogeneous nuclear ribonucleoprotein U OS=Rattus norvegicus GN=Hnrnpu PE=2 SV=1 - [Q6IMY8_RAT]	DNA binding; transporter activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	cell differentiation; transport; regulation of biological process	1.4	3.7	3.2	0.9	4.1	4.8	3.6	5.7	3.3	3.1
232	M0RAQ6	Hexokinase OS=Rattus norvegicus GN=Hk1 PE=3 SV=1 - [M0RAQ6_RAT]	nucleotide binding; catalytic activity	nucleus; mitochondrion; cytosol; membrane	metabolic process	2.0	3.2	3.3	1.4	4.1	6.3	2.5	12.9	5.2	4.1
233	P05708	Hexokinase-1 OS=Rattus norvegicus GN=Hk1 PE=1 SV=4 - [HXK1_RAT]	nucleotide binding; catalytic activity; protein binding	nucleus; mitochondrion; membrane; cytosol	response to stimulus; metabolic process; regulation of biological process	2.0	3.2	3.1	1.4	4.1	6.3	2.5	12.9	4.9	4.0
234	P27881	Hexokinase-2 OS=Rattus norvegicus GN=Hk2 PE=1 SV=1 - [HXK2_RAT]	nucleotide binding; catalytic activity	mitochondrion; membrane; cytosol	cellular homeostasis; response to stimulus; metabolic process; transport; cell organization and biogenesis; regulation of biological process	2.3	3.2	3.1	1.7	3.9			14.4	3.9	4.1
235	M0R5F8 ★	High mobility group nucleosome-binding domain-containing protein 5 OS=Rattus norvegicus GN=Hmgn5 PE=4 SV=1 - [M0R5F8_RAT]	DNA binding; protein binding; RNA binding	chromosome; nucleus	regulation of biological process		4.5	3.2						100.0	26.9
236	Q4QQW4	Histone deacetylase 1 OS=Rattus norvegicus GN=Hdac1 PE=1 SV=1 - [HDAC1_RAT]	DNA binding; protein binding; catalytic activity	chromosome; nucleus; cytosol	regulation of biological process; response to stimulus; metabolic process; cell differentiation; cell organization and biogenesis	2.0	2.9	2.7	1.3	2.8	3.7		7.2	3.0	2.8
237	F7ENH8	Histone deacetylase OS=Rattus norvegicus GN=Hdac2 PE=3 SV=1 - [F7ENH8_RAT]	DNA binding; protein binding; catalytic activity; RNA binding	chromosome; nucleus; cytoplasm	regulation of biological process; response to stimulus; cell organization and biogenesis; metabolic process; cell differentiation	1.9	3.0	2.8	1.6	2.8	3.9		7.3	2.9	2.9
238	Q71UF4	Histone-binding protein RBBP7 OS=Rattus norvegicus GN=Rbbp7 PE=2 SV=1 - [RBBP7_RAT]	RNA binding; protein binding	nucleus	regulation of biological process; metabolic process; cell organization and biogenesis; response to stimulus	2.3	5.1	6.5	5.5				4.5	52.0	10.8
239	D4A9J4 ★	Histone-lysine N-methyltransferase OS=Rattus norvegicus GN=LOC686349 PE=4 SV=2 - [D4A9J4_RAT]	protein binding; catalytic activity; metal ion binding; DNA binding	nucleus; membrane	regulation of biological process; cell organization and biogenesis; metabolic process	5.1	4.9	32.0	1.6	4.1	41.3		100.0	50.8	26.7
240	D4AA06 ★	Histone-lysine N-methyltransferase OS=Rattus norvegicus GN=Nsd1 PE=4 SV=1 - [D4AA06_RAT]	protein binding; catalytic activity; metal ion binding	nucleus	regulation of biological process; cell organization and biogenesis; metabolic process		6.4		1.6	2.8				53.2	12.8
241	D3ZK47 ★	Histone-lysine N-methyltransferase OS=Rattus norvegicus GN=Whsc1l1 PE=4 SV=1 - [D3ZK47_RAT]	protein binding; catalytic activity; metal ion binding	nucleus	cell organization and biogenesis; metabolic process; regulation of biological process		4.2		1.6	2.8				7.2	3.2
242	B0BN99 ★	Hmgb3 protein OS=Rattus norvegicus GN=Hmgb3 PE=2 SV=1 - [B0BN99_RAT]	DNA binding; protein binding; RNA binding	nucleus	cell organization and biogenesis; regulation of biological process	4.8	5.0	5.0	3.4					100.0	19.7
243	D4A4S1	Host cell factor 2 OS=Rattus norvegicus GN=Hcfc2 PE=4 SV=2 - [D4A4S1_RAT]	protein binding	cytoplasm		2.5	8.1	4.4	1.6					5.5	3.7
244	G3V8Y8	Huntingtin interacting protein 1, isoform CRA_a OS=Rattus norvegicus GN=Hip1 PE=4 SV=1 - [G3V8Y8_RAT]	protein binding	cytoplasm; Golgi	transport; cell death; metabolic process; regulation of biological process; cell organization and biogenesis; response to stimulus	2.4	3.0	3.2	1.6					2.4	2.1
245	F2Z3Q8	Importin subunit beta-1 OS=Rattus norvegicus GN=Kpnb1 PE=4 SV=1 - [F2Z3Q8_RAT]	protein binding; transporter activity	cytoplasm; membrane	transport	1.9	3.4	2.4	1.5	2.7	5.6	3.2	13.4	3.1	3.7

246	Q8CGX0 ★	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Rattus norvegicus GN=Igf2bp1 PE=1 SV=1 - [IF2B1_RAT]	nucleotide binding; RNA binding; translation regulator activity	nucleus; cytoplasm; membrane	regulation of biological process; transport; cell proliferation	3.2	100.0				100.0			100.0	60.6
247	G3V7J2	Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Rattus norvegicus GN=Prkra PE=4 SV=1 - [G3V7J2_RAT]	RNA binding; protein binding; catalytic activity	cytoplasm; membrane	metabolic process; cell death; response to stimulus; regulation of biological process	100.0	29.9	7.6	5.0					37.4	30.0
248	Q7TP98	Interleukin enhancer-binding factor 2 OS=Rattus norvegicus GN=Ilf2 PE=2 SV=1 - [ILF2_RAT]	DNA binding; RNA binding; nucleotide binding; catalytic activity	nucleus; cytoplasm; membrane	metabolic process; regulation of biological process; response to stimulus	5.8	6.6	5.3	4.0	2.6	4.9	4.9	7.0	3.4	4.5
249	Q9JIL3 ★	Interleukin enhancer-binding factor 3 OS=Rattus norvegicus GN=Ilf3 PE=1 SV=2 - [ILF3_RAT]	DNA binding; RNA binding; protein binding	nucleus; cytoplasm; mitochondrion; membrane	metabolic process; regulation of biological process; defense response; response to stimulus	0.9	2.3	2.1	0.7	2.8	5.3	3.1	8.5	3.0	2.9
250	F1LNF7	Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Rattus norvegicus GN=Idh3a PE=3 SV=1 - [F1LNF7_RAT]	metal ion binding; catalytic activity; nucleotide binding	mitochondrion	metabolic process	4.9	15.8	5.1	4.6					8.0	6.4
251	P56574	Isocitrate dehydrogenase [NADP], mitochondrial OS=Rattus norvegicus GN=Idh2 PE=1 SV=2 - [IDHP_RAT]	metal ion binding; catalytic activity; nucleotide binding	mitochondrion; membrane	metabolic process	3.0	2.8	2.7	3.5					3.5	2.6
252	P97924	Kalirin OS=Rattus norvegicus GN=Kalrn PE=1 SV=3 - [KALRN_RAT]	nucleotide binding; catalytic activity; protein binding; metal ion binding	cytoplasm; cytoskeleton	metabolic process; cell organization and biogenesis; regulation of biological process; response to stimulus	1.5	3.9		1.6		100.0			3.0	18.3
253	Q91V33	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Rattus norvegicus GN=Khdrbs1 PE=1 SV=1 - [KHDR1_RAT]	RNA binding; protein binding	nucleus; cytoplasm; membrane	metabolic process; regulation of biological process; response to stimulus	1.7	3.0	4.1	2.2	2.5	2.5	2.7	5.1	3.3	2.7
254	D3ZHG2	Kinesin light chain 1 OS=Rattus norvegicus GN=Klc1 PE=4 SV=2 - [D3ZHG2_RAT]	catalytic activity; motor activity; protein binding		metabolic process		100.0	4.9	1.2					10.7	23.4
255	Q2PQA9	Kinesin-1 heavy chain OS=Rattus norvegicus GN=Kif5b PE=1 SV=1 - [KINH_RAT]	nucleotide binding; catalytic activity; motor activity; protein binding; transporter activity	nucleus; cytoplasm; cytoskeleton; membrane	cell organization and biogenesis; metabolic process; cellular component movement; transport; cell differentiation; regulation of biological process		2.7	3.1	1.3					51.7	11.8
256	F1M8L1	Kinesin-like protein OS=Rattus norvegicus GN=Kif2a PE=3 SV=2 - [F1M8L1_RAT]	nucleotide binding; catalytic activity; motor activity; protein binding		cellular component movement; metabolic process	3.7	7.1	17.3	6.4	4.6	6.6		100.0	9.1	17.2
257	G3V7U4 ★	Lamin-B1 OS=Rattus norvegicus GN=Lmnb1 PE=3 SV=1 - [G3V7U4_RAT]	catalytic activity; motor activity; structural molecule activity; protein binding	nucleus; membrane	regulation of biological process	3.2	4.3	2.9	1.7	1.9	1.5		2.2	15.9	3.7
258	Q62733	Lamina-associated polypeptide 2, isoform beta OS=Rattus norvegicus GN=Tmpo PE=1 SV=3 - [LAP2_RAT]	DNA binding; protein binding	chromosome; nucleus; membrane	regulation of biological process; cell organization and biogenesis	2.2	3.4	3.3	2.2	2.9	1.5		4.4	3.4	2.6
259	F1LM33	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus GN=Lrpprc PE=4 SV=2 - [F1LM33_RAT]	DNA binding; RNA binding; protein binding	chromosome; nucleus; membrane; cytoplasm; mitochondrion; cytoskeleton	regulation of biological process; metabolic process; transport	2.3	4.4	3.2	1.9					4.0	2.6
260	Q5RJR8	Leucine-rich repeat-containing protein 59 OS=Rattus norvegicus GN=Lrrc59 PE=1 SV=1 - [LRC59_RAT]	protein binding; RNA binding	nucleus; endoplasmic reticulum; membrane		13.5	7.9	7.4	1.8					3.6	5.7
261	B1H227	LOC682908 protein OS=Rattus norvegicus GN=Rcc1 PE=2 SV=1 - [B1H227_RAT]	DNA binding; protein binding	chromosome; nucleus; cytoplasm; membrane	cell organization and biogenesis; regulation of biological process	3.8	7.7	54.8	2.9					4.5	12.3
262	O35547	Long-chain-fatty-acid--CoA ligase 4 OS=Rattus norvegicus GN=Acsl4 PE=1 SV=1 - [ACSL4_RAT]	nucleotide binding; catalytic activity	cytoplasm; mitochondrion; endoplasmic reticulum; membrane	metabolic process; response to stimulus; transport; cell differentiation; regulation of biological process		16.5		2.2					51.5	17.5
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	metabolic process; regulation of biological process; response to stimulus	1.9	2.9	2.4	1.8					3.9	2.2
264	Q6TUH4 ★	LRRGT00070 OS=Rattus norvegicus GN=Thoc1 PE=2 SV=1 - [Q6TUH4_RAT]	DNA binding; RNA binding; protein binding	nucleus; cytoplasm	regulation of biological process; metabolic process; transport; cell death; response to stimulus		15.2		1.2		1.2		100.0	6.7	20.7

265	D3ZJH9	Malic enzyme OS=Rattus norvegicus GN=Me2 PE=3 SV=1 - [D3ZJH9_RAT]	catalytic activity; metal ion binding; nucleotide binding	mitochondrion	metabolic process	2.6	55.3	2.9						100.0	32.2
266	Q9EPH2	MARCKS-related protein OS=Rattus norvegicus GN=Marcksl1 PE=2 SV=3 - [MRP_RAT]	protein binding	cytoplasm; membrane	regulation of biological process; transport	1.5	4.5	5.2	4.3					22.8	6.4
267	P43244	Matrin-3 OS=Rattus norvegicus GN=Matr3 PE=1 SV=2 - [MATR3_RAT]	nucleotide binding; RNA binding; metal ion binding	nucleus; cytoplasm; membrane		2.3	5.1	3.6	2.7	2.8	2.7	2.5	6.5	3.6	3.2
268	Q5XIU9	Membrane-associated progesterone receptor component 2 OS=Rattus norvegicus GN=Pgrmc2 PE=2 SV=1 - [PGRC2_RAT]		membrane			5.2	3.3						2.7	2.8
269	B2GV01	Metastasis-associated gene family, member 2 OS=Rattus norvegicus GN=Mta2 PE=2 SV=1 - [B2GV01_RAT]	DNA binding; protein binding; catalytic activity; metal ion binding	nucleus; membrane	regulation of biological process; metabolic process; cell organization and biogenesis	1.4	3.1	2.0	1.5	2.4	9.2			2.4	2.7
270	D3ZE72	Methionine aminopeptidase 1 OS=Rattus norvegicus GN=Metap1 PE=3 SV=1 - [D3ZE72_RAT]	catalytic activity; metal ion binding	nucleus; cytoplasm; ribosome	metabolic process		2.6	2.4						37.4	10.6
271	F7EY92	Methyl-CpG binding domain protein 3 (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Mbd3 PE=4 SV=1 - [F7EY92_RAT]	DNA binding; nucleotide binding; protein binding	chromosome; nucleus; cytoplasm	regulation of biological process; cell organization and biogenesis; response to stimulus; metabolic process	3.2	5.3	3.5	0.7					3.3	2.7
272	F1LWH6 ★	Methyl-CpG-binding protein 2 (Fragment) OS=Rattus norvegicus GN=Mecp2 PE=4 SV=1 - [F1LWH6_RAT]	DNA binding; RNA binding; protein binding; nucleotide binding	nucleus; cytoplasm; cytosol	defense response; response to stimulus; regulation of biological process; metabolic process; cell communication; cell organization and biogenesis; cell differentiation; transport	1.9	4.6	4.1	2.9	2.2	3.6	1.8		8.0	3.2
273	Q00566 ★	Methyl-CpG-binding protein 2 OS=Rattus norvegicus GN=Mecp2 PE=1 SV=1 - [MECP2_RAT]	DNA binding; RNA binding; protein binding; nucleotide binding	nucleus; cytoplasm; cytosol	regulation of biological process; defense response; response to stimulus; metabolic process; cell communication; cell organization and biogenesis; cell differentiation; transport	1.8	4.3	4.1	2.9	2.2	3.5	1.9	4.6	5.1	3.0
274	P34926	Microtubule-associated protein 1A OS=Rattus norvegicus GN=Map1a PE=1 SV=1 - [MAP1A_RAT]	protein binding; catalytic activity	cytoplasm; cytosol; cytoskeleton	cell organization and biogenesis; regulation of biological process; metabolic process	4.2	5.8	3.8	2.6	3.0	3.0		100.0	100.0	24.7
275	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=1 - [F1LRL9_RAT]	protein binding; catalytic activity	cytosol; membrane	cell organization and biogenesis; metabolic process; regulation of biological process; cellular component movement; transport; cell growth	1.6	5.0	2.8	2.7	2.6	3.3	2.5	35.6	6.5	6.3
276	P15205	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=2 - [MAP1B_RAT]	protein binding; catalytic activity	cytoplasm; cytosol; cytoskeleton; membrane	cell organization and biogenesis; regulation of biological process; metabolic process; response to stimulus; cellular component movement; transport; cell growth	1.6	4.4	2.6	2.8	2.9	3.5	9.4	100.0	6.4	13.4
277	P0C5W1	Microtubule-associated protein 1S OS=Rattus norvegicus GN=Map1s PE=1 SV=1 - [MAP1S_RAT]	DNA binding; catalytic activity; protein binding	nucleus; cytoplasm; cytosol; cytoskeleton	cell organization and biogenesis; cell death; metabolic process					2.3	3.2		5.9	22.3	8.4
278	Q5M7W5	Microtubule-associated protein 4 OS=Rattus norvegicus GN=Map4 PE=1 SV=1 - [MAP4_RAT]	protein binding; RNA binding	cytoplasm; cytoskeleton; membrane	cell organization and biogenesis; cellular component movement; cell division	2.4	5.1	4.0	3.8	100.0	31.9	100.0	24.9	9.5	28.2
279	Q63560	Microtubule-associated protein 6 OS=Rattus norvegicus GN=Map6 PE=1 SV=1 - [MAP6_RAT]	protein binding	cytoplasm; Golgi; cytoskeleton	cell organization and biogenesis; transport; regulation of biological process	1.5	4.3	3.1	1.9	100.0	2.0	1.4		3.2	13.1
280	F1MAQ5	Microtubule-associated protein OS=Rattus norvegicus GN=Map2 PE=4 SV=2 - [F1MAQ5_RAT]	protein binding	cytoplasm; endoplasmic reticulum; cytoskeleton	cell organization and biogenesis; metabolic process; response to stimulus	1.7	4.1	4.7	2.5	1.8	1.3	2.2	2.1	8.4	2.9
281	E9PT48 ★	Microtubule-associated protein OS=Rattus norvegicus GN=Mapt PE=4 SV=1 - [E9PT48_RAT]	protein binding	nucleus; cytoplasm; cytosol; cytoskeleton; membrane	cell organization and biogenesis; cellular component movement; cell death; response to stimulus; transport; regulation of biological process; cell differentiation; cell growth	2.1	3.9	2.9	2.3	2.2	1.3	1.0		5.7	2.4

282	D3ZKD9 ★	Microtubule-associated protein OS=Rattus norvegicus GN=Mapt PE=4 SV=2 - [D3ZKD9_RAT]	protein binding	nucleus; cytoplasm; cytosol; cytoskeleton; membrane	cell organization and biogenesis; cellular component movement; cell death; response to stimulus; transport; regulation of biological process; cell differentiation; cell growth	2.2	4.6	3.0	1.6	2.2	1.3	1.0	2.2	7.3	2.5
283	Q66HR2	Microtubule-associated protein RP/EB family member 1 OS=Rattus norvegicus GN=Mapre1 PE=1 SV=3 - [MARE1_RAT]	protein binding; RNA binding	cytoplasm; Golgi; cytoskeleton	cell organization and biogenesis; regulation of biological process; cell division			2.7		3.3	1.1		4.7		3.0
284	F1LN69	Misshapen-like kinase 1 (Fragment) OS=Rattus norvegicus GN=Mink1 PE=4 SV=2 - [F1LN69_RAT]	nucleotide binding; catalytic activity	cytoplasm; Golgi	regulation of biological process; metabolic process; cell organization and biogenesis	0.6	100.0	3.0	0.7	1.9	5.6			3.5	14.4
285	R9PXR4	Mitochondrial import receptor subunit TOM70 OS=Rattus norvegicus GN=Tomm70a PE=1 SV=1 - [R9PXR4_RAT]	protein binding	mitochondrion; membrane	transport	4.9	3.8	9.2	2.2	7.9				6.5	4.9
286	Q75Q39	Mitochondrial import receptor subunit TOM70 OS=Rattus norvegicus GN=Tomm70a PE=1 SV=1 - [TOM70_RAT]	protein binding	mitochondrion; membrane	transport	4.9	3.8	9.2	2.2					30.5	8.4
287	F1M754	Mitogen-activated protein kinase kinase kinase kinase 4 (Predicted) OS=Rattus norvegicus GN=Map4k4 PE=4 SV=2 - [F1M754_RAT]	catalytic activity; signal transducer activity; nucleotide binding	cytoplasm	metabolic process; response to stimulus; regulation of biological process; cell organization and biogenesis	0.9	3.1	1.8	0.8	1.9	4.4	2.1	7.9	2.8	2.6
288	O70437 ★	Mothers against decapentaplegic homolog 4 OS=Rattus norvegicus GN=Smad4 PE=1 SV=1 - [SMAD4_RAT]	DNA binding; protein binding; signal transducer activity; metal ion binding	nucleus; cytoplasm	response to stimulus; cell organization and biogenesis; regulation of biological process; metabolic process; cellular component movement; cell proliferation; cell differentiation		6.9	3.2						4.1	3.5
289	P51583	Multifunctional protein ADE2 OS=Rattus norvegicus GN=Paics PE=2 SV=3 - [PUR6_RAT]	nucleotide binding; catalytic activity; protein binding	membrane	metabolic process	6.5	5.0	100.0	2.5				51.2	66.2	33.1
290	O35821	Myb-binding protein 1A OS=Rattus norvegicus GN=Mybbp1a PE=2 SV=2 - [MBB1A_RAT]	DNA binding; catalytic activity; RNA binding	nucleus; cytoplasm; membrane	cell differentiation; metabolic process; regulation of biological process; transport; cell communication; response to stimulus	1.1	2.4	1.5	1.5	1.9	10.1	1.9	31.5	2.7	5.4
291	P70475 ★	Myelin transcription factor 1-like protein OS=Rattus norvegicus GN=Myt1l PE=1 SV=2 - [MYT1L_RAT]	DNA binding; metal ion binding	nucleus	metabolic process; regulation of biological process; development; cell differentiation	0.7	12.4						100.0	54.1	33.4
292	F1M8L4 ★	Myelin transcription factor 1-like protein OS=Rattus norvegicus GN=Myt1l PE=4 SV=2 - [F1M8L4_RAT]	metal ion binding	nucleus	regulation of biological process	0.7	12.4						100.0	21.5	26.9
293	Q64119	Myosin light polypeptide 6 OS=Rattus norvegicus GN=Myl6 PE=1 SV=3 - [MYL6_RAT]	catalytic activity; motor activity; metal ion binding; structural molecule activity		metabolic process; cellular component movement	21.3	8.3	18.8	8.2					7.1	10.6
294	Q9JLT0	Myosin-10 OS=Rattus norvegicus GN=Myh10 PE=2 SV=1 - [MYH10_RAT]	catalytic activity; motor activity; nucleotide binding; protein binding; transporter activity	nucleus; cytoplasm; mitochondrion; membrane; cytoskeleton	cell organization and biogenesis; cellular component movement; metabolic process; transport; cell proliferation; regulation of biological process	1.3	2.4	1.6	1.0	1.6	5.5	1.7	5.2	2.7	2.3
295	F1LMW7	Myristoylated alanine-rich C-kinase substrate OS=Rattus norvegicus GN=Marcks PE=4 SV=2 - [F1LMW7_RAT]	protein binding	cytoplasm; membrane; nucleus		1.6	10.3	8.9	4.1					58.0	13.8
296	Q66HF1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Rattus norvegicus GN=Ndufs1 PE=1 SV=1 - [NDUS1_RAT]	catalytic activity; metal ion binding	mitochondrion; membrane	transport; cell death; cell organization and biogenesis; metabolic process	35.5	4.3	3.6	3.1					7.1	9.0
297	P55161	Nck-associated protein 1 OS=Rattus norvegicus GN=Nckap1 PE=2 SV=1 - [NCKP1_RAT]	protein binding	membrane	cellular component movement; regulation of biological process; response to stimulus; cell organization and biogenesis	1.2	2.6	1.6	1.1	2.2	4.0		4.0	2.6	2.1
298	Q63689 ★	Neurogenic differentiation factor 2 OS=Rattus norvegicus GN=Neurod2 PE=1 SV=2 - [NDF2_RAT]	DNA binding; protein binding	nucleus	defense response; response to stimulus; metabolic process; regulation of biological process; development; cell differentiation		19.5	3.8	2.8					3.8	6.0
299	P42676	Neurolysin, mitochondrial OS=Rattus norvegicus GN=Nln PE=1 SV=1 - [NEUL_RAT]	catalytic activity; metal ion binding	cytoplasm; mitochondrion; membrane	regulation of biological process; metabolic process		46.6	2.4						2.3	12.8
300	P07936	Neuromodulin OS=Rattus norvegicus GN=Gap43 PE=1 SV=1 - [NEUM_RAT]	protein binding	cytoplasm; membrane	development; cellular component movement; cell differentiation; regulation of biological process; cell organization and biogenesis	0.6	6.3	13.8	2.7					51.7	12.5

301	G3V997	Neuronal migration protein doublecortin OS=Rattus norvegicus GN=Dcx PE=4 SV=1 - [G3V997_RAT]	protein binding	cytoplasm	cellular component movement; cell organization and biogenesis; regulation of biological process; response to stimulus; cell growth	3.2	6.5	5.8	4.2	2.5	2.4	3.7	6.8	4.8	4.0
302	D3ZPP8	Neuronal-specific septin-3 OS=Rattus norvegicus GN=Sept3 PE=3 SV=1 - [D3ZPP8_RAT]	nucleotide binding; catalytic activity			3.0	4.9	4.2	2.6		3.3			10.6	4.1
303	P55770	NHP2-like protein 1 OS=Rattus norvegicus GN=Nhp2l1 PE=2 SV=4 - [NH2L1_RAT]	RNA binding	nucleus; spliceosomal complex	metabolic process	10.5	12.8	25.2	10.9	2.4	3.9		7.2	45.0	13.1
304	Q56A27	Nuclear cap-binding protein subunit 1 OS=Rattus norvegicus GN=Ncbp1 PE=2 SV=1 - [NCBP1_RAT]	RNA binding; DNA binding; protein binding	nucleus; cytoplasm; mitochondrion; membrane	metabolic process; transport; regulation of biological process	2.5	3.3	2.2	1.9					51.9	10.3
305	P09414	Nuclear factor 1 A-type OS=Rattus norvegicus GN=Nfia PE=1 SV=2 - [NFIA_RAT]	DNA binding; protein binding	nucleus	regulation of biological process; metabolic process; response to stimulus; cell organization and biogenesis	4.2	6.4	3.0	1.5	2.6		10.8	23.8	3.9	6.2
306	O70187	Nuclear factor 1 OS=Rattus norvegicus GN=Nfib PE=2 SV=2 - [O70187_RAT]	DNA binding	nucleus	regulation of biological process; cell differentiation; metabolic process; cell organization and biogenesis; cellular component movement	1.8	4.2	2.7	1.9	2.8	5.6	10.8	23.8	2.9	5.6
307	F2Z3R4	Nuclear factor 1 OS=Rattus norvegicus GN=Nfix PE=3 SV=1 - [F2Z3R4_RAT]	DNA binding	nucleus	regulation of biological process; metabolic process; cell differentiation	1.7	4.4	3.4	1.8	3.4	4.7	4.5	12.5	3.4	4.0
308	F1LSL2	Nuclear pore complex protein Nup107 OS=Rattus norvegicus GN=Nup107 PE=4 SV=2 - [F1LSL2_RAT]	transporter activity; structural molecule activity	chromosome; nucleus; membrane	transport; cell organization and biogenesis		48.4		1.0				100.0	2.8	30.4
309	P70582 ★	Nuclear pore complex protein Nup54 OS=Rattus norvegicus GN=Nup54 PE=1 SV=1 - [NUP54_RAT]	transporter activity; protein binding	nucleus; membrane	transport	3.2	15.3	3.6	9.4					12.5	7.4
310	P49793 ★	Nuclear pore complex protein Nup98-Nup96 OS=Rattus norvegicus GN=Nup98 PE=1 SV=2 - [NUP98_RAT]	protein binding; structural molecule activity	chromosome; nucleus; membrane	cell organization and biogenesis; metabolic process; transport	1.6	2.0	1.5		3.7	20.6	100.0	7.9	3.4	15.6
311	G3V7F5	Nuclear receptor subfamily 2 group C member 2 OS=Rattus norvegicus GN=Nr2c2 PE=3 SV=1 - [G3V7F5_RAT]	DNA binding; receptor activity; signal transducer activity; metal ion binding; protein binding	nucleus	metabolic process; regulation of biological process; response to stimulus	100.0	5.6	5.7	5.0					16.6	22.1
312	F1MA52	Nuclear RNA export factor 1 OS=Rattus norvegicus GN=Nxf1 PE=4 SV=1 - [F1MA52_RAT]	nucleotide binding; RNA binding; transporter activity; protein binding	nucleus; cytoplasm	transport	2.9	3.5	1.6	1.8				8.0	5.8	3.4
313	Q9QZ86	Nucleolar protein 58 OS=Rattus norvegicus GN=Nop58 PE=1 SV=1 - [NOP58_RAT]	catalytic activity; RNA binding; protein binding	nucleus; cytoplasm; membrane	metabolic process; transport	2.0	3.6	3.6	1.7	5.9	8.4		100.0	3.0	14.2
314	Q4KLK7	Nucleolar protein 5A OS=Rattus norvegicus GN=Nop56 PE=2 SV=1 - [Q4KLK7_RAT]	RNA binding	membrane	metabolic process	1.9	4.4	4.0	1.0	5.8	5.1	100.0	100.0	2.7	22.5
315	Q3B8Q1	Nucleolar RNA helicase 2 OS=Rattus norvegicus GN=Ddx21 PE=2 SV=1 - [DDX21_RAT]	nucleotide binding; RNA binding; catalytic activity	nucleus; membrane	cell differentiation; metabolic process; response to stimulus	1.4	5.8	4.2	2.9	2.4	6.5	5.4	6.1	4.0	3.9
316	P25977 ★	Nucleolar transcription factor 1 OS=Rattus norvegicus GN=Ubtf PE=1 SV=1 - [UBF1_RAT]	DNA binding; protein binding; RNA binding	nucleus	regulation of biological process; cell organization and biogenesis; metabolic process	3.2	2.7	5.2	1.2					5.6	3.0
317	P13383	Nucleolin OS=Rattus norvegicus GN=Ncl PE=1 SV=3 - [NUCL_RAT]	nucleotide binding; DNA binding; RNA binding; protein binding	nucleus; cytoplasm; membrane	regulation of biological process	2.2	5.4	3.5	1.6	1.6	2.1	1.0	3.0	28.4	4.9
318	P13084	Nucleophosmin OS=Rattus norvegicus GN=Npm1 PE=1 SV=1 - [NPM_RAT]	DNA binding; RNA binding; enzyme regulator activity; protein binding	nucleus; cytoplasm; cytosol; cytoskeleton; membrane	transport; metabolic process; response to stimulus; cell organization and biogenesis; cellular homeostasis; regulation of biological process; cell growth	8.9	11.3	14.1	10.5	1.9	1.3	1.8	3.7	7.8	6.1
319	D4A7R3	Nucleoporin 205kDa (Predicted) OS=Rattus norvegicus GN=Nup205 PE=4 SV=1 - [D4A7R3_RAT]	transporter activity; structural molecule activity	cytoplasm; membrane	transport; cell organization and biogenesis	1.6	2.9	10.2	0.7	2.3	8.0	2.1	7.9	3.1	3.9
320	Q68FY1 ★	Nucleoporin NUP53 OS=Rattus norvegicus GN=Nup35 PE=1 SV=1 - [NUP53_RAT]	transporter activity; protein binding	nucleus; membrane; cytoskeleton	transport		23.4	100.0	3.8					51.9	35.8

321	F1MA98	Nucleoprotein TPR OS=Rattus norvegicus GN=Tpr PE=1 SV=1 - [TPR_RAT]	RNA binding; catalytic activity; motor activity; transporter activity; nucleotide binding; protein binding	chromosome; nucleus; cytoplasm; cytoskeleton; membrane	regulation of biological process; transport; metabolic process; cell organization and biogenesis; response to stimulus; cell division	0.7	2.1	1.2	0.6	1.4	100.0		14.2	3.2	13.7
322	P19804	Nucleoside diphosphate kinase B OS=Rattus norvegicus GN=Nme2 PE=1 SV=1 - [NDKB_RAT]	nucleotide binding; catalytic activity; protein binding; metal ion binding	nucleus; cytoplasm; mitochondrion; cytosol; membrane	regulation of biological process; metabolic process; response to stimulus; cell organization and biogenesis; cellular homeostasis	4.3	10.8	4.0	9.4					20.4	8.2
323	A1L1I3	Numb-like protein OS=Rattus norvegicus GN=Numbl PE=1 SV=1 - [NUMBL_RAT]	protein binding	cytoplasm	development; cell proliferation; cell organization and biogenesis; regulation of biological process; response to stimulus; metabolic process; cell division		4.1	4.5		3.2	2.5		100.0	18.7	19.0
324	G3V6F4	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase), isoform CRA_b OS=Rattus norvegicus GN=Ogt PE=4 SV=2 - [G3V6F4_RAT]	protein binding; enzyme regulator activity; catalytic activity	nucleus; cytoplasm; mitochondrion; cytosol; membrane	regulation of biological process; metabolic process; cell death; response to stimulus; cell organization and biogenesis; cellular homeostasis	2.7	3.1	1.9	2.3					3.7	2.3
325	D3ZJ19	One cut domain family member OS=Rattus norvegicus GN=Satb2 PE=3 SV=1 - [D3ZJ19_RAT]	DNA binding	nucleus; cytoplasm	regulation of biological process; cellular component movement; cell organization and biogenesis; metabolic process; response to stimulus	1.9	4.5	3.2	1.6					6.8	3.0
326	F2Z3T0	Parafibromin OS=Rattus norvegicus GN=Cdc73 PE=4 SV=1 - [F2Z3T0_RAT]	protein binding	nucleus	regulation of biological process; metabolic process; cell organization and biogenesis; response to stimulus	2.3	24.3	3.7	1.8					7.1	6.5
327	F1SW39 ★	PC4 and SFRS1 interacting protein 1 OS=Rattus norvegicus GN=Psip1 PE=2 SV=1 - [F1SW39_RAT]	protein binding; RNA binding; DNA binding	nucleus	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	3.0	6.3	6.7	3.3	2.9	2.3	2.4	7.5	9.7	4.4
328	Q812D1 ★	PC4 and SFRS1-interacting protein OS=Rattus norvegicus GN=Psip1 PE=2 SV=1 - [PSIP1_RAT]	DNA binding; protein binding; RNA binding	nucleus	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	3.0	6.3	4.6	3.5	2.8	2.5			37.6	7.6
329	P10111	Peptidyl-prolyl cis-trans isomerase A OS=Rattus norvegicus GN=Ppia PE=1 SV=2 - [PPIA_RAT]	catalytic activity; RNA binding	extracellular; nucleus; cytoplasm; cytosol; membrane	metabolic process; cell differentiation; regulation of biological process; cell organization and biogenesis	1.1	7.0	5.5	1.6	4.5	4.7	4.0	100.0	19.6	14.8
330	D4A5R0	Peptidyl-prolyl cis-trans isomerase OS=Rattus norvegicus GN=Ppih PE=3 SV=2 - [D4A5R0_RAT]	catalytic activity	cytoplasm	metabolic process; regulation of biological process	100.0	30.0	100.0	0.7					100.0	55.1
331	P97852	Peroxisomal multifunctional enzyme type 2 OS=Rattus norvegicus GN=Hsd17b4 PE=1 SV=3 - [DHB4_RAT]	nucleotide binding; catalytic activity; protein binding	mitochondrion; membrane	metabolic process; cell differentiation	0.7	1.4	1.2	0.7	100.0	6.4		100.0	3.0	23.7
332	F1LWX5	PHD finger protein 2 (Predicted) OS=Rattus norvegicus GN=Phf2 PE=4 SV=2 - [F1LWX5_RAT]	metal ion binding; protein binding; catalytic activity	nucleus; cytoplasm	metabolic process; cell organization and biogenesis; regulation of biological process	10.6	95.3	2.6	3.3					4.2	19.3
333	Q4V9H5	PHD finger protein 20-like protein 1 OS=Rattus norvegicus GN=Phf20l1 PE=2 SV=2 - [P20L1_RAT]	protein binding; metal ion binding				100.0	100.0						51.4	62.8
334	D3ZKI5	PHD finger protein 3 (Predicted) OS=Rattus norvegicus GN=Phf3 PE=4 SV=1 - [D3ZKI5_RAT]	protein binding; metal ion binding	nucleus	metabolic process		22.0				18.4		100.0	16.9	31.5
335	P83871 ★	PHD finger-like domain-containing protein 5A OS=Rattus norvegicus GN=Phf5a PE=2 SV=1 - [PHF5A_RAT]	DNA binding; RNA binding	nucleus; spliceosomal complex	metabolic process; regulation of biological process	3.6	5.8	5.0	1.2					3.7	3.2
336	G3V741	Phosphate carrier protein, mitochondrial OS=Rattus norvegicus GN=Slc25a3 PE=3 SV=1 - [G3V741_RAT]	transporter activity; protein binding	mitochondrion; membrane	transport	1.4	4.4	3.2	1.5					2.6	2.2
337	O55012 ★	Phosphatidylinositol-binding clathrin assembly protein OS=Rattus norvegicus GN=Picalm PE=1 SV=1 - [PICAL_RAT]	protein binding	nucleus; endosome; Golgi; membrane	transport; cell organization and biogenesis; cell proliferation; regulation of biological process; metabolic process	5.0	4.3	100.0	2.1					52.0	27.2
338	F1LPG3	Phosphofurin acidic cluster sorting protein 1 OS=Rattus norvegicus GN=Pacs1 PE=4 SV=1 - [F1LPG3_RAT]	protein binding	Golgi	transport; cell organization and biogenesis	9.0	2.3	4.4		2.5	4.1		100.0	5.9	16.0
339	Q6AXS5	Plasminogen activator inhibitor 1 RNA-binding protein OS=Rattus norvegicus GN=Serbp1 PE=1 SV=2 - [PAIRB_RAT]	RNA binding	nucleus; cytoplasm; membrane	regulation of biological process	100.0	9.3	10.2	4.1					8.5	22.0

340	D3ZT07	Platelet glycoprotein Ib beta chain OS=Rattus norvegicus GN=Sept5 PE=3 SV=2 - [D3ZT07_RAT]	nucleotide binding; catalytic activity; protein binding	membrane	regulation of biological process; cell division	5.6	7.1	12.0	2.6					55.8	13.8
341	P63004 ★	Platelet-activating factor acetylhydrolase IB subunit alpha OS=Rattus norvegicus GN=Pafah1b1 PE=1 SV=2 - [LIS1_RAT]	protein binding; catalytic activity	chromosome; nucleus; cytoplasm; cytosol; cytoskeleton; membrane	cell organization and biogenesis; cellular component movement; regulation of biological process; metabolic process; transport; cell communication; development; cell proliferation; response to stimulus; cell division; cell differentiation	2.7	4.4	2.6	2.0					50.7	10.4
342	P27008	Poly [ADP-ribose] polymerase 1 OS=Rattus norvegicus GN=Parp1 PE=1 SV=4 - [PARP1_RAT]	DNA binding; catalytic activity; protein binding; metal ion binding; RNA binding; nucleotide binding	nucleus; cytoplasm; membrane	cell organization and biogenesis; metabolic process; response to stimulus; regulation of biological process	1.5	2.7	4.8	0.7		100.0		11.0	7.2	16.0
343	G3V7Z8 ★	Poly(A) binding protein, nuclear 1, isoform CRA_a OS=Rattus norvegicus GN=Pabpn1 PE=4 SV=1 - [G3V7Z8_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm	transport		33.7	25.6	0.6	1.5	3.4	2.1		1.9	8.6
344	Q6AYU5	Poly(RC) binding protein 2 OS=Rattus norvegicus GN=Pcbp2 PE=2 SV=1 - [Q6AYU5_RAT]	RNA binding; protein binding	nucleus; cytoplasm; membrane	metabolic process; regulation of biological process	5.4	9.0	16.4	8.1	4.4	5.5	100.0	34.1	11.2	19.4
345	Q6AY48 ★	Poly(RC) binding protein 3 OS=Rattus norvegicus GN=Pcbp3 PE=2 SV=1 - [Q6AY48_RAT]	RNA binding	nucleus; mitochondrion; cytosol		5.3	6.9	14.5	6.3	4.8	6.8	100.0	100.0	10.4	25.5
346	Q9EPH8	Polyadenylate-binding protein 1 OS=Rattus norvegicus GN=Pabpc1 PE=1 SV=1 - [PABP1_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex; cytoplasm; membrane	metabolic process; regulation of biological process	2.6	3.8	4.3	2.3					51.7	10.8
347	G3V9N0	Polyadenylate-binding protein OS=Rattus norvegicus GN=Pabpc4 PE=2 SV=2 - [G3V9N0_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm		2.6	5.3	3.0	2.4					100.0	18.9
348	D4A2B0 ★	Polymerase (DNA-directed), delta interacting protein 3 (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Poldip3 PE=4 SV=1 - [D4A2B0_RAT]	nucleotide binding; RNA binding	nucleus	transport; regulation of biological process	4.8	6.5	10.5	4.1				100.0	5.2	18.7
349	D3ZB30	Polypyrimidine tract binding protein 1, isoform CRA_c OS=Rattus norvegicus GN=Ptbp1 PE=4 SV=1 - [D3ZB30_RAT]	nucleotide binding; DNA binding; RNA binding; catalytic activity	nucleus; membrane	regulation of biological process; metabolic process	2.0	2.9	3.4	2.4					3.9	2.4
350	Q66H20 ★	Polypyrimidine tract-binding protein 2 OS=Rattus norvegicus GN=Ptbp2 PE=2 SV=1 - [PTBP2_RAT]	nucleotide binding; RNA binding	nucleus; spliceosomal complex	cell organization and biogenesis; metabolic process; regulation of biological process	1.5	2.2	3.4	2.2	1.9	1.6		2.9	3.2	2.1
351	F1M7A3 ★	POU domain protein (Fragment) OS=Rattus norvegicus GN=Pou3f3 PE=3 SV=2 - [F1M7A3_RAT]	DNA binding; protein binding	nucleus	regulation of biological process; cellular component movement; cell division; cell differentiation	3.7	5.1	80.4	3.8					55.9	24.8
352	G3V6U5 ★	POU domain protein OS=Rattus norvegicus GN=Pou3f2 PE=3 SV=1 - [G3V6U5_RAT]	DNA binding; protein binding	nucleus	metabolic process; regulation of biological process; cellular component movement; cell division; cell differentiation; response to stimulus	3.7	6.2	6.0	4.3					59.1	13.2
353	P20267 ★	POU domain, class 3, transcription factor 1 OS=Rattus norvegicus GN=Pou3f1 PE=2 SV=2 - [PO3F1_RAT]	DNA binding	nucleus	regulation of biological process; metabolic process; cell differentiation	4.0	5.9	6.0	3.8					100.0	20.0
354	D3ZJ92	Pre-mRNA processing factor 40 homolog A (Yeast) (Predicted) OS=Rattus norvegicus GN=Prpf40a PE=4 SV=1 - [D3ZJ92_RAT]	protein binding; RNA binding	nucleus; cytoplasm; membrane	cell organization and biogenesis; regulation of biological process; cellular component movement	3.4	3.2	6.1	1.3	2.0	3.1	2.9	3.6	8.8	3.4
355	Q9JMJ4	Pre-mRNA-processing factor 19 OS=Rattus norvegicus GN=Prpf19 PE=1 SV=2 - [PRP19_RAT]	DNA binding; catalytic activity; protein binding	nucleus; spliceosomal complex; cytoplasm; cytoskeleton; membrane	metabolic process; cell organization and biogenesis; cell proliferation; response to stimulus; regulation of biological process	2.8	3.4	2.6	1.6	3.0	3.1	15.2	100.0	3.6	13.5
356	A1A5S1	Pre-mRNA-processing factor 6 OS=Rattus norvegicus GN=Prpf6 PE=2 SV=1 - [PRP6_RAT]	RNA binding; protein binding	nucleus; spliceosomal complex; membrane	cell organization and biogenesis; metabolic process; regulation of biological process	1.3	4.4	3.2	0.6	2.5	5.8	2.6	5.8	3.9	3.0
357	Q6AYD3	Proliferation-associated protein 2G4 OS=Rattus norvegicus GN=Pa2g4 PE=1 SV=1 - [PA2G4_RAT]	DNA binding; RNA binding; protein binding	nucleus; cytoplasm; membrane	metabolic process; regulation of biological process	2.7	6.3	100.0						2.6	22.3

358	Q56B11 ★	Proline-, glutamic acid- and leucine-rich protein 1 OS=Rattus norvegicus GN=Pelp1 PE=2 SV=2 - [PELP1_RAT]	protein binding; RNA binding	nucleus; cytoplasm; membrane	metabolic process; regulation of biological process; response to stimulus		2.1		0.7	100.0	22.0			2.6	21.2
359	E9PST5	Protein Acin1 OS=Rattus norvegicus GN=Acin1 PE=1 SV=1 - [E9PST5_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm; membrane	cell differentiation; cell organization and biogenesis; metabolic process; regulation of biological process	2.9	4.3	100.0	2.7	2.3	2.5		5.6	14.4	15.0
360	D3ZRN3	Protein Actbl2 OS=Rattus norvegicus GN=Actbl2 PE=3 SV=1 - [D3ZRN3_RAT]	nucleotide binding	cytoplasm; cytoskeleton		3.2	3.9	5.9	3.7	2.9	3.0	2.9	4.1	6.7	3.6
361	D3ZIE9	Protein Aldh18a1 OS=Rattus norvegicus GN=Aldh18a1 PE=4 SV=1 - [D3ZIE9_RAT]	catalytic activity; RNA binding	cytoplasm; mitochondrion	metabolic process	2.0	3.5	2.7	1.9					3.9	2.3
362	F1M9N9	Protein Ank2 (Fragment) OS=Rattus norvegicus GN=Ank2 PE=4 SV=2 - [F1M9N9_RAT]	structural molecule activity; protein binding	cytoskeleton; membrane	regulation of biological process; response to stimulus; cell organization and biogenesis	1.5	2.5	2.5	2.6	2.8	5.6		100.0	5.5	13.7
363	F1LM42	Protein Ank2 OS=Rattus norvegicus GN=Ank2 PE=4 SV=2 - [F1LM42_RAT]	structural molecule activity; protein binding	cytoplasm; cytoskeleton; membrane	regulation of biological process; cellular homeostasis; response to stimulus; cell organization and biogenesis; transport; cell communication	1.3	2.5	2.5	2.5	3.1	5.6		100.0	5.6	13.7
364	F1LXQ7	Protein Arhgap21 (Fragment) OS=Rattus norvegicus GN=Arhgap21 PE=1 SV=2 - [F1LXQ7_RAT]	protein binding	Golgi	cell organization and biogenesis; regulation of biological process; response to stimulus; cellular component movement; transport	0.8	66.2				8.1			100.0	35.0
365	D3ZJU0 ★	Protein Arid2 OS=Rattus norvegicus GN=Arid2 PE=4 SV=2 - [D3ZJU0_RAT]	DNA binding; metal ion binding	nucleus; membrane	cell organization and biogenesis; regulation of biological process	0.8	2.6	98.4			13.5	3.0	6.9	3.7	16.1
366	D3ZSY3 ★	Protein Bcl11a OS=Rattus norvegicus GN=Bcl11a PE=4 SV=1 - [D3ZSY3_RAT]	DNA binding; metal ion binding; protein binding	nucleus	regulation of biological process; metabolic process; cell differentiation	1.2	5.1	2.1	0.9	5.2	3.6		10.6	3.8	3.6
367	D3ZGX8	Protein Brd4 OS=Rattus norvegicus GN=Brd4 PE=4 SV=2 - [D3ZGX8_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	regulation of biological process; cell proliferation; cell organization and biogenesis; metabolic process; response to stimulus	1.2	4.0	2.0	1.4		6.7	2.7	22.9	5.4	5.1
368	F7FMD6	Protein Camlg OS=Rattus norvegicus GN=Camlg PE=4 SV=1 - [F7FMD6_RAT]	protein binding	endoplasmic reticulum	metabolic process; regulation of biological process; response to stimulus	2.9	1.5	2.8	1.3					3.9	2.1
369	D4A2P1	Protein Ccar1 OS=Rattus norvegicus GN=Ccar1 PE=4 SV=2 - [D4A2P1_RAT]	metal ion binding; RNA binding		regulation of biological process; cell death; cell division	1.3	2.7	2.1	1.8	4.3	7.7		11.2	10.4	4.6
370	D4AC23	Protein Cct7 OS=Rattus norvegicus GN=Cct7 PE=3 SV=1 - [D4AC23_RAT]	nucleotide binding; protein binding	cytoplasm; mitochondrion	metabolic process; transport	2.8	4.4	4.5	2.8	3.4	5.1		11.9	4.5	4.4
371	B5DEG7	Protein Champ1 OS=Rattus norvegicus GN=Champ1 PE=2 SV=1 - [B5DEG7_RAT]	metal ion binding	chromosome; nucleus	cell organization and biogenesis	4.3	4.5	5.8	3.0	2.6	3.1		100.0	7.4	14.5
372	F1LPP8 ★	Protein Chd3 (Fragment) OS=Rattus norvegicus GN=Chd3 PE=4 SV=2 - [F1LPP8_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding; metal ion binding	nucleus; cytoplasm; cytoskeleton	metabolic process; cell organization and biogenesis; regulation of biological process	0.8	1.9	1.4	1.7	3.1	7.1		11.4	3.2	3.4
373	E9PU01	Protein Chd4 OS=Rattus norvegicus GN=Chd4 PE=4 SV=2 - [E9PU01_RAT]	protein binding; DNA binding; catalytic activity; nucleotide binding; metal ion binding	nucleus; cytoplasm	metabolic process; cell organization and biogenesis; regulation of biological process; response to stimulus	0.7	2.1	1.7	1.7	1.8	5.0		8.7	3.4	2.8
374	F1M949	Protein Ckap5 OS=Rattus norvegicus GN=Ckap5 PE=4 SV=2 - [F1M949_RAT]		membrane	cell organization and biogenesis	3.2	3.0	2.1	2.1	2.3	6.9	2.1	18.3	5.3	4.5
375	F1LNR0	Protein Clasp1 OS=Rattus norvegicus GN=Clasp1 PE=4 SV=2 - [F1LNR0_RAT]	protein binding			2.2	4.7	11.7	1.6					3.6	4.0
376	D4A6H8	Protein Ctnna2 (Fragment) OS=Rattus norvegicus GN=Ctnna2 PE=4 SV=2 - [D4A6H8_RAT]	structural molecule activity; protein binding	cytoplasm; cytoskeleton; membrane	cell organization and biogenesis; cellular component movement; regulation of biological process	3.5	3.9	29.2	0.7					62.0	16.6
377	E9PT29	Protein Ddx17 OS=Rattus norvegicus GN=Ddx17 PE=3 SV=2 - [E9PT29_RAT]	nucleotide binding; catalytic activity		metabolic process	2.1	3.2	2.9	1.5	3.5	3.9	3.3		2.8	2.6
378	D3ZN21	Protein Ddx3y OS=Rattus norvegicus GN=Ddx3y PE=3 SV=1 - [D3ZN21_RAT]	nucleotide binding; DNA binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; membrane	metabolic process; regulation of biological process; response to stimulus; cell organization and biogenesis; defense response	2.3	2.9	2.5	1.3	3.3	3.5	9.6	4.0	3.1	3.2

379	Q6AXS3	Protein DEK OS=Rattus norvegicus GN=Dek PE=2 SV=1 - [DEK_RAT]	DNA binding; protein binding; RNA binding	nucleus	cell organization and biogenesis; regulation of biological process	1.9	6.2	4.9	4.6					100.0	19.6
380	D3ZWL9	Protein Dido1 OS=Rattus norvegicus GN=Dido1 PE=4 SV=1 - [D3ZWL9_RAT]	protein binding; metal ion binding	nucleus	metabolic process; regulation of biological process; response to stimulus	1.8	5.6	4.2	3.4					6.4	3.6
381	P11598	Protein disulfide-isomerase A3 OS=Rattus norvegicus GN=Pdia3 PE=1 SV=2 - [PDIA3_RAT]	catalytic activity; RNA binding	nucleus; endoplasmic reticulum; organelle lumen; cell surface	metabolic process; response to stimulus; regulation of biological process; cellular homeostasis	1.5	2.2	2.7	2.3	9.1	3.2	2.4	19.8	5.1	4.8
382	Q63081	Protein disulfide-isomerase A6 OS=Rattus norvegicus GN=Pdia6 PE=1 SV=2 - [PDIA6_RAT]	catalytic activity; metal ion binding	endoplasmic reticulum; organelle lumen; membrane	metabolic process; response to stimulus; transport; cellular homeostasis; regulation of biological process	1.2	2.3	1.8	1.2	17.8			100.0	6.2	16.3
383	F1LM66	Protein Eftud2 OS=Rattus norvegicus GN=Eftud2 PE=4 SV=1 - [F1LM66_RAT]	nucleotide binding; catalytic activity; RNA binding	nucleus; cytoplasm; membrane; spliceosomal complex	metabolic process	1.4	2.5	2.8	2.2	3.4	3.9	20.4	7.4	3.3	4.7
384	D4A005 ★	Protein Ehmt1 OS=Rattus norvegicus GN=Ehmt1 PE=4 SV=2 - [D4A005_RAT]	protein binding; catalytic activity; metal ion binding	nucleus; chromosome	regulation of biological process; metabolic process; cell organization and biogenesis		5.4		3.1					3.7	3.0
385	D4AE02	Protein Fam98b OS=Rattus norvegicus GN=Fam98b PE=4 SV=2 - [D4AE02_RAT]				3.5	3.4	100.0						6.8	22.7
386	F1LQ48	Protein Fblim1 OS=Rattus norvegicus GN=Hnrnpl PE=4 SV=2 - [F1LQ48_RAT]	nucleotide binding; RNA binding; DNA binding	nucleus; membrane	metabolic process	2.8	5.3	4.2	2.9	2.6	2.8	3.1	6.6	4.4	3.5
387	D3ZVA5	Protein Fbll1 OS=Rattus norvegicus GN=Fbll1 PE=3 SV=2 - [D3ZVA5_RAT]	RNA binding; catalytic activity		metabolic process	2.4	3.6	100.0	0.7	2.9	3.2	1.1	14.0	2.2	13.0
388	M0R7H8	Protein Fsd1 OS=Rattus norvegicus GN=Fsd1 PE=4 SV=1 - [M0R7H8_RAT]		cytoplasm		3.9	7.5		3.4					100.0	23.0
389	D3ZC90	Protein Fsd1l (Fragment) OS=Rattus norvegicus GN=Fsd1l PE=4 SV=2 - [D3ZC90_RAT]	protein binding			100.0	5.0	100.0	8.4	8.9	2.2			7.0	28.9
390	D4A0I2	Protein Fsd1l (Fragment) OS=Rattus norvegicus GN=Fsd1l PE=4 SV=2 - [D4A0I2_RAT]	protein binding			1.0	5.0	31.3	8.4	6.5	2.2			9.0	7.9
391	G3V829	Protein Fubp3 OS=Rattus norvegicus GN=Fubp3 PE=4 SV=1 - [G3V829_RAT]	RNA binding	nucleus; cytoplasm	metabolic process; regulation of biological process	1.5	2.6		1.3	1.1	2.5		3.4	4.8	2.2
392	D3ZVD8	Protein Hdac6 OS=Rattus norvegicus GN=Hdac6 PE=4 SV=2 - [D3ZVD8_RAT]	metal ion binding; catalytic activity		metabolic process	1.5	4.7	3.7	1.4	100.0	34.2			4.1	18.7
393	D4A9T3 ★	Protein Hmg1l1 OS=Rattus norvegicus GN=Hmg1l1 PE=4 SV=2 - [D4A9T3_RAT]	DNA binding; protein binding	chromosome; nucleus; cell surface	regulation of biological process; defense response; response to stimulus; metabolic process	4.3	4.4	4.7	3.1					13.4	5.0
394	F1M3H8	Protein Hnrnpa0 OS=Rattus norvegicus GN=Hnrnpa0 PE=4 SV=2 - [F1M3H8_RAT]	nucleotide binding; RNA binding; protein binding	nucleus	defense response; response to stimulus; regulation of biological process	2.2	3.2	2.4	1.3	1.7	1.6	2.0	2.3	3.7	2.0
395	D4A3E1 ★	Protein Hnrnpll OS=Rattus norvegicus GN=Hnrnpll PE=4 SV=1 - [D4A3E1_RAT]	nucleotide binding; RNA binding	nucleus; membrane	metabolic process; regulation of biological process	2.3	3.6	4.5	1.6	4.0	12.9	2.9	8.0	5.8	4.6
396	D4ABT8	Protein Hnrnpul2 OS=Rattus norvegicus GN=Hnrnpul2 PE=1 SV=1 - [D4ABT8_RAT]	protein binding; nucleotide binding; catalytic activity; RNA binding	nucleus; membrane		1.7	4.0	3.0	1.1	3.1	4.6	2.5	5.9	4.1	3.0
397	D3ZZQ6	Protein Ints4 OS=Rattus norvegicus GN=Ints4 PE=4 SV=1 - [D3ZZQ6_RAT]			transport; metabolic process	2.8	9.3	4.6						52.6	13.9
398	D4AD67	Protein Ktn1 OS=Rattus norvegicus GN=Ktn1 PE=4 SV=2 - [D4AD67_RAT]	protein binding		cellular component movement	1.3	5.6	1.4	1.4	3.7	9.3			2.7	3.2
399	D3ZJT9 ★	Protein L3mbtl3 OS=Rattus norvegicus GN=L3mbtl3 PE=4 SV=1 - [D3ZJT9_RAT]	protein binding	nucleus	regulation of biological process; cell differentiation		4.1				8.0		19.8	51.9	16.8
400	F1LWZ8	Protein Lemd3 OS=Rattus norvegicus GN=Lemd3 PE=4 SV=2 - [F1LWZ8_RAT]	nucleotide binding	membrane	cellular component movement; cell organization and biogenesis; regulation of biological process; cell differentiation	14.8		5.6	4.4	8.5	100.0			61.3	27.8
401	D3ZZK1	Protein LOC100359563 OS=Rattus norvegicus GN=LOC100359563 PE=3 SV=1 - [D3ZZK1_RAT]	RNA binding; structural molecule activity	cytoplasm; ribosome; membrane	metabolic process	4.0	23.2	6.9	4.9					4.7	7.3
402	F7FLF2	Protein LOC100360057 (Fragment) OS=Rattus norvegicus GN=LOC100363800 PE=4 SV=1 - [F7FLF2_RAT]	structural molecule activity	cytoplasm; ribosome	metabolic process; cell differentiation	1.8	3.4	2.8	1.3	1.6	2.3		100.0	3.6	13.0

403	D3ZFY8	Protein LOC100362142 OS=Rattus norvegicus GN=LOC100912618 PE=4 SV=1 - [D3ZFY8_RAT]	catalytic activity; protein binding	nucleus; cytoplasm	metabolic process; response to stimulus; regulation of biological process	2.1		18.4						54.2	18.7
404	D3ZZR5 ★	Protein LOC100364748 OS=Rattus norvegicus GN=Snrpa1 PE=4 SV=1 - [D3ZZR5_RAT]	protein binding; RNA binding	nucleus; spliceosomal complex		2.4	100.0	5.4	0.8					7.8	19.4
405	D4ABI7	Protein LOC100365676 OS=Rattus norvegicus GN=LOC100365676 PE=4 SV=2 - [D4ABI7_RAT]	catalytic activity; protein binding	endoplasmic reticulum	regulation of biological process; response to stimulus; metabolic process	1.5	4.2	2.5	1.5					2.5	2.0
406	D3ZLL8	Protein LOC100909878 OS=Rattus norvegicus GN=LOC691716 PE=3 SV=1 - [D3ZLL8_RAT]	structural molecule activity	ribosome	metabolic process	2.2	3.5	2.6	2.1					12.7	3.8
407	D4A0F5	Protein LOC100910754 OS=Rattus norvegicus GN=Sept7 PE=3 SV=2 - [D4A0F5_RAT]	nucleotide binding			1.6	3.0	3.4	0.7	2.7	5.4	100.0	24.4	3.5	14.5
408	Q5BJP4	Protein LOC100910882 OS=Rattus norvegicus GN=Rbm39 PE=2 SV=1 - [Q5BJP4_RAT]	nucleotide binding; RNA binding	nucleus; cytoskeleton; membrane	metabolic process	1.4	2.1	2.0	1.7	5.3	4.8		100.0	10.3	14.2
409	M0R3M4 ★	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	metabolic process; regulation of biological process; transport	2.5	16.3	2.7	2.6	5.9	100.0		100.0	4.0	26.0
410	Q5FVG4 ★	Protein LOC100911440 OS=Rattus norvegicus GN=LOC100911440 PE=2 SV=1 - [Q5FVG4_RAT]	transporter activity	nucleus; mitochondrion; membrane	transport		4.5	3.0						11.5	4.8
411	D4A510	Protein LOC685179 OS=Rattus norvegicus GN=Smarcc2 PE=4 SV=2 - [D4A510_RAT]	DNA binding; protein binding	nucleus		1.2	2.7	1.7	1.3	1.9	2.6	3.5	6.1	2.6	2.4
412	D3Z8C1	Protein Lsm14b OS=Rattus norvegicus GN=Lsm14b PE=4 SV=1 - [D3Z8C1_RAT]					62.0	64.3						6.7	33.3
413	D3ZS48	Protein Lsm14b OS=Rattus norvegicus GN=Lsm14b PE=4 SV=1 - [D3ZS48_RAT]					62.0	64.3						9.9	34.1
414	Q27W02	Protein mago nashi homolog OS=Rattus norvegicus GN=Magoh PE=2 SV=1 - [MGN_RAT]	RNA binding	nucleus; spliceosomal complex; cytoplasm	metabolic process; regulation of biological process; transport	42.5	40.5	100.0	18.8					54.5	42.7
415	D3ZAG3	Protein Map9 OS=Rattus norvegicus GN=Map9 PE=4 SV=1 - [D3ZAG3_RAT]		nucleus; cytoplasm; Golgi; cytoskeleton	regulation of biological process; cell organization and biogenesis		5.0	9.7	3.2					7.8	5.1
416	D3ZBD0	Protein Msl1 OS=Rattus norvegicus GN=Msl1 PE=4 SV=1 - [D3ZBD0_RAT]		nucleus	cell organization and biogenesis; metabolic process		5.8	4.1	2.6					4.0	3.3
417	D4AEI5	Protein Myef2 OS=Rattus norvegicus GN=Myef2 PE=4 SV=1 - [D4AEI5_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm; Golgi	cell differentiation	5.6	10.0	11.2	2.5		14.9	2.0	6.0	54.7	11.9
418	F1M6E5	Protein Nacad OS=Rattus norvegicus GN=Nacad PE=4 SV=2 - [F1M6E5_RAT]				1.9	8.3		4.9					20.3	7.1
419	F1LPV0	Protein Nars OS=Rattus norvegicus GN=Nars PE=3 SV=2 - [F1LPV0_RAT]	nucleotide binding; catalytic activity	cytoplasm; mitochondrion	metabolic process	3.2	4.9	3.2	2.4	100.0	100.0			7.6	27.7
420	F1M4H5	Protein Nova2 (Fragment) OS=Rattus norvegicus GN=Nova2 PE=4 SV=2 - [F1M4H5_RAT]	RNA binding	nucleus		1.2	2.2	3.0	1.6	3.2	4.2		12.7	54.8	9.2
421	F2Z3S9	Protein Nr2f1 OS=Rattus norvegicus GN=Nr2f1 PE=3 SV=1 - [F2Z3S9_RAT]	DNA binding; receptor activity; signal transducer activity; metal ion binding	nucleus	regulation of biological process; cellular component movement; metabolic process; response to stimulus	2.1	4.1	2.6	2.4	3.1	5.3	3.6	7.2	3.8	3.4
422	F1LW91	Protein Numa1 (Fragment) OS=Rattus norvegicus GN=Numa1 PE=4 SV=1 - [F1LW91_RAT]	catalytic activity; receptor activity; signal transducer activity; protein binding	membrane; nucleus; cytoplasm	cell organization and biogenesis; regulation of biological process; response to stimulus; metabolic process; cell differentiation	1.1	2.6	1.6	1.1	1.5	4.9	1.7	6.8	2.9	2.4
423	D3Z8B2	Protein Nup133 (Fragment) OS=Rattus norvegicus GN=Nup133 PE=4 SV=2 - [D3Z8B2_RAT]	transporter activity		transport; cell organization and biogenesis		2.7		1.5	5.7	100.0		100.0	3.3	30.5
424	D3ZBL6	Protein Nup160 OS=Rattus norvegicus GN=Nup160 PE=4 SV=2 - [D3ZBL6_RAT]	transporter activity	chromosome	transport		3.1	2.7	1.4	2.7	19.9	23.9	12.1	3.1	7.7
425	D4ACK1	Protein Nup214 (Fragment) OS=Rattus norvegicus GN=Nup214 PE=4 SV=2 - [D4ACK1_RAT]	transporter activity; protein binding		transport; regulation of biological process	1.2	4.5	2.0	1.6			2.0	100.0	4.8	14.5
426	D4A8C8	Protein Paxbp1 OS=Rattus norvegicus GN=Paxbp1 PE=4 SV=1 - [D4A8C8_RAT]	DNA binding; protein binding	nucleus; cytosol	regulation of biological process	3.3	5.6	2.0						52.6	12.7
427	D3ZT52	Protein Pbrm1 OS=Rattus norvegicus GN=Pbrm1 PE=4 SV=1 - [D3ZT52_RAT]	DNA binding; protein binding	chromosome	regulation of biological process	1.5	3.7	2.8	2.1	3.5	23.3	2.6	30.5	4.1	7.4
428	D3ZNI3	Protein Pdcd11 OS=Rattus norvegicus GN=Pdcd11 PE=4 SV=1 - [D3ZNI3_RAT]	RNA binding; protein binding	nucleus; cytosol	metabolic process		16.4			1.6	100.0	1.9	10.8	2.7	19.0

429	M0R464	Protein Phf6 OS=Rattus norvegicus GN=Phf6 PE=4 SV=1 - [M0R464_RAT]	protein binding; metal ion binding; RNA binding	nucleus		2.1	7.3		3.4	5.9	27.3	10.1	100.0	4.0	17.8
430	G3V629	Protein Ppp1r18 OS=Rattus norvegicus GN=Ppp1r18 PE=2 SV=2 - [G3V629_RAT]	protein binding			3.9		6.5	100.0					52.1	32.5
431	Q5XI34	Protein Ppp2r1a OS=Rattus norvegicus GN=Ppp2r1a PE=2 SV=1 - [Q5XI34_RAT]	catalytic activity; protein binding	cytosol	regulation of biological process; metabolic process	2.2	4.0	3.1	1.8					3.7	2.5
432	D3ZHI9	Protein Ppp2r5e OS=Rattus norvegicus GN=Ppp2r5e PE=4 SV=1 - [D3ZHI9_RAT]	enzyme regulator activity	cytoplasm	regulation of biological process; response to stimulus		2.8	3.0						100.0	26.4
433	D4A6M5	Protein Prr12 OS=Rattus norvegicus GN=Prr12 PE=4 SV=2 - [D4A6M5_RAT]	DNA binding			1.8	4.5	3.7	2.2					5.8	3.0
434	B0BNK1	Protein Rab5c OS=Rattus norvegicus GN=Rab5c PE=2 SV=1 - [B0BNK1_RAT]	nucleotide binding; catalytic activity	nucleus; cytoplasm; membrane; endosome	transport; cell organization and biogenesis; regulation of biological process; response to stimulus		15.1	9.3	1.7					13.4	7.9
435	E9PTI6	Protein Raly OS=Rattus norvegicus GN=Raly PE=4 SV=1 - [E9PTI6_RAT]	nucleotide binding	spliceosomal complex		1.8	3.9	2.4	1.3	1.4	1.1	2.0	2.8	2.4	1.9
436	B5DFB2	Protein Rbbp4 OS=Rattus norvegicus GN=Rbbp4 PE=2 SV=1 - [B5DFB2_RAT]	DNA binding; protein binding; catalytic activity	nucleus	metabolic process; cell organization and biogenesis; response to stimulus	2.4	5.1	6.8	5.7				100.0	18.5	19.8
437	M0R3Z8	Protein Rbm15 OS=Rattus norvegicus GN=Rbm15 PE=1 SV=1 - [M0R3Z8_RAT]	nucleotide binding	nucleus	regulation of biological process	0.9	2.9	2.6	1.4		19.2	2.5	24.9	2.9	6.4
438	D3ZHD6	Protein Rbm15b OS=Rattus norvegicus GN=Rbm15b PE=4 SV=2 - [D3ZHD6_RAT]	nucleotide binding; RNA binding	nucleus	regulation of biological process; transport	1.4	19.2	2.7						17.6	8.2
439	Q6AY02	Protein Rbm17 OS=Rattus norvegicus GN=Rbm17 PE=2 SV=1 - [Q6AY02_RAT]	nucleotide binding	nucleus; cytoplasm	metabolic process	100.0	21.6	58.3	6.4					3.9	31.7
440	D3Z8R4	Protein Rbm25l1 OS=Rattus norvegicus GN=Rbm25l1 PE=4 SV=2 - [D3Z8R4_RAT]	nucleotide binding; RNA binding	spliceosomal complex	regulation of biological process	2.4	3.7	2.6	3.1	7.1	17.7		15.5	53.4	11.7
441	D3Z9W9	Protein Rbm26 OS=Rattus norvegicus GN=Rbm26 PE=4 SV=2 - [D3Z9W9_RAT]	nucleotide binding; RNA binding; metal ion binding		metabolic process	2.5	3.5	9.4	3.6					5.8	4.1
442	F1LWJ2	Protein Rbm27 (Fragment) OS=Rattus norvegicus GN=Rbm27 PE=4 SV=1 - [F1LWJ2_RAT]	nucleotide binding; RNA binding; metal ion binding			2.4	15.6	4.9						60.2	16.6
443	D4ACW0	Protein Rbm6 OS=Rattus norvegicus GN=Rbm6 PE=4 SV=1 - [D4ACW0_RAT]	nucleotide binding; RNA binding; metal ion binding	nucleus		100.0	21.6		5.9					4.1	26.3
444	Q6AXX5	Protein Rdh11 OS=Rattus norvegicus GN=Rdh11 PE=2 SV=1 - [Q6AXX5_RAT]	nucleotide binding; catalytic activity	membrane	metabolic process; regulation of biological process		19.5	9.5						50.3	19.8
445	D3ZKC9	Protein RGD1559904 (Fragment) OS=Rattus norvegicus GN=RGD1559904 PE=4 SV=2 - [D3ZKC9_RAT]					100.0				3.5			3.7	26.8
446	D4A6W6	Protein RGD1561333 OS=Rattus norvegicus GN=RGD1561333 PE=3 SV=1 - [D4A6W6_RAT]	RNA binding; structural molecule activity	ribosome	metabolic process	1.4	2.9	2.3	2.1					2.2	1.8
447	D3ZPT0	Protein RGD1566084 OS=Rattus norvegicus GN=Prr36 PE=4 SV=2 - [D3ZPT0_RAT]				100.0	7.3	4.6	4.9					67.1	30.6
448	F1M5X1	Protein Rrbp1 OS=Rattus norvegicus GN=Rrbp1 PE=4 SV=2 - [F1M5X1_RAT]			transport	1.0	3.1	1.6	1.1	1.6	3.0	2.7	61.4	2.9	7.8
449	G3V8T5	Protein Ruvbl2 OS=Rattus norvegicus GN=Ruvbl2 PE=4 SV=1 - [G3V8T5_RAT]	nucleotide binding; DNA binding; catalytic activity; protein binding	nucleus; cytoplasm	metabolic process; response to stimulus; cell organization and biogenesis; regulation of biological process	3.3	7.7	100.0	4.3	6.2	2.6		8.8	52.5	20.6
450	M0R6E6	Protein Safb2 (Fragment) OS=Rattus norvegicus GN=Safb2 PE=4 SV=1 - [M0R6E6_RAT]	nucleotide binding; protein binding			8.2	4.6			4.1	5.4		3.8	3.9	4.3
451	F1LPT8	Protein SCAF8 OS=Rattus norvegicus GN=Scaf8 PE=4 SV=2 - [F1LPT8_RAT]	nucleotide binding; protein binding	nucleus			100.0		4.7					18.4	30.8
452	G3V7S5	Protein Senp3 OS=Rattus norvegicus GN=Senp3 PE=4 SV=1 - [G3V7S5_RAT]	catalytic activity	nucleus	metabolic process	62.2	3.9		2.7					2.6	14.3
453	B5DFG5	Protein Sept6 OS=Rattus norvegicus GN=Sept6 PE=2 SV=1 - [B5DFG5_RAT]	nucleotide binding	cytoplasm		3.1	4.8	7.5	4.2	1.9				23.0	6.4
454	Q4KLI7	Protein Sf3a3 OS=Rattus norvegicus GN=Sf3a3 PE=2 SV=1 - [Q4KLI7_RAT]	RNA binding; metal ion binding	nucleus; spliceosomal complex	metabolic process	3.7	5.2	6.4	3.1				4.6	7.5	4.4
455	E9PT66	Protein Sf3b3 OS=Rattus norvegicus GN=Sf3b3 PE=4 SV=2 - [E9PT66_RAT]	RNA binding; protein binding	nucleus; spliceosomal complex	metabolic process	1.9	3.5	2.6	1.1	2.9	5.4	2.8	5.9	2.6	2.9

456	D4A5T1	Protein Sf3b5 OS=Rattus norvegicus GN=Sf3b5 PE=4 SV=1 - [D4A5T1_RAT]		nucleus; spliceosomal complex		3.8	4.8	14.1	5.2					50.1	13.0
457	D3ZBP2	Protein Sin3a OS=Rattus norvegicus GN=Sin3a PE=4 SV=1 - [D3ZBP2_RAT]	DNA binding; protein binding; RNA binding; catalytic activity	chromosome; nucleus; cytoplasm	regulation of biological process; cell differentiation; metabolic process; response to stimulus; cell organization and biogenesis; cellular homeostasis	1.6	2.4	2.0	1.1	10.7	100.0		100.0	3.4	24.6
458	D4AE49	Protein Skiv2l2 (Fragment) OS=Rattus norvegicus GN=Skiv2l2 PE=4 SV=2 - [D4AE49_RAT]	nucleotide binding; catalytic activity	nucleus; spliceosomal complex	metabolic process	1.6	100.0	10.2	1.7					10.2	20.6
459	D3ZIE5	Protein Smarca1 OS=Rattus norvegicus GN=Smarca1 PE=4 SV=2 - [D3ZIE5_RAT]	DNA binding; catalytic activity; nucleotide binding; protein binding	nucleus	metabolic process; cell organization and biogenesis; cell differentiation; regulation of biological process	1.6	5.5	2.1	2.0	2.5	4.0			4.5	2.8
460	E9PTG1	Protein Smarca2 OS=Rattus norvegicus GN=Smarca2 PE=4 SV=1 - [E9PTG1_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding	nucleus; cytoskeleton	cell organization and biogenesis; regulation of biological process; metabolic process; cell differentiation	1.2	2.8	2.4	1.7	1.7	7.9			3.6	2.7
461	F1LNL2	Protein Smarca5 OS=Rattus norvegicus GN=Smarca5 PE=4 SV=2 - [F1LNL2_RAT]	DNA binding; catalytic activity; nucleotide binding; protein binding	chromosome; nucleus	regulation of biological process; metabolic process; response to stimulus; cell organization and biogenesis	1.8	3.2	1.9	2.1	3.0	4.1			4.7	2.6
462	Q4KLI0	Protein Smarcb1 OS=Rattus norvegicus GN=Smarcb1 PE=1 SV=1 - [Q4KLI0_RAT]	DNA binding; protein binding	chromosome; nucleus	cell organization and biogenesis; regulation of biological process; cell differentiation; metabolic process	6.2	4.8	100.0	4.0				10.3	100.0	32.2
463	D3ZJU5	Protein Smarcc1 OS=Rattus norvegicus GN=Smarcc1 PE=4 SV=1 - [D3ZJU5_RAT]	DNA binding; protein binding	chromosome; nucleus	cell organization and biogenesis; regulation of biological process; response to stimulus	1.4	2.9	3.2			3.1			3.7	2.4
464	D3ZBS9	Protein Smarcd1 OS=Rattus norvegicus GN=Smarcd1 PE=4 SV=1 - [D3ZBS9_RAT]	protein binding; structural molecule activity	nucleus	cell organization and biogenesis; regulation of biological process; response to stimulus	2.4	6.7	100.0	2.0	3.4	4.3		39.7	6.2	18.3
465	Q5U3Y2	Protein Smarcd3 OS=Rattus norvegicus GN=Smarcd3 PE=2 SV=1 - [Q5U3Y2_RAT]	protein binding	nucleus; cytoplasm	regulation of biological process; cell organization and biogenesis; metabolic process; cell differentiation	2.6	100.0	5.5	3.1					6.6	19.6
466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	regulation of biological process; cell organization and biogenesis			2.6	2.5	2.1	31.5		100.0	9.5	24.7
467	B5DES0	Protein Snrpd2 OS=Rattus norvegicus GN=Snrpd2 PE=2 SV=1 - [B5DES0_RAT]	RNA binding	spliceosomal complex; cytosol	cell organization and biogenesis; metabolic process	1.2	1.6	1.4	0.9	1.8	2.6	1.1	2.9	3.1	1.7
468	G3V6S0	Protein Sptbn1 OS=Rattus norvegicus GN=Sptbn1 PE=4 SV=2 - [G3V6S0_RAT]	protein binding; structural molecule activity	nucleus; cytoplasm; membrane; cytoskeleton	cell organization and biogenesis; metabolic process; transport	1.2	2.6	1.6	0.9	1.7	4.5	1.5	6.2	2.2	2.2
469	M0R7E6	Protein Srrt OS=Rattus norvegicus GN=Srrt PE=4 SV=1 - [M0R7E6_RAT]	DNA binding	cytoplasm	regulation of biological process; cell proliferation; metabolic process	2.2	3.4	3.2	3.1	5.2	6.3	2.6		17.1	4.8
470	D4A9L2	Protein Srsf1 OS=Rattus norvegicus GN=Srsf1 PE=4 SV=1 - [D4A9L2_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex	cell organization and biogenesis; regulation of biological process; metabolic process	5.4	5.7	6.1	3.9	1.3	1.1		1.8	10.8	4.0
471	Q0ZFS8	Protein Srsf3 OS=Rattus norvegicus GN=Srsf3 PE=2 SV=1 - [Q0ZFS8_RAT]	nucleotide binding; protein binding; RNA binding			2.6	4.8	3.2	2.8	2.3	2.0		2.2	51.9	8.0
472	G3V798	Protein Srsf4 OS=Rattus norvegicus GN=Srsf4 PE=4 SV=1 - [G3V798_RAT]	nucleotide binding; RNA binding	nucleus	cell differentiation; regulation of biological process	2.2	4.1	2.4	0.8	1.0	1.7	1.3	2.8	3.4	2.0
473	D4A720	Protein Srsf7 OS=Rattus norvegicus GN=Srsf7 PE=4 SV=1 - [D4A720_RAT]	nucleotide binding; metal ion binding; RNA binding	nucleus	regulation of biological process	3.6	10.5	6.2	2.9	1.1			25.9	3.7	6.7
474	D3ZTT7	Protein Sun2 OS=Rattus norvegicus GN=Sun2 PE=4 SV=1 - [D3ZTT7_RAT]	protein binding	chromosome; membrane	cell organization and biogenesis; regulation of biological process; cellular component movement	1.1	5.3	78.1	0.7					3.5	14.8
475	M0R7D8	Protein Suz12 OS=Rattus norvegicus GN=Suz12 PE=4 SV=1 - [M0R7D8_RAT]					10.9	0.8			100.0			59.4	34.2
476	F1LSH0	Protein Sympk OS=Rattus norvegicus GN=Sympk PE=4 SV=2 - [F1LSH0_RAT]		nucleus; cytoplasm; membrane	metabolic process; regulation of biological process	1.8	4.1	3.4	1.7					54.0	10.8
477	I6L9G6	Protein Tardbp OS=Rattus norvegicus GN=Tardbp PE=2 SV=1 - [I6L9G6_RAT]	nucleotide binding; DNA binding; RNA binding; protein binding	nucleus; cytoplasm	metabolic process; regulation of biological process; response to stimulus	1.8	12.4	6.0	2.6	3.5	6.0	3.2	17.7	11.4	6.5

478	A0A096MJZ2	Protein Tbl2 OS=Rattus norvegicus GN=Tbl2 PE=4 SV=1 - [A0A096MJZ2_RAT]	protein binding; RNA binding				81.1	18.9						7.2	26.8
479	D4A206	Protein Tcof1 OS=Rattus norvegicus GN=Tcof1 PE=1 SV=2 - [D4A206_RAT]	protein binding	nucleus; cytoplasm	metabolic process	1.0	3.4	1.9	2.3			0.9	100.0	2.8	14.0
480	D3ZJF7	Protein Terf2 OS=Rattus norvegicus GN=Terf2 PE=4 SV=2 - [D3ZJF7_RAT]	DNA binding; protein binding	nucleus; cytoplasm; Golgi	cell organization and biogenesis; metabolic process; response to stimulus; regulation of biological process	4.1	4.2	24.0	4.2	100.0	1.9			100.0	29.8
481	Q52KJ9	Protein Tmx1 OS=Rattus norvegicus GN=Tmx1 PE=2 SV=1 - [Q52KJ9_RAT]	catalytic activity	endoplasmic reticulum; membrane	metabolic process; response to stimulus; regulation of biological process; cellular homeostasis	2.6	3.6	2.8	1.3					19.5	5.0
482	D3ZZQ0	Protein Tnik OS=Rattus norvegicus GN=Tnik PE=4 SV=1 - [D3ZZQ0_RAT]	nucleotide binding; catalytic activity; signal transducer activity	nucleus; cytoplasm; cytoskeleton; membrane	regulation of biological process; metabolic process; response to stimulus; cell organization and biogenesis	0.6	2.5	2.0	0.6	1.4	3.4		13.2	3.5	3.0
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	metabolic process; response to stimulus; regulation of biological process	1.4	3.3	2.9	2.5	5.3	6.4	4.2	100.0	4.1	13.0
484	A0A096MKD9	Protein Trim46 (Fragment) OS=Rattus norvegicus GN=Trim46 PE=4 SV=1 - [A0A096MKD9_RAT]				2.0	3.7	2.9	2.5	100.0	100.0			2.8	26.7
485	D3ZA17	Protein Trim46 OS=Rattus norvegicus GN=Trim46 PE=4 SV=2 - [D3ZA17_RAT]	protein binding; metal ion binding			2.2	4.1	2.9	2.4	100.0	58.6			2.7	21.6
486	F1M0Z1	Protein Trio OS=Rattus norvegicus GN=Trio PE=4 SV=2 - [F1M0Z1_RAT]	catalytic activity; protein binding; nucleotide binding		metabolic process; regulation of biological process	1.5	3.9		1.6	6.3	18.3			3.5	5.0
487	B4F7C2	Protein Tubb4a OS=Rattus norvegicus GN=Tubb4a PE=2 SV=1 - [B4F7C2_RAT]	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cell organization and biogenesis	1.6	4.1	4.2	2.9	9.5	4.1	2.8	9.2	3.4	4.2
488	Q3KR55	Protein U2af1 OS=Rattus norvegicus GN=U2af1 PE=2 SV=1 - [Q3KR55_RAT]	nucleotide binding; RNA binding; metal ion binding; protein binding	nucleus; spliceosomal complex		5.2	23.3	5.1	3.7	2.2	3.3	4.4	8.6	3.5	5.9
489	F2Z3T9	Protein U2af2 OS=Rattus norvegicus GN=U2af2 PE=4 SV=1 - [F2Z3T9_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex	metabolic process; regulation of biological process	2.7	6.4	27.6	1.6	3.2	2.6		19.3	52.8	12.9
490	D4A4B4	Protein U2surp OS=Rattus norvegicus GN=U2surp PE=4 SV=1 - [D4A4B4_RAT]	nucleotide binding; RNA binding	nucleus	metabolic process	2.1	4.4	4.3	1.5					4.5	2.8
491	F7F1N8	Protein Usp39 OS=Rattus norvegicus GN=Usp39 PE=4 SV=1 - [F7F1N8_RAT]	catalytic activity; metal ion binding		metabolic process	1.3	1.6	1.8	1.1	2.4	8.3		4.2	4.2	2.8
492	D3ZPY0	Protein Wtap OS=Rattus norvegicus GN=Wtap PE=4 SV=1 - [D3ZPY0_RAT]		nucleus; membrane	regulation of biological process; metabolic process	15.1		100.0	61.0					53.5	45.9
493	Q8CHJ4	Protein Yy1 OS=Rattus norvegicus GN=Yy1 PE=2 SV=1 - [Q8CHJ4_RAT]	DNA binding; RNA binding; protein binding; metal ion binding	nucleus; cytoplasm; membrane	regulation of biological process; metabolic process; response to stimulus; cell organization and biogenesis		100.0	100.0						50.1	62.5
494	F1M0V0	Protein Zfp280d OS=Rattus norvegicus GN=Zfp280d PE=4 SV=2 - [F1M0V0_RAT]	metal ion binding								100.0	4.2		100.0	68.1
495	D3ZQL4	Protein Zfp346 OS=Rattus norvegicus GN=Zfp346 PE=4 SV=2 - [D3ZQL4_RAT]	RNA binding; metal ion binding; protein binding	nucleus	cell death; regulation of biological process		100.0		5.2					4.6	27.5
496	D4A169	Protein Zfp462 OS=Rattus norvegicus GN=Zfp462 PE=4 SV=2 - [D4A169_RAT]	metal ion binding			1.6	4.9		1.9		6.6		25.2	3.9	6.3
497	D3ZIF0	Protein Zfp512 OS=Rattus norvegicus GN=Zfp512 PE=4 SV=1 - [D3ZIF0_RAT]	metal ion binding	nucleus		0.9	5.3	5.1	1.5	3.1	3.5	2.7	14.5	3.0	4.0
498	D4A0U3	Protein Zfp638 OS=Rattus norvegicus GN=Zfp638 PE=4 SV=1 - [D4A0U3_RAT]	nucleotide binding; metal ion binding; RNA binding	nucleus		2.3	4.3	3.5	2.4	3.3	4.7	2.3	16.2	6.1	4.5
499	D4A069	Protein Zmym4 OS=Rattus norvegicus GN=Zmym4 PE=4 SV=1 - [D4A069_RAT]	metal ion binding		cell organization and biogenesis; regulation of biological process		5.6	3.2						5.3	3.5
500	D4A7J8	PRP4 pre-mRNA processing factor 4 homolog (Yeast) OS=Rattus norvegicus GN=Prpf4 PE=4 SV=1 - [D4A7J8_RAT]	protein binding; RNA binding	nucleus	metabolic process	2.7	4.0	3.4	1.6			1.9	100.0	3.7	14.7
501	Q5BJS0	Putative ATP-dependent RNA helicase DHX30 OS=Rattus norvegicus GN=Dhx30 PE=1 SV=1 - [DHX30_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; mitochondrion	metabolic process		4.1				100.0			3.6	26.9

502	Q5RKH0	Putative oxidoreductase GLYR1 OS=Rattus norvegicus GN=Glyr1 PE=2 SV=1 - [GLYR1_RAT]	nucleotide binding; DNA binding; catalytic activity; protein binding	nucleus; cytoplasm; Golgi	metabolic process	7.2	5.3	6.5	1.0					51.4	11.9
503	Q6AY23	Pyrroline-5-carboxylate reductase 2 OS=Rattus norvegicus GN=Pycr2 PE=2 SV=1 - [P5CR2_RAT]	nucleotide binding; catalytic activity	cytoplasm	metabolic process		5.9		21.0	6.7	100.0			3.7	22.9
504	D3ZXI0	Pyrroline-5-carboxylate reductase OS=Rattus norvegicus GN=Pycr1 PE=3 SV=1 - [D3ZXI0_RAT]	nucleotide binding; catalytic activity; protein binding	cytoplasm; mitochondrion	metabolic process; response to stimulus; regulation of biological process		95.9		4.3					3.7	26.0
505	P11980	Pyruvate kinase PKM OS=Rattus norvegicus GN=Pkm PE=1 SV=3 - [KPYM_RAT]	nucleotide binding; metal ion binding; catalytic activity; protein binding; RNA binding	nucleus; cytoplasm; mitochondrion; membrane	response to stimulus; metabolic process; cell death		3.2	100.0	2.5					58.9	32.9
506	Q6RUV5	Ras-related C3 botulinum toxin substrate 1 OS=Rattus norvegicus GN=Rac1 PE=1 SV=1 - [RAC1_RAT]	nucleotide binding; catalytic activity; protein binding	membrane; cytoplasm; cytosol	regulation of biological process; cell organization and biogenesis; cellular component movement; response to stimulus; metabolic process; transport; cell proliferation; cell differentiation	3.0	2.9	3.9	2.2					3.1	2.5
507	Q6NYB7	Ras-related protein Rab-1A OS=Rattus norvegicus GN=Rab1A PE=1 SV=3 - [RAB1A_RAT]	nucleotide binding; catalytic activity	membrane; nucleus; cytoplasm; mitochondrion; endosome; endoplasmic reticulum; Golgi; cytosol	cell organization and biogenesis; metabolic process; transport; regulation of biological process; response to stimulus; cellular component movement; defense response	3.9	8.0	3.9	3.8				1.9	4.7	3.7
508	M0RC99	Ras-related protein Rab-5A OS=Rattus norvegicus GN=Rab5a PE=2 SV=1 - [RAB5A_RAT]	nucleotide binding; catalytic activity; protein binding	nucleus; cytoplasm; endosome; cytosol; membrane; cytoskeleton	metabolic process; transport; cell organization and biogenesis; regulation of biological process; response to stimulus		3.6	9.3	5.7					29.8	9.7
509	G3V9N1	RCG21137 OS=Rattus norvegicus GN=Pgam5 PE=4 SV=1 - [G3V9N1_RAT]	catalytic activity; enzyme regulator activity; protein binding	mitochondrion; membrane	metabolic process; regulation of biological process; cell death	4.2	5.2	24.3	1.5	1.6	1.5		4.7	2.8	5.1
510	G3V7C6	RCG45400 OS=Rattus norvegicus GN=Tubb4b PE=3 SV=1 - [G3V7C6_RAT]	nucleotide binding; RNA binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cell organization and biogenesis	1.6	4.2	4.2	2.6	4.0	3.8	3.4	6.3	3.3	3.3
511	D4AD82	Rho GTPase-activating protein 35 OS=Rattus norvegicus GN=Arhgap35 PE=4 SV=2 - [D4AD82_RAT]	nucleotide binding		regulation of biological process; response to stimulus		100.0	2.3	4.3	7.2	8.1			6.1	18.3
512	O55215	Ribosomal protein S2 OS=Rattus norvegicus GN=Rps2-ps6 PE=2 SV=1 - [O55215_RAT]	RNA binding; structural molecule activity; protein binding	nucleus; cytoplasm; ribosome; membrane	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	2.3	3.5	3.0	2.2					2.8	2.3
513	Q4V886	RNA polymerase II-associated factor 1 homolog OS=Rattus norvegicus GN=Paf1 PE=2 SV=1 - [PAF1_RAT]	protein binding	nucleus; mitochondrion	regulation of biological process; metabolic process; cell organization and biogenesis; response to stimulus		40.1	18.1						4.7	15.7
514	B2GV05	RNA-binding protein 5 OS=Rattus norvegicus GN=Rbm5 PE=2 SV=1 - [RBM5_RAT]	nucleotide binding; RNA binding; metal ion binding	nucleus; spliceosomal complex	cell organization and biogenesis; regulation of biological process; metabolic process; cell death	1.5	2.6	2.6						3.5	2.1
515	P60123	RuvB-like 1 OS=Rattus norvegicus GN=Ruvbl1 PE=1 SV=1 - [RUVB1_RAT]	nucleotide binding; catalytic activity	nucleus; cytoplasm; Golgi	metabolic process; response to stimulus; regulation of biological process; cell organization and biogenesis; cell division	3.1	5.8	10.6	4.0	6.4	6.7	6.6	100.0	37.3	18.1
516	Q6PEC4	S-phase kinase-associated protein 1 OS=Rattus norvegicus GN=Skp1 PE=2 SV=3 - [SKP1_RAT]	catalytic activity	cytosol	metabolic process; cell organization and biogenesis	100.0	9.1	8.0	33.0	100.0	100.0			18.6	46.1
517	Q6AY30	Saccharopine dehydrogenase-like oxidoreductase OS=Rattus norvegicus GN=Sccpdh PE=2 SV=1 - [SCPDL_RAT]	nucleotide binding; catalytic activity	nucleus; mitochondrion; membrane	metabolic process	16.3	6.7		4.0					4.8	6.4
518	P11507	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Rattus norvegicus GN=Atp2a2 PE=1 SV=1 - [AT2A2_RAT]	nucleotide binding; catalytic activity; transporter activity; metal ion binding; protein binding	endoplasmic reticulum; membrane	regulation of biological process; metabolic process; transport; cellular homeostasis; response to stimulus; cell organization and biogenesis	1.2	2.8	1.9	1.2				100.0	3.9	15.8
519	O88453	Scaffold attachment factor B1 OS=Rattus norvegicus GN=Safb PE=1 SV=2 - [SAFB1_RAT]	nucleotide binding; DNA binding; RNA binding; protein binding	nucleus	metabolic process; regulation of biological process; response to stimulus	0.7	2.9	4.7	0.9	4.4	5.4		20.3	4.3	4.9

520	B3GNI6	Septin-11 OS=Rattus norvegicus GN=Sept11 PE=1 SV=1 - [SEP11_RAT]	nucleotide binding	cytoplasm; cytoskeleton	cell organization and biogenesis; cell division	3.5	4.5	8.2	4.7	1.9	2.2		7.7	53.2	9.6
521	Q5RJR9	Serine (Or cysteine) proteinase inhibitor, clade H, member 1, isoform CRA_b OS=Rattus norvegicus GN=Serpinh1 PE=2 SV=1 - [Q5RJR9_RAT]	enzyme regulator activity; protein binding; RNA binding	cytoplasm; endoplasmic reticulum; organelle lumen	response to stimulus; regulation of biological process; cell organization and biogenesis; metabolic process	5.0	5.8	4.6	3.0					12.4	5.1
522	Q5U3Z7	Serine hydroxymethyltransferase OS=Rattus norvegicus GN=Shmt2 PE=2 SV=1 - [Q5U3Z7_RAT]	catalytic activity; protein binding	mitochondrion; membrane; organelle lumen; cytoskeleton	metabolic process; regulation of biological process; cell organization and biogenesis	1.5	4.4	3.2	1.6	2.8	2.9		38.4	2.4	6.3
523	Q6P799	Serine--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Sars PE=1 SV=3 - [SYSC_RAT]	nucleotide binding; catalytic activity	cytoplasm; mitochondrion	metabolic process	18.9	5.5	24.1	4.8					50.5	17.3
524	B2DD29	Serine/threonine-protein kinase BRSK1 OS=Rattus norvegicus GN=Brsk1 PE=1 SV=1 - [BRSK1_RAT]	nucleotide binding; metal ion binding; catalytic activity; protein binding	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; response to stimulus; transport; cell organization and biogenesis; cell differentiation			100.0		100.0	100.0			100.0	100.0
525	O08875	Serine/threonine-protein kinase DCLK1 OS=Rattus norvegicus GN=Dclk1 PE=2 SV=1 - [DCLK1_RAT]	nucleotide binding; catalytic activity		cellular component movement; metabolic process; development; cell organization and biogenesis; response to stimulus; cell differentiation; cell growth	4.8	6.3	6.8	3.5		3.3		15.7	5.9	5.8
526	E9PSS1	Serine/threonine-protein kinase DCLK2 OS=Rattus norvegicus GN=Dclk2 PE=1 SV=2 - [E9PSS1_RAT]	nucleotide binding; catalytic activity		metabolic process; regulation of biological process; response to stimulus	3.5	7.8	9.0	4.6			100.0	28.2	6.2	19.9
527	O08678	Serine/threonine-protein kinase MARK1 OS=Rattus norvegicus GN=Mark1 PE=1 SV=1 - [MARK1_RAT]	nucleotide binding; metal ion binding; catalytic activity; protein binding	cytoplasm; cytoskeleton; membrane	cell organization and biogenesis; cellular component movement; metabolic process; regulation of biological process; response to stimulus			5.4			100.0		7.7	7.7	37.7
528	O88664	Serine/threonine-protein kinase TAO1 OS=Rattus norvegicus GN=Taok1 PE=1 SV=1 - [TAOK1_RAT]	nucleotide binding; catalytic activity; signal transducer activity; protein binding; enzyme regulator activity	cytoplasm	metabolic process; regulation of biological process; response to stimulus; cell death		3.5	2.2						2.8	2.1
529	F1M9G6	Serine/threonine-protein kinase TAO1 OS=Rattus norvegicus GN=Taok1 PE=4 SV=2 - [F1M9G6_RAT]	nucleotide binding; catalytic activity		metabolic process; response to stimulus; regulation of biological process		18.6	2.2						3.0	5.9
530	O55000	Serine/threonine-protein phosphatase 1 regulatory subunit 10 OS=Rattus norvegicus GN=Ppp1r10 PE=1 SV=1 - [PP1RA_RAT]	DNA binding; RNA binding; enzyme regulator activity; protein binding; metal ion binding	chromosome; nucleus	metabolic process; regulation of biological process	1.0	4.2	5.1	2.0			1.9	100.0	51.4	20.7
531	P62716	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Rattus norvegicus GN=Ppp2cb PE=1 SV=1 - [PP2AB_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; chromosome; cytoplasm; cytoskeleton	metabolic process; cell organization and biogenesis; regulation of biological process; response to stimulus	2.2	3.3	17.6	0.8					20.6	7.4
532	P63329	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform OS=Rattus norvegicus GN=Ppp3ca PE=1 SV=1 - [PP2BA_RAT]	catalytic activity; metal ion binding; protein binding; enzyme regulator activity	nucleus; cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	response to stimulus; regulation of biological process; metabolic process; transport; cellular homeostasis	1.3	17.6	3.5	2.1					2.3	4.5
533	P62138	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Rattus norvegicus GN=Ppp1ca PE=1 SV=1 - [PP1A_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; cytoplasm; cytosol; membrane	metabolic process; regulation of biological process; response to stimulus; cell division	3.8	5.2	5.0	3.4					15.6	5.5
534	P62142	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Rattus norvegicus GN=Ppp1cb PE=1 SV=3 - [PP1B_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; cytoplasm; cytosol	metabolic process; regulation of biological process; response to stimulus; cell division	5.8	19.5	7.1	3.4					12.3	8.0
535	P63088	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit OS=Rattus norvegicus GN=Ppp1cc PE=1 SV=1 - [PP1G_RAT]	catalytic activity; protein binding; RNA binding; metal ion binding	chromosome; nucleus; cytoplasm; mitochondrion; membrane; cytosol	metabolic process; cell differentiation; regulation of biological process; response to stimulus; cell division	7.7	19.5	7.5	3.4					23.7	10.3
536	P29457	Serpin H1 OS=Rattus norvegicus GN=Serpinh1 PE=1 SV=1 - [SERPH_RAT]	enzyme regulator activity; protein binding; RNA binding	cytoplasm; endoplasmic reticulum; organelle lumen	response to stimulus; regulation of biological process; cell organization and biogenesis; metabolic process	4.5	5.6	4.6	3.0					12.4	5.0
537	A4L9P7	Sister chromatid cohesion protein PDS5 homolog A OS=Rattus norvegicus GN=Pds5a PE=2 SV=1 - [PDS5A_RAT]		chromosome; nucleus; membrane	cell organization and biogenesis; regulation of biological process; cell division	1.5	3.0	2.9	1.3					4.2	2.1

538	Q6TRW4	Sister chromatid cohesion protein PDS5 homolog B OS=Rattus norvegicus GN=Pds5b PE=2 SV=2 - [PDS5B_RAT]	DNA binding	chromosome; nucleus	cell organization and biogenesis; regulation of biological process; cell division	1.5	3.6	2.2	1.9	1.5	38.6		100.0	3.1	16.9
539	D4A208	SLIT-ROBO Rho GTPase-activating protein 2 OS=Rattus norvegicus GN=Srgap2 PE=1 SV=1 - [SRGP2_RAT]	enzyme regulator activity; protein binding	nucleus; cytoplasm; membrane; cytosol	cell organization and biogenesis; regulation of biological process; response to stimulus; cell proliferation	12.8	75.3	5.6	4.5	2.7	5.2	2.5	14.8	14.1	13.8
540	F1M2K3	Small ubiquitin-related modifier (Fragment) OS=Rattus norvegicus PE=3 SV=1 - [F1M2K3_RAT]	protein binding	nucleus	metabolic process	1.5	2.8	2.7	6.1					4.3	2.9
541	Q5XIF4	Small ubiquitin-related modifier 3 OS=Rattus norvegicus GN=Sumo3 PE=3 SV=1 - [SUMO3_RAT]	protein binding; catalytic activity	nucleus; cytoplasm	metabolic process; regulation of biological process	1.6	2.6	2.6	6.1					4.3	2.9
542	P16086	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 - [SPTN1_RAT]	protein binding; metal ion binding	cytoplasm; cytosol; cytoskeleton; membrane	cell organization and biogenesis; regulation of biological process	0.9	1.8	1.4	0.7	1.6	2.7	1.7	3.1	2.5	1.6
543	D3ZDD7	Spermatid perinuclear RNA binding protein, isoform CRA_a OS=Rattus norvegicus GN=Strbp PE=4 SV=1 - [D3ZDD7_RAT]	DNA binding; RNA binding	nucleus; cytoplasm; cytoskeleton	cellular component movement; development; response to stimulus; cell differentiation	1.7	4.7	3.3	1.2	4.1	6.6	3.2	11.4	5.8	4.2
544	Q63413	Spliceosome RNA helicase Ddx39b OS=Rattus norvegicus GN=Ddx39b PE=1 SV=3 - [DX39B_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; spliceosomal complex; cytoplasm	cell organization and biogenesis; metabolic process; transport; regulation of biological process	2.4	3.9	4.1	2.4	2.2	2.2	1.5	5.1	5.6	2.9
545	Q5BJP2	Spliceosome-associated protein CWC15 homolog OS=Rattus norvegicus GN=Cwc15 PE=2 SV=1 - [CWC15_RAT]	RNA binding	nucleus; spliceosomal complex	metabolic process		14.1	30.8						100.0	36.2
546	F1LSM7	Splicing factor, arginine/serine-rich 15 OS=Rattus norvegicus GN=Scaf4 PE=4 SV=2 - [F1LSM7_RAT]	nucleotide binding	nucleus			47.9	4.7	4.8			2.3	1.6	3.7	9.3
547	F1M994	Splicing factor, arginine/serine-rich 15 OS=Rattus norvegicus GN=Scaf4 PE=4 SV=2 - [F1M994_RAT]	nucleotide binding			1.1	15.9	2.8	4.8			2.3	1.8	4.4	4.1
548	Q02769	Squalene synthase OS=Rattus norvegicus GN=Fdft1 PE=2 SV=1 - [FDFT_RAT]	catalytic activity	endoplasmic reticulum; membrane	metabolic process	2.7	15.6	6.4	2.3					5.5	5.4
549	Q66X93	Staphylococcal nuclease domain-containing protein 1 OS=Rattus norvegicus GN=Snd1 PE=2 SV=1 - [SND1_RAT]	catalytic activity; RNA binding	nucleus; cytoplasm; mitochondrion; membrane	cell differentiation; metabolic process; regulation of biological process	2.4	5.0	5.9	3.0	3.1	4.9		8.0	6.2	4.3
550	F1M953	Stress-70 protein, mitochondrial OS=Rattus norvegicus GN=Hspa9 PE=3 SV=1 - [F1M953_RAT]	nucleotide binding; protein binding; RNA binding	mitochondrion; cell surface	cell organization and biogenesis; metabolic process; transport; response to stimulus	1.7	3.2	6.1	2.6					15.2	4.8
551	O35814	Stress-induced-phosphoprotein 1 OS=Rattus norvegicus GN=Stip1 PE=1 SV=1 - [STIP1_RAT]	protein binding; RNA binding	nucleus; cytoplasm		100.0	13.4	5.9	4.5					28.1	25.3
552	F1LM47	Succinyl-CoA ligase subunit beta OS=Rattus norvegicus GN=Sucla2 PE=3 SV=1 - [F1LM47_RAT]	catalytic activity; nucleotide binding; metal ion binding	mitochondrion	metabolic process	13.5	7.9			4.1	3.6			6.4	5.9
553	Q68FU8	SURP and G-patch domain-containing protein 1 OS=Rattus norvegicus GN=Sugp1 PE=2 SV=1 - [SUGP1_RAT]	RNA binding	nucleus; spliceosomal complex	metabolic process		2.3	100.0						100.0	50.6
554	Q4QQU6	Survival of motor neuron-related-splicing factor 30 OS=Rattus norvegicus GN=Smndc1 PE=2 SV=1 - [SPF30_RAT]	RNA binding	nucleus; spliceosomal complex; cytoplasm; cytoskeleton	cell organization and biogenesis; metabolic process; cell death	29.4	6.0	65.1	7.9					59.0	27.9
555	O54772	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2 OS=Rattus norvegicus GN=Smarcd2 PE=2 SV=3 - [SMRD2_RAT]	DNA binding; protein binding	nucleus	cell organization and biogenesis; metabolic process; regulation of biological process	2.2	100.0	100.0						50.8	50.6
556	P09951	Synapsin-1 OS=Rattus norvegicus GN=Syn1 PE=1 SV=3 - [SYN1_RAT]	protein binding; catalytic activity; nucleotide binding	Golgi; cytosol; membrane	transport; metabolic process	0.6	1.8	1.2	1.0	2.0	4.5	100.0	1.9	2.7	11.6
557	P28480	T-complex protein 1 subunit alpha OS=Rattus norvegicus GN=Tcp1 PE=1 SV=1 - [TCPA_RAT]	nucleotide binding; protein binding; RNA binding	nucleus; cytoplasm; Golgi; cytoskeleton; membrane	metabolic process; transport; regulation of biological process	2.7	3.9	5.3	4.5	5.6	6.6			52.2	10.1
558	Q5XIM9	T-complex protein 1 subunit beta OS=Rattus norvegicus GN=Cct2 PE=1 SV=3 - [TCPB_RAT]	nucleotide binding; protein binding	nucleus; cytoplasm	metabolic process; cell organization and biogenesis; transport	2.1	4.1	5.2	2.7					13.9	4.7
559	Q7TPB1	T-complex protein 1 subunit delta OS=Rattus norvegicus GN=Cct4 PE=1 SV=3 - [TCPD_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; cytoskeleton	metabolic process; transport	3.0	4.5	5.5	2.8					5.4	3.5

560	Q6P502	T-complex protein 1 subunit gamma OS=Rattus norvegicus GN=Cct3 PE=1 SV=1 - [TCPG_RAT]	nucleotide binding; RNA binding; protein binding	cytoplasm; membrane	metabolic process; cell organization and biogenesis; transport	5.0	4.7	10.1	5.6				20.3	6.7	7.5
561	Q5EAN7	Telomeric repeat-binding factor 2-interacting protein 1 OS=Rattus norvegicus GN=Terf2ip PE=2 SV=1 - [TE2IP_RAT]	DNA binding	nucleus; chromosome; cytoplasm	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	5.6	6.8	53.7	0.9					54.9	20.3
562	P59924	THO complex subunit 1 OS=Rattus norvegicus GN=Thoc1 PE=2 SV=1 - [THOC1_RAT]	DNA binding; RNA binding; protein binding	nucleus; cytoplasm	regulation of biological process; metabolic process; transport; cell death; response to stimulus	2.0	3.1	2.4						3.8	2.3
563	Q6AY87	THO complex subunit 6 homolog OS=Rattus norvegicus GN=Thoc6 PE=2 SV=1 - [THOC6_RAT]	RNA binding; protein binding	nucleus	metabolic process; transport; cell death; development; regulation of biological process	5.0	2.0	3.7		2.9	6.4	1.7	57.9	4.2	9.3
564	Q5XHY5	Threonine--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Tars PE=2 SV=1 - [SYTC_RAT]	nucleotide binding; catalytic activity; metal ion binding	cytoplasm; cytoskeleton	metabolic process	3.3	11.1	4.3	1.2		5.2			3.9	4.1
565	Q5M7V8	Thyroid hormone receptor-associated protein 3 OS=Rattus norvegicus GN=Thrap3 PE=1 SV=1 - [TR150_RAT]	nucleotide binding; DNA binding; receptor activity; RNA binding; protein binding	nucleus	regulation of biological process; metabolic process; response to stimulus	1.5	2.8	2.4	1.6	1.1	1.2	1.1	4.0	4.5	2.0
566	G3V790	Transcription activator BRG1 OS=Rattus norvegicus GN=Smarca4 PE=4 SV=2 - [G3V790_RAT]	DNA binding; protein binding; catalytic activity; nucleotide binding	nucleus; membrane	regulation of biological process; cell organization and biogenesis; cell differentiation; metabolic process	1.2	3.2	2.5	1.0	1.8	4.2	1.8	6.4	3.3	2.5
567	F1LQ90	Transcription factor 4 OS=Rattus norvegicus GN=Tcf4 PE=4 SV=2 - [F1LQ90_RAT]	DNA binding; protein binding	nucleus	regulation of biological process; metabolic process; cell organization and biogenesis	1.8	2.6	2.8	4.0					5.3	2.7
568	O08629	Transcription intermediary factor 1-beta OS=Rattus norvegicus GN=Trim28 PE=1 SV=2 - [TIF1B_RAT]	DNA binding; catalytic activity; protein binding; metal ion binding; RNA binding	chromosome; nucleus	regulation of biological process; cell organization and biogenesis; metabolic process; response to stimulus; defense response	1.6	3.2	3.5	1.6	7.6	3.7		32.5	5.3	6.6
569	Q9R1D1	Transcriptional repressor CTCF OS=Rattus norvegicus GN=Ctcf PE=2 SV=1 - [CTCF_RAT]	DNA binding; metal ion binding	chromosome; nucleus	regulation of biological process; metabolic process; cell organization and biogenesis	1.8	5.7		4.0					2.9	2.9
570	P62997	Transformer-2 protein homolog beta OS=Rattus norvegicus GN=Tra2b PE=1 SV=1 - [TRA2B_RAT]	nucleotide binding; RNA binding; protein binding	nucleus	response to stimulus; regulation of biological process; metabolic process	2.4	7.3	100.0	2.7					51.2	27.3
571	P61589	Transforming protein RhoA OS=Rattus norvegicus GN=Rhoa PE=1 SV=1 - [RHOA_RAT]	nucleotide binding; catalytic activity; signal transducer activity; protein binding	nucleus; cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	cell organization and biogenesis; response to stimulus; metabolic process; regulation of biological process; cellular component movement; cell differentiation; cell division	2.1	19.4	6.3						3.6	6.3
572	P37805	Transgelin-3 OS=Rattus norvegicus GN=Tagln3 PE=1 SV=2 - [TAGL3_RAT]	protein binding	nucleus	regulation of biological process	6.7	10.7	38.2	2.7					2.1	10.1
573	P46462	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus GN=Vcp PE=1 SV=3 - [TERA_RAT]	nucleotide binding; catalytic activity; RNA binding; protein binding; enzyme regulator activity	proteasome; nucleus; cytoplasm; endoplasmic reticulum; membrane; cytosol	metabolic process; response to stimulus; transport; regulation of biological process; cell organization and biogenesis	4.7	5.6	9.8	4.7			4.3	1.5	54.3	10.6
574	P63029	Translationally-controlled tumor protein OS=Rattus norvegicus GN=Tpt1 PE=1 SV=1 - [TCTP_RAT]	metal ion binding; protein binding; RNA binding	nucleus; cytoplasm; endosome	cell proliferation; response to stimulus; regulation of biological process	62.1	8.8		3.5					100.0	34.9
575	Q9Z142	Transmembrane protein 33 OS=Rattus norvegicus GN=Tmem33 PE=2 SV=1 - [TMM33_RAT]		membrane		2.9	4.7	2.8	2.7					50.9	10.7
576	P32089	Tricarboxylate transport protein, mitochondrial OS=Rattus norvegicus GN=Slc25a1 PE=1 SV=1 - [TXTP_RAT]	transporter activity	nucleus; mitochondrion; membrane	transport		2.5	2.2	2.6					2.9	2.0
577	Q64428	Trifunctional enzyme subunit alpha, mitochondrial OS=Rattus norvegicus GN=Hadha PE=1 SV=2 - [ECHA_RAT]	catalytic activity; protein binding; nucleotide binding	cytoplasm; mitochondrion; membrane; organelle lumen	metabolic process; response to stimulus	1.7	3.9	2.9	2.5		100.0			3.7	16.4
578	G3V8D6	Tripartite motif protein 3, isoform CRA_a OS=Rattus norvegicus GN=Trim3 PE=4 SV=1 - [G3V8D6_RAT]	catalytic activity; protein binding; metal ion binding	cytoplasm; endosome	transport; metabolic process	2.6	3.7	4.2						4.4	3.0
579	Q64560	Tripeptidyl-peptidase 2 OS=Rattus norvegicus GN=Tpp2 PE=2 SV=3 - [TPP2_RAT]	catalytic activity	nucleus; cytoplasm	metabolic process	3.9	4.0	12.3	2.0					2.8	4.2

580	Q6AZ25	Tropomyosin 1, alpha OS=Rattus norvegicus GN=Tpm1 PE=2 SV=1 - [Q6AZ25_RAT]	protein binding; structural molecule activity	cytoplasm; cytoskeleton	regulation of biological process; cellular component movement; cell organization and biogenesis; cell communication; response to stimulus; metabolic process	1.2	3.5	6.0	3.1					51.7	10.9
581	P04692	Tropomyosin alpha-1 chain OS=Rattus norvegicus GN=Tpm1 PE=1 SV=3 - [TPM1_RAT]	protein binding	cytoplasm; cytoskeleton	regulation of biological process; cellular component movement; cell organization and biogenesis; response to stimulus	4.9	6.3	10.0	3.5					53.4	13.0
582	Q63610	Tropomyosin alpha-3 chain OS=Rattus norvegicus GN=Tpm3 PE=1 SV=2 - [TPM3_RAT]	protein binding	cytoplasm; cytoskeleton		4.9	6.3	24.5	18.8					53.1	17.9
583	P09495	Tropomyosin alpha-4 chain OS=Rattus norvegicus GN=Tpm4 PE=1 SV=3 - [TPM4_RAT]	protein binding; metal ion binding	cytoplasm; cytoskeleton; membrane	cell differentiation; response to stimulus	1.2	6.3	6.0	3.5					50.1	11.2
584	P68370	Tubulin alpha-1A chain OS=Rattus norvegicus GN=Tuba1a PE=1 SV=1 - [TBA1A_RAT]	nucleotide binding; catalytic activity; structural molecule activity; protein binding	nucleus; cytoplasm; cytoskeleton; endosome	metabolic process; cellular component movement; cell organization and biogenesis	2.2	4.6	3.5	2.6	3.5	4.5	2.9	6.8	3.5	3.4
585	P85108	Tubulin beta-2A chain OS=Rattus norvegicus GN=Tubb2a PE=1 SV=1 - [TBB2A_RAT]	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis	1.6	6.8	4.2	2.5	3.4	3.1	3.4	6.4	3.7	3.5
586	Q3KRE8	Tubulin beta-2B chain OS=Rattus norvegicus GN=Tubb2b PE=1 SV=1 - [TBB2B_RAT]	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	cellular component movement; metabolic process; cell organization and biogenesis	1.6	6.8	4.2	2.5	3.4	3.1	3.4	6.4	3.5	3.5
587	Q4QRB4	Tubulin beta-3 chain OS=Rattus norvegicus GN=Tubb3 PE=1 SV=1 - [TBB3_RAT]	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis; cell differentiation	1.9	4.2	3.9	2.5	5.1	2.6	2.8	13.4	3.3	4.0
588	P69897	Tubulin beta-5 chain OS=Rattus norvegicus GN=Tubb5 PE=1 SV=1 - [TBB5_RAT]	nucleotide binding; catalytic activity; structural molecule activity; protein binding	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis	1.6	5.8	4.2	2.6	3.4	3.1	3.4	6.4	3.7	3.4
589	D3ZCL3	U1 small nuclear ribonucleoprotein C OS=Rattus norvegicus GN=Snrpc PE=3 SV=1 - [RU1C_RAT]	RNA binding; metal ion binding; protein binding	spliceosomal complex; nucleus	cell organization and biogenesis; metabolic process		9.7	26.2						100.0	34.0
590	M3ZCQ2	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Rattus norvegicus GN=Snrnp200 PE=1 SV=1 - [M3ZCQ2_RAT]	nucleotide binding; DNA binding; catalytic activity; protein binding; RNA binding	nucleus; spliceosomal complex; membrane	metabolic process; cell differentiation	1.1	2.7	1.4	1.0	3.9	20.8	20.0	7.1	2.6	6.1
591	M0RD75	Uncharacterized protein (Fragment) OS=Rattus norvegicus GN=Rps6 PE=4 SV=1 - [M0RD75_RAT]	structural molecule activity; protein binding	nucleus; cytoplasm; ribosome	metabolic process; regulation of biological process; response to stimulus	2.6	4.7	83.9	1.5					12.1	17.5
592	M0R6L7	Uncharacterized protein (Fragment) OS=Rattus norvegicus PE=4 SV=1 - [M0R6L7_RAT]	protein binding			3.7	98.5	100.0	2.0					5.2	34.9
593	M0R735	Uncharacterized protein (Fragment) OS=Rattus norvegicus PE=4 SV=1 - [M0R735_RAT]				2.1	3.0	4.2	1.3	1.9	2.0	1.9	3.8	4.1	2.4
594	M0R750	Uncharacterized protein (Fragment) OS=Rattus norvegicus PE=4 SV=1 - [M0R750_RAT]	DNA binding						2.1			4.4	100.0	52.4	39.7
595	F1LT30	Uncharacterized protein OS=Rattus norvegicus GN=Rbm25 PE=4 SV=2 - [F1LT30_RAT]	RNA binding	spliceosomal complex	regulation of biological process; metabolic process	2.2	5.3	6.8	4.1		2.5		10.8	7.2	4.9
596	F1LQJ1	Uncharacterized protein OS=Rattus norvegicus GN=Ylpm1 PE=4 SV=2 - [F1LQJ1_RAT]		nucleus	regulation of biological process	0.9	2.8	1.7	0.5	1.6	16.0		7.4	3.9	3.9
597	D4A7G0	Uncharacterized protein OS=Rattus norvegicus GN=Zc3h14 PE=4 SV=2 - [D4A7G0_RAT]	metal ion binding				3.1	4.5						57.5	16.3
598	M0R5J4	Uncharacterized protein OS=Rattus norvegicus PE=3 SV=1 - [M0R5J4_RAT]	metal ion binding; catalytic activity		metabolic process	7.6	4.2	7.8	3.3					27.5	8.4
599	M0RCH8	Uncharacterized protein OS=Rattus norvegicus PE=4 SV=1 - [M0RCH8_RAT]	RNA binding			5.0	100.0	5.4						100.0	42.1
600	D3ZXI2	Uncharacterized protein OS=Rattus norvegicus PE=4 SV=2 - [D3ZXI2_RAT]	RNA binding	cytosol	transport; cellular homeostasis; regulation of biological process; cell growth	8.6	12.8	11.7	7.4		1.0			19.2	8.7
601	D4A567	Uncharacterized protein OS=Rattus norvegicus PE=4 SV=2 - [D4A567_RAT]	protein binding	chromosome; nucleus	cell organization and biogenesis; regulation of biological process	3.8	5.0	4.4	0.7	18.5	18.7			4.3	6.9

602	Q9QYF3	Unconventional myosin-Va OS=Rattus norvegicus GN=Myo5a PE=1 SV=1 - [MYO5A_RAT]	catalytic activity; motor activity; protein binding; nucleotide binding; metal ion binding; RNA binding	extracellular; cytoplasm; vacuole; endosome; endoplasmic reticulum; Golgi; cytosol; membrane	cell organization and biogenesis; metabolic process; transport; cell communication; regulation of biological process; cellular component movement; cell differentiation; response to stimulus	1.0	2.5	1.5	1.2	1.8	8.2	3.1	5.3	2.3	2.7
603	Q04462	Valine--tRNA ligase OS=Rattus norvegicus GN=Vars PE=2 SV=2 - [SYVC_RAT]	nucleotide binding; catalytic activity; protein binding	cytoplasm; mitochondrion; cytosol	metabolic process; regulation of biological process	1.5	3.2	1.5	1.1	3.3	8.0	100.0	18.1	2.4	13.9
604	Q9Z270	Vesicle-associated membrane protein-associated protein A OS=Rattus norvegicus GN=Vapa PE=1 SV=3 - [VAPA_RAT]	signal transducer activity; structural molecule activity; protein binding	membrane; endoplasmic reticulum; cytoskeleton	transport; cell organization and biogenesis; regulation of biological process; response to stimulus; cell death; metabolic process	2.1	7.2	3.2	1.3					15.9	4.9
605	Q9Z269	Vesicle-associated membrane protein-associated protein B OS=Rattus norvegicus GN=Vapb PE=1 SV=3 - [VAPB_RAT]	structural molecule activity; protein binding	membrane; endoplasmic reticulum; Golgi	cellular homeostasis; transport; response to stimulus; regulation of biological process; cell organization and biogenesis		26.0	3.0	2.3					51.2	16.5
606	Q4KM74	Vesicle-trafficking protein SEC22b OS=Rattus norvegicus GN=Sec22b PE=1 SV=3 - [SC22B_RAT]	protein binding	membrane; endoplasmic reticulum; Golgi	transport; regulation of biological process; cell organization and biogenesis	7.3	7.5	26.7	4.4					6.2	8.7
607	P31000	Vimentin OS=Rattus norvegicus GN=Vim PE=1 SV=2 - [VIME_RAT]	protein binding; RNA binding; structural molecule activity	nucleus; cytoplasm; cytosol; cytoskeleton; membrane	cell organization and biogenesis; metabolic process; response to stimulus; regulation of biological process; cell differentiation	1.7	2.5	2.2	1.0	1.6	1.9		4.6	3.7	2.1
608	Q9Z2L0	Voltage-dependent anion-selective channel protein 1 OS=Rattus norvegicus GN=Vdac1 PE=1 SV=4 - [VDAC1_RAT]	nucleotide binding; transporter activity; protein binding	nucleus; mitochondrion; membrane	defense response; response to stimulus; transport; cell death; cell communication; cell differentiation; regulation of biological process		5.8	9.1	2.7					100.0	23.5
609	Q5BJU7	Wiskott-Aldrich syndrome protein family member 1 OS=Rattus norvegicus GN=Wasf1 PE=1 SV=1 - [WASF1_RAT]	protein binding	cytoplasm; mitochondrion; membrane; cytoskeleton	regulation of biological process; response to stimulus; cell organization and biogenesis	2.5	3.3	2.2	1.5	16.9			100.0	3.1	16.2
610	G3V6J7	Zinc finger and BTB domain-containing protein 18 OS=Rattus norvegicus GN=Zfp238 PE=4 SV=2 - [G3V6J7_RAT]	protein binding; DNA binding; metal ion binding	nucleus; cytoskeleton	regulation of biological process; metabolic process	3.8	5.5	4.8	4.0					6.0	4.0
611	Q7TMD5	Zinc finger CCCH domain-containing protein 14 OS=Rattus norvegicus GN=Zc3h14 PE=2 SV=1 - [ZC3HE_RAT]	RNA binding; metal ion binding	nucleus; cytoplasm			3.5	4.5						100.0	27.0
612	Q62806	Zinc finger protein 148 OS=Rattus norvegicus GN=Znf148 PE=2 SV=1 - [ZN148_RAT]	DNA binding; metal ion binding	nucleus; Golgi	regulation of biological process; metabolic process; cell organization and biogenesis	1.6	4.2	17.7						2.7	5.3
613	O88553	Zinc finger protein 37 OS=Rattus norvegicus GN=Zfp37 PE=2 SV=1 - [ZFP37_RAT]	DNA binding; metal ion binding	nucleus	metabolic process; regulation of biological process; cell proliferation; cell differentiation		21.9	100.0	3.0					4.1	25.8
614	Q562A2	Zinc finger RNA-binding protein OS=Rattus norvegicus GN=Zfr PE=1 SV=2 - [ZFR_RAT]	DNA binding; RNA binding; metal ion binding	nucleus; chromosome; cytoplasm	development	1.9	4.3	2.2	1.9	2.5	9.3	29.0	100.0	3.2	15.4

Table S3

Hit list: 100μM CysNO-treated neuronal cytoplasmic extracts

470 proteins

Hit Number	Uniprot ID	Description	Molecular Function	Cellular Component	Biological Process	100μM CysNO/Cys
1	P10687	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1 OS=Rattus norvegicus GN=Plcb1 PE=1 SV=1 - [PLCB1_RAT]	catalytic activity; enzyme regulator activity; metal ion binding; protein binding; signal transducer activity	chromosome; cytoplasm; cytosol; membrane; nucleus; organelle lumen	cell communication; cell differentiation; cellular component movement; development; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	4.2
2	P62260	14-3-3 protein epsilon OS=Rattus norvegicus GN=Ywhae PE=1 SV=1 - [1433E_RAT]	enzyme regulator activity; protein binding	cytoplasm; cytoskeleton; mitochondrion	cell communication; cell differentiation; cellular component movement; development; metabolic process; regulation of biological process; response to stimulus; transport	4.2
3	P68511	14-3-3 protein eta OS=Rattus norvegicus GN=Ywhah PE=1 SV=2 - [1433F_RAT]	protein binding	cytoplasm	cell communication; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus; transport	4.2
4	P61983	14-3-3 protein gamma OS=Rattus norvegicus GN=Ywhag PE=1 SV=2 - [1433G_RAT]	enzyme regulator activity; protein binding	cytoplasm	cell communication; cell differentiation; development; metabolic process; regulation of biological process; response to stimulus; transport	3.7
5	P68255	14-3-3 protein theta OS=Rattus norvegicus GN=Ywhaq PE=1 SV=1 - [1433T_RAT]	protein binding	cytoplasm	cell communication; metabolic process; regulation of biological process; response to stimulus; transport	3.9
6	P63102	14-3-3 protein zeta/delta OS=Rattus norvegicus GN=Ywhaz PE=1 SV=1 - [1433Z_RAT]	protein binding	cytoplasm; cytoskeleton; mitochondrion; nucleus	cell communication; cell death; cell organization and biogenesis; defense response; regulation of biological process; response to stimulus; transport	3.7
7	Q5XI78	2-oxoglutarate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Ogdh PE=1 SV=1 - [ODO1_RAT]	catalytic activity; protein binding	cytoplasm; membrane; mitochondrion; organelle lumen	cell differentiation; cellular component movement; development; metabolic process	2.2
8	G3V8B6	26S proteasome non-ATPase regulatory subunit 1 OS=Rattus norvegicus GN=Psmd1 PE=4 SV=1 - [G3V8B6_RAT]	enzyme regulator activity	proteasome	metabolic process; regulation of biological process	3.3
9	Q4FZT9	26S proteasome non-ATPase regulatory subunit 2 OS=Rattus norvegicus GN=Psmd2 PE=2 SV=1 - [PSMD2_RAT]	enzyme regulator activity	proteasome	metabolic process; regulation of biological process	2.3
10	P51639	3-hydroxy-3-methylglutaryl-coenzyme A reductase OS=Rattus norvegicus GN=Hmgcr PE=1 SV=2 - [HMDH_RAT]	catalytic activity; nucleotide binding; protein binding; receptor activity; signal transducer activity	cytoplasm; endoplasmic reticulum; membrane	cell communication; cell death; cell differentiation; cell organization and biogenesis; cell proliferation; cellular homeostasis; development; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	2.2

11	B0BMW2	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Rattus norvegicus GN=Hsd17b10 PE=2 SV=1 - [B0BMW2_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; endoplasmic reticulum; membrane; mitochondrion	cell differentiation; cell organization and biogenesis; development; metabolic process; reproduction	2.4
12	P07871	3-ketoacyl-CoA thiolase B, peroxisomal OS=Rattus norvegicus GN=Acaa1b PE=2 SV=2 - [THIKB_RAT]	catalytic activity; protein binding	cytoplasm; mitochondrion	metabolic process	6.1
13	P97532	3-mercaptopyruvate sulfurtransferase OS=Rattus norvegicus GN=Mpst PE=1 SV=3 - [THTM_RAT]	catalytic activity	cytoplasm; membrane; mitochondrion	metabolic process	4.1
14	Q9Z1N4	3'(2'),5'-bisphosphate nucleotidase 1 OS=Rattus norvegicus GN=Bpnt1 PE=1 SV=1 - [BPNT1_RAT]	catalytic activity; metal ion binding		metabolic process	6.1
15	Q9JLJ3	4-trimethylaminobutyraldehyde dehydrogenase OS=Rattus norvegicus GN=Aldh9a1 PE=1 SV=1 - [AL9A1_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; cytosol; membrane; mitochondrion	cell communication; development; metabolic process	4.1
16	P62859	40S ribosomal protein S28 OS=Rattus norvegicus GN=Rps28 PE=1 SV=1 - [RS28_RAT]	RNA binding; structural molecule activity	cytoplasm; cytosol; ribosome	metabolic process; transport	2.7
17	P63039	60 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspd1 PE=1 SV=1 - [CH60_RAT]	nucleotide binding; protein binding	cell surface; cytoplasm; cytosol; endoplasmic reticulum; endosome; extracellular; Golgi; membrane; mitochondrion; nucleus; organelle lumen	cell communication; cell death; cell proliferation; defense response; development; metabolic process; regulation of biological process; response to stimulus	3.9
18	P19945	60S acidic ribosomal protein P0 OS=Rattus norvegicus GN=Rplp0 PE=1 SV=2 - [RLA0_RAT]	structural molecule activity	cytoplasm; cytosol; nucleus; ribosome	metabolic process; response to stimulus	8.5
19	D4A9M6	A kinase (PRKA) anchor protein 1, isoform CRA_b OS=Rattus norvegicus GN=Akap1 PE=4 SV=2 - [D4A9M6_RAT]	catalytic activity; protein binding; RNA binding; structural molecule activity	cytoplasm; membrane; mitochondrion; organelle lumen	cell communication; metabolic process; regulation of biological process; response to stimulus; transport	2.6
20	Q7TQ85	Ac1164 OS=Rattus norvegicus GN=Pdhx PE=2 SV=1 - [Q7TQ85_RAT]	catalytic activity	cytoplasm; extracellular; mitochondrion	metabolic process	3.8
21	Q9JMI1	Acetoacetyl-CoA synthetase OS=Rattus norvegicus GN=Aacs PE=1 SV=1 - [AACS_RAT]	catalytic activity; nucleotide binding	cytoplasm; cytosol	cell communication; cell differentiation; cellular homeostasis; development; metabolic process; regulation of biological process; response to stimulus; transport	2.6
22	P60711	Actin, cytoplasmic 1 OS=Rattus norvegicus GN=Actb PE=1 SV=1 - [ACTB_RAT]	nucleotide binding; protein binding	cytoplasm; cytoskeleton; cytosol; extracellular; nucleus; organelle lumen	cell differentiation; cell organization and biogenesis; development	3.7
23	P63269	Actin, gamma-enteric smooth muscle OS=Rattus norvegicus GN=Actg2 PE=2 SV=1 - [ACTH_RAT]	nucleotide binding	cytoplasm; cytoskeleton		3.6
24	G3V9E4	Acylamino-acid-releasing enzyme OS=Rattus norvegicus GN=Apeh PE=4 SV=1 - [G3V9E4_RAT]	catalytic activity	cytoplasm; membrane; nucleus	metabolic process	2.8
25	P61751	ADP-ribosylation factor 4 OS=Rattus norvegicus GN=Arf4 PE=2 SV=2 - [ARF4_RAT]	nucleotide binding; signal transducer activity	cytoplasm; Golgi; membrane; nucleus	cell communication; development; regulation of biological process; response to stimulus; transport	2.4
26	O35889	Afadin OS=Rattus norvegicus GN=Mllt4 PE=1 SV=1 - [AFAD_RAT]	protein binding	cytoplasm; cytosol; membrane; nucleus; organelle lumen	cell communication; regulation of biological process; response to stimulus	2.2
27	Q8CG45	Aflatoxin B1 aldehyde reductase member 2 OS=Rattus norvegicus GN=Akr7a2 PE=1 SV=2 - [ARK72_RAT]	catalytic activity	cytoplasm; Golgi; mitochondrion	metabolic process	2.1
28	P50475	Alanine--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Aars PE=1 SV=3 - [SYAC_RAT]	catalytic activity; metal ion binding; nucleotide binding; RNA binding	cytoplasm	cell communication; cell death; development; metabolic process; regulation of biological process; response to stimulus	3.9
29	Q5XI97	Alanyl-tRNA editing protein Aarsd1 OS=Rattus norvegicus GN=Aarsd1 PE=2 SV=1 - [AASD1_RAT]	catalytic activity; metal ion binding; nucleotide binding	cytoplasm	metabolic process; regulation of biological process	5.9
30	D3ZZ99	Alpha-adducin OS=Rattus norvegicus GN=Add1 PE=2 SV=2 - [D3ZZ99_RAT]				2.2
31	Q64057	Alpha-aminoadipic semialdehyde dehydrogenase OS=Rattus norvegicus GN=Aldh7a1 PE=1 SV=2 - [AL7A1_RAT]	catalytic activity	cytoplasm; cytosol; mitochondrion; nucleus	metabolic process	4.0
32	G3V6V1	Aminopeptidase B OS=Rattus norvegicus GN=Rnpep PE=4 SV=1 - [G3V6V1_RAT]	catalytic activity; metal ion binding	cell surface; cytoplasm; extracellular; Golgi; membrane	development; metabolic process	2.5

33	O35430	Amyloid beta A4 precursor protein-binding family A member 1 OS=Rattus norvegicus GN=Apba1 PE=1 SV=1 - [APBA1_RAT]	protein binding	membrane; nucleus	cell communication; development; metabolic process; regulation of biological process; response to stimulus; transport	3.5
34	D4ABR6	Annexin (Fragment) OS=Rattus norvegicus GN=Anxa6 PE=2 SV=2 - [D4ABR6_RAT]	metal ion binding			4.0
35	Q07936	Annexin A2 OS=Rattus norvegicus GN=Anxa2 PE=1 SV=2 - [ANXA2_RAT]	enzyme regulator activity; metal ion binding; protein binding	cytoplasm; endosome; extracellular; membrane	cell organization and biogenesis; cell proliferation; coagulation; development; metabolic process; regulation of biological process; response to stimulus; transport	5.8
36	P0C1X8	AP2-associated protein kinase 1 OS=Rattus norvegicus GN=Aak1 PE=1 SV=1 - [AAK1_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; membrane	cell communication; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport	2.9
37	G3V7H6	Arginase 2 OS=Rattus norvegicus GN=Arg2 PE=3 SV=1 - [G3V7H6_RAT]	catalytic activity; metal ion binding; protein binding	cytoplasm; mitochondrion	cell death; defense response; development; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	5.3
38	P40329	Arginine--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Rars PE=1 SV=2 - [SYRC_RAT]	catalytic activity; nucleotide binding; RNA binding	cytoplasm; mitochondrion; nucleus; organelle lumen	metabolic process	2.1
39	B4F7F3	Arvcf protein OS=Rattus norvegicus GN=Arvcf PE=2 SV=1 - [B4F7F3_RAT]	protein binding	cytoplasm; membrane; nucleus		3.8
40	P49088	Asparagine synthetase [glutamine-hydrolyzing] OS=Rattus norvegicus GN=Asns PE=2 SV=3 - [ASNS_RAT]	catalytic activity; nucleotide binding; protein binding		cell communication; cell death; development; metabolic process; regulation of biological process; response to stimulus	2.4
41	D3ZD23	ATP-binding cassette, sub-family E (OABP), member 1 OS=Rattus norvegicus GN=Abce1 PE=3 SV=1 - [D3ZD23_RAT]	catalytic activity; nucleotide binding	cytoplasm; mitochondrion	metabolic process	2.2
42	Q641Y8	ATP-dependent RNA helicase DDX1 OS=Rattus norvegicus GN=Ddx1 PE=2 SV=1 - [DDX1_RAT]	catalytic activity; DNA binding; nucleotide binding; protein binding; RNA binding	cytoplasm; nucleus; organelle lumen	development; metabolic process; regulation of biological process; response to stimulus	2.7
43	B2GUV5	ATPase, H transporting, lysosomal V1 subunit G1 OS=Rattus norvegicus GN=Atp6v1g1 PE=4 SV=1 - [B2GUV5_RAT]	catalytic activity; protein binding; transporter activity	cytoplasm; cytosol; membrane; vacuole	metabolic process; transport	3.5
44	D4A9L5	Band 4.1-like protein 1 OS=Rattus norvegicus GN=Epb41l1 PE=2 SV=2 - [D4A9L5_RAT]				6.3
45	F8WFS9	Beta-adducin OS=Rattus norvegicus GN=Add2 PE=4 SV=1 - [F8WFS9_RAT]	metal ion binding; protein binding; structural molecule activity	cytoplasm; cytoskeleton; membrane	cell organization and biogenesis; development; regulation of biological process; transport	2.2
46	Q8VIJ5	Bifunctional protein NCOAT OS=Rattus norvegicus GN=Mgea5 PE=1 SV=1 - [NCOAT_RAT]	catalytic activity	cytoplasm; mitochondrion; nucleus	cell communication; cell death; cell organization and biogenesis; cellular homeostasis; metabolic process; regulation of biological process; response to stimulus; transport	2.3
47	O35567	Bifunctional purine biosynthesis protein PURH OS=Rattus norvegicus GN=Atic PE=1 SV=2 - [PUR9_RAT]	catalytic activity; protein binding	cytoplasm; mitochondrion	development; metabolic process; response to stimulus	3.4
48	F1LQC5	Bone morphogenic protein receptor, type II (Serine/threonine kinase) OS=Rattus norvegicus GN=Bmpr2 PE=4 SV=2 - [F1LQC5_RAT]	catalytic activity; nucleotide binding; protein binding; receptor activity; signal transducer activity	cell surface; cytoplasm; membrane	cell communication; cell differentiation; cell growth; cell organization and biogenesis; cell proliferation; cellular component movement; development; metabolic process; regulation of biological process; response to stimulus	7.9
49	P54690	Branched-chain-amino-acid aminotransferase, cytosolic OS=Rattus norvegicus GN=Bcat1 PE=1 SV=1 - [BCAT1_RAT]	catalytic activity; protein binding	cytoplasm; cytosol; mitochondrion	metabolic process	5.0
50	D4A631	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Rattus norvegicus GN=Arfgef1 PE=1 SV=1 - [BIG1_RAT]	enzyme regulator activity; protein binding	cytoplasm; cytosol; Golgi; membrane; nucleus; organelle lumen	cell communication; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport	2.7

51	Q7TSU1	Brefeldin A-inhibited guanine nucleotide-exchange protein 2 OS=Rattus norvegicus GN=Arfgef2 PE=1 SV=1 - [BIG2_RAT]	enzyme regulator activity; protein binding	cytoplasm; cytoskeleton; cytosol; endosome; Golgi; membrane	cell communication; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport	2.3
52	G3V6S5	C-1-tetrahydrofolate synthase, cytoplasmic OS=Rattus norvegicus GN=Mthfd1 PE=3 SV=1 - [G3V6S5_RAT]	catalytic activity; nucleotide binding	cytoplasm; mitochondrion	metabolic process	3.0
53	Q6AZ26	C-terminal binding protein 1 OS=Rattus norvegicus GN=Ctbp1 PE=2 SV=1 - [Q6AZ26_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; cytosol; nucleus; organelle lumen	cell differentiation; cell organization and biogenesis; metabolic process; regulation of biological process	4.2
54	Q62717	Calcium-dependent secretion activator 1 OS=Rattus norvegicus GN=Cadps PE=1 SV=1 - [CAPS1_RAT]	metal ion binding; protein binding	cytoplasm; membrane	cell communication; cell organization and biogenesis; regulation of biological process; transport	2.2
55	Q64566	Calcium-transporting ATPase type 2C member 1 OS=Rattus norvegicus GN=Atp2c1 PE=2 SV=1 - [AT2C1_RAT]	catalytic activity; metal ion binding; nucleotide binding; signal transducer activity; transporter activity	cytoplasm; Golgi; membrane	cell communication; cell organization and biogenesis; cellular homeostasis; development; metabolic process; regulation of biological process; response to stimulus; transport	2.9
56	Q6AYK6	Calcyclin-binding protein OS=Rattus norvegicus GN=Cacybp PE=1 SV=1 - [CYBP_RAT]	protein binding	cytoplasm; nucleus	cell death; cell differentiation; development; metabolic process; regulation of biological process; response to stimulus	5.0
57	Q07009	Calpain-2 catalytic subunit OS=Rattus norvegicus GN=Capn2 PE=1 SV=3 - [CAN2_RAT]	catalytic activity; metal ion binding; protein binding	chromosome; cytoplasm; membrane; nucleus	cell differentiation; development; metabolic process; response to stimulus	3.3
58	P37397	Calponin-3 OS=Rattus norvegicus GN=Cnn3 PE=1 SV=1 - [CNN3_RAT]	protein binding	cytoskeleton	cell organization and biogenesis; metabolic process; regulation of biological process	3.0
59	F1LR80	CaM kinase-like vesicle-associated protein OS=Rattus norvegicus GN=Camkv PE=2 SV=2 - [F1LR80_RAT]	catalytic activity; nucleotide binding		metabolic process	3.8
60	P68182	cAMP-dependent protein kinase catalytic subunit beta OS=Rattus norvegicus GN=Prkacb PE=1 SV=2 - [KAPCB_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding	cytoplasm; cytoskeleton; cytosol; membrane; nucleus	metabolic process; regulation of biological process; reproduction; response to stimulus	4.6
61	F1M9X5	cAMP-dependent protein kinase type I-beta regulatory subunit OS=Rattus norvegicus GN=Prkar1b PE=2 SV=2 - [F1M9X5_RAT]				3.3
62	P12369	cAMP-dependent protein kinase type II-beta regulatory subunit OS=Rattus norvegicus GN=Prkar2b PE=1 SV=3 - [KAP3_RAT]	catalytic activity; enzyme regulator activity; nucleotide binding; protein binding	cytoplasm; cytoskeleton; membrane; mitochondrion	cell communication; metabolic process; regulation of biological process; response to stimulus	3.4
63	F1M1T9	cAMP-specific 3',5'-cyclic phosphodiesterase 4B (Fragment) OS=Rattus norvegicus GN=Pde4b PE=2 SV=1 - [F1M1T9_RAT]	catalytic activity; metal ion binding	membrane	cell communication; metabolic process; regulation of biological process; response to stimulus	2.5
64	Q5M9G3	Caprin-1 OS=Rattus norvegicus GN=Caprin1 PE=1 SV=2 - [CAPR1_RAT]	RNA binding	cytoplasm; cytosol	cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process	2.0
65	P04762	Catalase OS=Rattus norvegicus GN=Cat PE=1 SV=3 - [CATA_RAT]	antioxidant activity; catalytic activity; metal ion binding; nucleotide binding; protein binding	cytoplasm; cytosol; endoplasmic reticulum; Golgi; membrane; mitochondrion; vacuole	cell communication; cell death; cell division; cell organization and biogenesis; development; metabolic process; regulation of biological process; reproduction; response to stimulus	2.6
66	Q5U302	Catenin (Cadherin associated protein), alpha 1 OS=Rattus norvegicus GN=Ctnna1 PE=2 SV=1 - [Q5U302_RAT]	protein binding; structural molecule activity	cytoplasm; cytoskeleton; membrane	cell communication; cell death; cell differentiation; cell organization and biogenesis; cell proliferation; development; regulation of biological process; reproduction; response to stimulus	5.0
67	D3ZZZ9	Catenin (Cadherin associated protein), delta 1 (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Ctnnd1 PE=4 SV=1 - [D3ZZZ9_RAT]	protein binding	cytoplasm; cytosol; membrane; nucleus	cell communication; cell differentiation; development; regulation of biological process; response to stimulus	2.1
68	F1M787	Catenin delta-2 (Fragment) OS=Rattus norvegicus GN=Ctnnd2 PE=2 SV=2 - [F1M787_RAT]				2.1

69	G3V9U1	Centaurin, gamma 2 (Predicted) OS=Rattus norvegicus GN=Agap1 PE=4 SV=1 - [G3V9U1_RAT]	catalytic activity; enzyme regulator activity; metal ion binding; nucleotide binding; protein binding	membrane	cell communication; metabolic process; regulation of biological process; response to stimulus	2.4
70	G3V9Z5	Centaurin, gamma 3 (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Agap3 PE=4 SV=1 - [G3V9Z5_RAT]	catalytic activity; enzyme regulator activity; metal ion binding; protein binding	cytoplasm; nucleus	metabolic process; regulation of biological process; response to stimulus; transport	2.1
71	Q3MHS9	Chaperonin containing Tcp1, subunit 6A (Zeta 1) OS=Rattus norvegicus GN=Cct6a PE=2 SV=1 - [Q3MHS9_RAT]	nucleotide binding; protein binding	cytoplasm; cytoskeleton; cytosol	metabolic process; reproduction	3.5
72	D4ACB8	Chaperonin subunit 8 (Theta) (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Cct8 PE=3 SV=1 - [D4ACB8_RAT]	nucleotide binding; protein binding	cytoplasm; cytoskeleton; cytosol	metabolic process; reproduction	4.6
73	F1LRK0	Clathrin coat assembly protein AP180 OS=Rattus norvegicus GN=Snap91 PE=2 SV=2 - [F1LRK0_RAT]				2.8
74	Q99JD4	CLIP-associating protein 2 OS=Rattus norvegicus GN=Clasp2 PE=2 SV=1 - [CLAP2_RAT]	protein binding	chromosome; cytoplasm; cytoskeleton; Golgi; membrane	cell division; cell organization and biogenesis; cellular component movement; regulation of biological process	2.2
75	P23514	Coatomer subunit beta OS=Rattus norvegicus GN=Copb1 PE=1 SV=1 - [COPB_RAT]	protein binding; structural molecule activity	cytoplasm; endoplasmic reticulum; Golgi; membrane	transport	2.5
76	D4ABY2	Coatomer subunit gamma OS=Rattus norvegicus GN=Copg2 PE=2 SV=2 - [D4ABY2_RAT]				2.4
77	Q4AEF8	Coatomer subunit gamma-1 OS=Rattus norvegicus GN=Copg1 PE=2 SV=1 - [COPG1_RAT]	structural molecule activity	cytoplasm; Golgi; membrane; nucleus	cellular component movement; transport	2.4
78	P45592	Cofilin-1 OS=Rattus norvegicus GN=Cfl1 PE=1 SV=3 - [COF1_RAT]	protein binding	cytoplasm; cytoskeleton; membrane; nucleus; organelle lumen	cell differentiation; cell division; cell organization and biogenesis; cellular component movement; development; metabolic process; regulation of biological process; response to stimulus; transport	2.6
79	P18395	Cold shock domain-containing protein E1 OS=Rattus norvegicus GN=Csde1 PE=2 SV=1 - [CSDE1_RAT]	DNA binding; RNA binding	cytoplasm; membrane; mitochondrion	metabolic process; regulation of biological process	2.9
80	Q9Z1T4	Connector enhancer of kinase suppressor of ras 2 OS=Rattus norvegicus GN=Cnksr2 PE=1 SV=1 - [CNKR2_RAT]	protein binding	cytoplasm; membrane	cell communication; regulation of biological process; response to stimulus	2.6
81	G3V624	Coronin OS=Rattus norvegicus GN=Coro1c PE=3 SV=1 - [G3V624_RAT]	protein binding			2.3
82	Q91ZN1	Coronin-1A OS=Rattus norvegicus GN=Coro1a PE=1 SV=3 - [COR1A_RAT]	protein binding	cytoplasm; cytoskeleton; membrane; nucleus	cell differentiation; cell organization and biogenesis; cell proliferation; cellular component movement; development; regulation of biological process; response to stimulus; transport	4.0
83	Q66HL2	Cortactin OS=Rattus norvegicus GN=Cttn PE=1 SV=1 - [Q66HL2_RAT]	protein binding	cytoplasm; cytoskeleton	development; transport	2.8
84	B5DF89	Cullin-3 OS=Rattus norvegicus GN=Cul3 PE=1 SV=2 - [CUL3_RAT]	catalytic activity; protein binding	cytoplasm; cytoskeleton; Golgi; nucleus	cell communication; cell differentiation; cell division; cell organization and biogenesis; cellular component movement; development; metabolic process; regulation of biological process; response to stimulus; transport	2.4
85	P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	protein binding	cytoplasm; membrane; nucleus	cell differentiation; cell organization and biogenesis; metabolic process; regulation of biological process; transport	2.3
86	F1LMD9	Cyclin-G-associated kinase OS=Rattus norvegicus GN=Gak PE=2 SV=1 - [F1LMD9_RAT]	catalytic activity; nucleotide binding; protein binding		metabolic process	2.3
87	G3V9K0	Cysteinyl-tRNA synthetase (Predicted), isoform CRA_b OS=Rattus norvegicus GN=Cars PE=3 SV=1 - [G3V9K0_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding; RNA binding	cytoplasm; cytosol	metabolic process	2.3

88	D3ZU74	Cytoplasmic dynein 1 intermediate chain 2 OS=Rattus norvegicus GN=Dync1i2 PE=4 SV=1 - [D3ZU74_RAT]	catalytic activity; motor activity; protein binding	cytoplasm; cytoskeleton	cellular component movement; transport	2.6
89	Q62698	Cytoplasmic dynein 1 light intermediate chain 2 OS=Rattus norvegicus GN=Dync1li2 PE=1 SV=1 - [DC1L2_RAT]	catalytic activity; motor activity; nucleotide binding	cytoplasm; cytoskeleton	cell organization and biogenesis; cellular component movement; transport	3.0
90	Q6Q0N1	Cytosolic non-specific dipeptidase OS=Rattus norvegicus GN=Cndp2 PE=1 SV=1 - [CNDP2_RAT]	catalytic activity; metal ion binding	cytoplasm	metabolic process	4.3
91	Q2KN99	Cytospin-A OS=Rattus norvegicus GN=Specc1l PE=2 SV=1 - [CYTSA_RAT]	protein binding	cytoplasm; cytoskeleton	cell division; cell organization and biogenesis; cellular component movement; regulation of biological process	2.5
92	O08651	D-3-phosphoglycerate dehydrogenase OS=Rattus norvegicus GN=Phgdh PE=1 SV=3 - [SERA_RAT]	catalytic activity; nucleotide binding		cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process	6.7
93	Q7M0E3	Destrin OS=Rattus norvegicus GN=Dstn PE=1 SV=3 - [DEST_RAT]	protein binding	cytoplasm; cytoskeleton	cell division; cell organization and biogenesis; cellular component movement; regulation of biological process	4.5
94	P08461	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Rattus norvegicus GN=Dlat PE=1 SV=3 - [ODP2_RAT]	catalytic activity; nucleotide binding	cytoplasm; mitochondrion; organelle lumen	metabolic process	3.5
95	Q9JHU0	Dihydropyrimidinase-related protein 5 OS=Rattus norvegicus GN=Dpysl5 PE=1 SV=1 - [DPYL5_RAT]	catalytic activity; protein binding	cytoplasm	cell differentiation; development; metabolic process	3.6
96	Q9ES71	Dihydroxyacetone phosphate acyltransferase OS=Rattus norvegicus GN=Gnpat PE=2 SV=1 - [GNPAT_RAT]	catalytic activity; protein binding	cytoplasm; membrane; mitochondrion	cell communication; cell organization and biogenesis; cellular homeostasis; development; metabolic process; response to stimulus	2.7
97	Q6P730	Disabled homolog 2-interacting protein OS=Rattus norvegicus GN=Dab2ip PE=1 SV=1 - [DAB2P_RAT]	enzyme regulator activity; protein binding	cytoplasm; membrane	cell communication; cell death; cell differentiation; cell growth; cell organization and biogenesis; cell proliferation; cellular component movement; development; metabolic process; regulation of biological process; response to stimulus; transport	2.3
98	G3V8Y5	DNA-directed RNA polymerase OS=Rattus norvegicus GN=Polr2b PE=3 SV=1 - [G3V8Y5_RAT]	catalytic activity; DNA binding	nucleus; organelle lumen	metabolic process	2.2
99	D4A0I5	DnaJ (Hsp40) homolog, subfamily C, member 6 (Predicted) OS=Rattus norvegicus GN=Dnajc6 PE=4 SV=1 - [D4A0I5_RAT]	protein binding			2.4
100	G3V8B8	DnaJ (Hsp40) homolog, subfamily C, member 7, isoform CRA_a OS=Rattus norvegicus GN=Dnajc7 PE=4 SV=1 - [G3V8B8_RAT]	protein binding	cytoplasm; nucleus; organelle lumen	metabolic process	2.4
101	P63036	DnaJ homolog subfamily A member 1 OS=Rattus norvegicus GN=Dnaja1 PE=2 SV=1 - [DNJA1_RAT]	metal ion binding; nucleotide binding; protein binding	membrane	cell communication; cellular component movement; metabolic process; regulation of biological process; reproduction; response to stimulus	2.6
102	Q6AYH5	Dynactin subunit 2 OS=Rattus norvegicus GN=Dctn2 PE=1 SV=1 - [DCTN2_RAT]	catalytic activity; motor activity	chromosome; cytoplasm; cytoskeleton; membrane	cell organization and biogenesis; cell proliferation	2.6
103	F1MAP9	E3 ubiquitin-protein ligase HUWE1 OS=Rattus norvegicus GN=Huwe1 PE=2 SV=2 - [F1MAP9_RAT]				2.1
104	F1LQ82	E3 ubiquitin-protein ligase NEDD4 (Fragment) OS=Rattus norvegicus GN=Nedd4 PE=2 SV=2 - [F1LQ82_RAT]				2.5
105	Q62940	E3 ubiquitin-protein ligase NEDD4 OS=Rattus norvegicus GN=Nedd4 PE=1 SV=1 - [NEDD4_RAT]	catalytic activity; protein binding	chromosome; cytoplasm; cytosol; Golgi; membrane	cell communication; cell differentiation; cell organization and biogenesis; cellular homeostasis; development; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	2.5

106	Q91ZY8	E3 ubiquitin-protein ligase TRIM9 OS=Rattus norvegicus GN=Trim9 PE=1 SV=1 - [TRIM9_RAT]	catalytic activity; metal ion binding; protein binding	cytoplasm; cytoskeleton	cell communication; cell organization and biogenesis; metabolic process; regulation of biological process; transport	2.2
107	Q4KLM4	Ectoderm-neural cortex protein 2 OS=Rattus norvegicus GN=Klhl25 PE=2 SV=1 - [ENC2_RAT]	protein binding	cytoplasm		2.2
108	B5DF91	ELAV (Embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R) OS=Rattus norvegicus GN=Elavl1 PE=2 SV=1 - [B5DF91_RAT]	nucleotide binding; protein binding; RNA binding	cytoplasm; nucleus	metabolic process; regulation of biological process	3.0
109	Q68FR6	Elongation factor 1-gamma OS=Rattus norvegicus GN=Eef1g PE=1 SV=3 - [EF1G_RAT]	protein binding; RNA binding	cytoplasm	metabolic process; response to stimulus	2.2
110	P05197	Elongation factor 2 OS=Rattus norvegicus GN=Eef2 PE=1 SV=4 - [EF2_RAT]	catalytic activity; nucleotide binding; RNA binding	cytoplasm	metabolic process	3.8
111	P85834	Elongation factor Tu, mitochondrial OS=Rattus norvegicus GN=Tufm PE=1 SV=1 - [EFTU_RAT]	catalytic activity; nucleotide binding; RNA binding	cytoplasm; membrane; mitochondrion; organelle lumen	metabolic process	2.3
112	F1M8I7	Ena/VASP-like protein (Fragment) OS=Rattus norvegicus GN=Evl PE=2 SV=1 - [F1M8I7_RAT]	protein binding	cytoskeleton	cell organization and biogenesis	2.3
113	O35964	Endophilin-A2 OS=Rattus norvegicus GN=Sh3gl1 PE=1 SV=1 - [SH3G1_RAT]	protein binding	cytoplasm; cytoskeleton; endosome; membrane	transport	4.0
114	D4A7V1	Endophilin-B2 OS=Rattus norvegicus GN=Sh3glb2 PE=2 SV=2 - [D4A7V1_RAT]				3.8
115	A3E0T0	Erythrocyte protein band 4.1-like 3 OS=Rattus norvegicus GN=Epb41l3 PE=2 SV=1 - [A3E0T0_RAT]	protein binding; structural molecule activity	cytoplasm; cytoskeleton; membrane	cell communication; cell differentiation; cell organization and biogenesis; cellular homeostasis; development; regulation of biological process	3.5
116	P81795	Eukaryotic translation initiation factor 2 subunit 3 OS=Rattus norvegicus GN=Eif2s3 PE=1 SV=2 - [IF2G_RAT]	catalytic activity; nucleotide binding; RNA binding		metabolic process	5.5
117	D4A554	Eukaryotic translation initiation factor 4 gamma, 3 (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Eif4g3 PE=4 SV=2 - [D4A554_RAT]	DNA binding; enzyme regulator activity; protein binding; RNA binding		metabolic process; regulation of biological process; reproduction	2.4
118	Q6P3V8	Eukaryotic translation initiation factor 4A1 OS=Rattus norvegicus GN=Eif4a1 PE=2 SV=1 - [Q6P3V8_RAT]	catalytic activity; nucleotide binding; RNA binding	cytoplasm	development; metabolic process	3.5
119	O54924	Exocyst complex component 8 OS=Rattus norvegicus GN=Exoc8 PE=1 SV=1 - [EXOC8_RAT]	protein binding	cytoplasm; nucleus	transport	3.1
120	Q5XI32	F-actin-capping protein subunit beta OS=Rattus norvegicus GN=Capzb PE=1 SV=1 - [CAPZB_RAT]	protein binding	cytoplasm; cytoskeleton; membrane	cell communication; cell differentiation; cell organization and biogenesis; development; regulation of biological process; response to stimulus	2.3
121	Q5MJ12	F-box/LRR-repeat protein 16 OS=Rattus norvegicus GN=Fbxl16 PE=2 SV=1 - [FXL16_RAT]	protein binding			6.0
122	Q924K2	FAS-associated factor 1 OS=Rattus norvegicus GN=Faf1 PE=2 SV=1 - [FAF1_RAT]	protein binding	cytoplasm; cytosol; endoplasmic reticulum; membrane; nucleus	cell communication; cell death; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport	2.4
123	F1LYQ8	FERM, RhoGEF and pleckstrin domain-containing protein 1 OS=Rattus norvegicus GN=Farp1 PE=1 SV=2 - [FARP1_RAT]	enzyme regulator activity; protein binding	cytoplasm; cytoskeleton; cytosol; membrane	cell communication; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus	2.3
124	D3ZEA0	Fibronectin type III domain containing 3a (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Fndc3a PE=4 SV=2 - [D3ZEA0_RAT]	protein binding	cytoplasm; cytosol; Golgi; membrane	cell differentiation; development; reproduction	2.7
125	C0JPT7	Filamin alpha OS=Rattus norvegicus GN=Flna PE=2 SV=1 - [C0JPT7_RAT]	protein binding; signal transducer activity	chromosome; cytoplasm; cytoskeleton; cytosol; extracellular; membrane; nucleus	cell communication; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus; transport	2.9

126	D4A8D5	Filamin, beta (Predicted) OS=Rattus norvegicus GN=Flnb PE=4 SV=1 - [D4A8D5_RAT]	protein binding	cytoplasm; cytoskeleton; membrane	development	2.2
127	O35346	Focal adhesion kinase 1 OS=Rattus norvegicus GN=Ptk2 PE=1 SV=1 - [FAK1_RAT]	catalytic activity; nucleotide binding; protein binding; signal transducer activity	cytoplasm; cytoskeleton; cytosol; membrane; nucleus; organelle lumen	cell communication; cell death; cell differentiation; cell growth; cell organization and biogenesis; cell proliferation; cellular component movement; cellular homeostasis; development; metabolic process; regulation of biological process; response to stimulus; transport	2.2
128	Q6AYD5	G1 to S phase transition 1 OS=Rattus norvegicus GN=Gspt1 PE=2 SV=1 - [Q6AYD5_RAT]	catalytic activity; nucleotide binding; RNA binding		metabolic process	5.5
129	Q5RKH2	Galactokinase 1 OS=Rattus norvegicus GN=Galk1 PE=2 SV=1 - [Q5RKH2_RAT]	catalytic activity; nucleotide binding	cytoplasm; membrane	metabolic process	7.7
130	B4F774	Ganglioside-induced differentiation-associated protein 1-like 1 (Predicted) OS=Rattus norvegicus GN=Gdap1l1 PE=2 SV=1 - [B4F774_RAT]	protein binding			2.6
131	P41542	General vesicular transport factor p115 OS=Rattus norvegicus GN=Uso1 PE=1 SV=1 - [USO1_RAT]	catalytic activity; motor activity; protein binding; transporter activity	cytoplasm; cytoskeleton; cytosol; Golgi; membrane	cell organization and biogenesis; transport	2.1
132	P05370	Glucose-6-phosphate 1-dehydrogenase OS=Rattus norvegicus GN=G6pdx PE=1 SV=3 - [G6PD_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; cytoskeleton; cytosol; membrane; nucleus	cell death; cell differentiation; development; metabolic process; regulation of biological process; response to stimulus	3.5
133	G3V746	Glutamate receptor ionotropic, NMDA 2B OS=Rattus norvegicus GN=Grin2b PE=4 SV=1 - [G3V746_RAT]	metal ion binding; protein binding; receptor activity; signal transducer activity; transporter activity	cell surface; cytoplasm; cytoskeleton; membrane	cell communication; cell death; cell organization and biogenesis; cellular homeostasis; defense response; development; regulation of biological process; response to stimulus; transport	2.4
134	Q9JLZ1	Glutaredoxin-3 OS=Rattus norvegicus GN=Glrx3 PE=1 SV=2 - [GLRX3_RAT]	catalytic activity; metal ion binding; protein binding	cytoplasm; nucleus; spliceosomal complex	cell organization and biogenesis; cellular homeostasis; regulation of biological process	2.8
135	P35571	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Rattus norvegicus GN=Gpd2 PE=1 SV=1 - [GPDM_RAT]	catalytic activity; metal ion binding	cytoplasm; membrane; mitochondrion	metabolic process	2.1
136	G3V7G8	Glycine--tRNA ligase OS=Rattus norvegicus GN=Gars PE=3 SV=1 - [G3V7G8_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; mitochondrion	metabolic process	3.4
137	P18266	Glycogen synthase kinase-3 beta OS=Rattus norvegicus GN=Gsk3b PE=1 SV=1 - [GSK3B_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; cytoskeleton; cytosol; membrane; nucleus; organelle lumen	cell communication; cell death; cell differentiation; cell organization and biogenesis; cellular component movement; development; metabolic process; regulation of biological process; response to stimulus; transport	2.1
138	Q3KR56	GRAM domain-containing protein 1A OS=Rattus norvegicus GN=Gramd1a PE=2 SV=2 - [GRM1A_RAT]		membrane		2.4
139	M0R4R4	Growth arrest-specific protein 7 (Fragment) OS=Rattus norvegicus GN=Gas7 PE=4 SV=1 - [M0R4R4_RAT]				4.4
140	P20171	GTPase HRas OS=Rattus norvegicus GN=Hras1 PE=1 SV=2 - [RASH_RAT]	catalytic activity; nucleotide binding; protein binding; transporter activity	cytoplasm; Golgi; membrane	cell communication; cell death; cell differentiation; cell organization and biogenesis; cell proliferation; cellular component movement; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	2.6
141	Q04970	GTPase NRas OS=Rattus norvegicus GN=Nras PE=1 SV=1 - [RASN_RAT]	catalytic activity; nucleotide binding; protein binding; transporter activity	cytoplasm; Golgi; membrane	cell communication; cell death; cell differentiation; cell organization and biogenesis; cell proliferation; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	2.5
142	P10824	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Rattus norvegicus GN=Gnai1 PE=1 SV=3 - [GNAI1_RAT]	catalytic activity; enzyme regulator activity; metal ion binding; nucleotide binding; protein binding; signal transducer activity	cytoplasm; cytoskeleton; Golgi; membrane; nucleus	cell communication; cell differentiation; cell division; cellular homeostasis; development; metabolic process; regulation of biological process; response to stimulus; transport	2.6

143	P04897	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Rattus norvegicus GN=Gnai2 PE=1 SV=3 - [GNAI2_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding; signal transducer activity	cytoplasm; cytoskeleton; cytosol; membrane; nucleus	cell communication; cell division; cell proliferation; metabolic process; regulation of biological process; response to stimulus; transport	2.6
144	P08753	Guanine nucleotide-binding protein G(k) subunit alpha OS=Rattus norvegicus GN=Gnai3 PE=1 SV=3 - [GNAI3_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding; signal transducer activity	cytoplasm; cytoskeleton; Golgi; membrane	cell communication; cell division; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport	2.5
145	P59215	Guanine nucleotide-binding protein G(o) subunit alpha OS=Rattus norvegicus GN=Gnao1 PE=1 SV=2 - [GNAO_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding; signal transducer activity	membrane	cell communication; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus; transport	3.0
146	P63095	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Rattus norvegicus GN=Gnas PE=1 SV=1 - [GNAS2_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding; signal transducer activity	cytoplasm; cytosol; endosome; extracellular; membrane	cell communication; cell differentiation; development; metabolic process; regulation of biological process; response to stimulus; transport	2.6
147	P19686	Guanylate cyclase soluble subunit alpha-3 OS=Rattus norvegicus GN=Gucy1a3 PE=1 SV=1 - [GCYA3_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; cytosol	cell communication; metabolic process; regulation of biological process; response to stimulus	3.8
148	F1LRV4	Heat shock 70 kDa protein 4 OS=Rattus norvegicus GN=Hspa4 PE=2 SV=1 - [F1LRV4_RAT]	nucleotide binding	nucleus	cell organization and biogenesis; transport	10.4
149	D3ZC55	Heat shock 70kDa protein 12A (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Hspa12a PE=4 SV=1 - [D3ZC55_RAT]	catalytic activity		metabolic process; response to stimulus	3.0
150	Q66HA8	Heat shock protein 105 kDa OS=Rattus norvegicus GN=Hsph1 PE=2 SV=1 - [HS105_RAT]	nucleotide binding; protein binding	cytoplasm; cytoskeleton; nucleus; organelle lumen	metabolic process; response to stimulus	5.6
151	P82995	Heat shock protein HSP 90-alpha OS=Rattus norvegicus GN=Hsp90aa1 PE=1 SV=3 - [HS90A_RAT]	catalytic activity; enzyme regulator activity; nucleotide binding; protein binding; RNA binding	cell surface; cytoplasm; cytosol; membrane	cell death; cell differentiation; cell organization and biogenesis; cellular component movement; development; metabolic process; regulation of biological process; response to stimulus; transport	3.8
152	P34058	Heat shock protein HSP 90-beta OS=Rattus norvegicus GN=Hsp90ab1 PE=1 SV=4 - [HS90B_RAT]	nucleotide binding; protein binding	cell surface; cytoplasm; cytosol; membrane; mitochondrion; nucleus	cell communication; cell death; cell organization and biogenesis; defense response; development; metabolic process; regulation of biological process; response to stimulus; transport	3.6
153	D4ACN3	Hect (Homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 2 (Predicted) OS=Rattus norvegicus GN=Herc2 PE=4 SV=2 - [D4ACN3_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding	cytoplasm; membrane; mitochondrion; nucleus	metabolic process; reproduction; response to stimulus	2.5
154	P01946	Hemoglobin subunit alpha-1/2 OS=Rattus norvegicus GN=Hba1 PE=1 SV=3 - [HBA_RAT]	antioxidant activity; catalytic activity; metal ion binding; protein binding; transporter activity	cytoplasm; cytosol; ribosome	cell death; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus; transport	8.1
155	P05708	Hexokinase-1 OS=Rattus norvegicus GN=Hk1 PE=1 SV=4 - [HXK1_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; cytosol; membrane; mitochondrion; nucleus; organelle lumen	cell death; metabolic process; regulation of biological process; transport	2.9
156	Q3KRF2	High density lipoprotein binding protein (Vigilin) OS=Rattus norvegicus GN=Hdlbp PE=2 SV=1 - [Q3KRF2_RAT]	RNA binding	cytoplasm; extracellular; nucleus	metabolic process; transport	3.2
157	Q9Z214	Homer protein homolog 1 OS=Rattus norvegicus GN=Homer1 PE=1 SV=2 - [HOME1_RAT]	catalytic activity; nucleotide binding; protein binding; structural molecule activity	cytoplasm; cytoskeleton; membrane	cell communication; cell differentiation; development; metabolic process; regulation of biological process; response to stimulus; transport	2.4
158	Q6IMX7	Hsp70-binding protein 1 OS=Rattus norvegicus GN=Hspbp1 PE=2 SV=1 - [HPBP1_RAT]			metabolic process; regulation of biological process	3.2

159	P17425	Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Rattus norvegicus GN=Hmgcs1 PE=1 SV=1 - [HMCS1_RAT]	catalytic activity; protein binding	cytoplasm; cytosol; membrane; nucleus; organelle lumen	development; metabolic process; reproduction; response to stimulus	6.5
160	Q56R18	Importin subunit alpha OS=Rattus norvegicus GN=Kpna3 PE=2 SV=1 - [Q56R18_RAT]	protein binding; transporter activity	cytoplasm; nucleus	transport	2.5
161	Q56R17	Importin subunit alpha OS=Rattus norvegicus GN=Kpna4 PE=2 SV=1 - [Q56R17_RAT]	protein binding; transporter activity	cytoplasm; nucleus	transport	2.7
162	P83953	Importin subunit alpha-5 OS=Rattus norvegicus GN=Kpna1 PE=1 SV=1 - [IMA5_RAT]	protein binding; transporter activity	cytoplasm; nucleus	regulation of biological process; transport	4.7
163	F2Z3Q8	Importin subunit beta-1 OS=Rattus norvegicus GN=Kpnb1 PE=4 SV=1 - [F2Z3Q8_RAT]	protein binding; transporter activity		transport	2.2
164	Q62688	Inactive phospholipase C-like protein 1 OS=Rattus norvegicus GN=Plcl1 PE=1 SV=1 - [PLCL1_RAT]	catalytic activity; metal ion binding; protein binding; signal transducer activity	cytoplasm	cell communication; metabolic process; regulation of biological process; response to stimulus	4.1
165	E9PU28	Inosine-5'-monophosphate dehydrogenase 2 OS=Rattus norvegicus GN=Impdh2 PE=3 SV=1 - [IMDH2_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding	cytoplasm; membrane; nucleus	cell organization and biogenesis; cell proliferation; development; metabolic process	2.7
166	P35559	Insulin-degrading enzyme OS=Rattus norvegicus GN=Ide PE=1 SV=1 - [IDE_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding	cell surface; cytoplasm; cytosol; extracellular; membrane; mitochondrion; nucleus; organelle lumen; proteasome	cell organization and biogenesis; cellular homeostasis; development; metabolic process; regulation of biological process	3.3
167	G3V7J2	Interferon-inducible double stranded RNA-dependent protein kinase activator A OS=Rattus norvegicus GN=Prkra PE=4 SV=1 - [G3V7J2_RAT]	catalytic activity; protein binding; RNA binding	cytoplasm	cell death; development; metabolic process; regulation of biological process; response to stimulus	3.1
168	F1LNF7	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Rattus norvegicus GN=Idh3a PE=2 SV=1 - [F1LNF7_RAT]	catalytic activity; metal ion binding; nucleotide binding	cytoplasm; mitochondrion	metabolic process	2.9
169	P41562	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Rattus norvegicus GN=Idh1 PE=1 SV=1 - [IDHC_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding	cytoplasm; cytosol; mitochondrion	development; metabolic process; reproduction; response to stimulus	3.4
170	Q08877-8	Isoform 13 of Dynamin-3 OS=Rattus norvegicus GN=Dnm3 - [DYN3_RAT]	catalytic activity; nucleotide binding			3.6
171	Q05140-2	Isoform 2 of Clathrin coat assembly protein AP180 OS=Rattus norvegicus GN=Snap91 - [AP180_RAT]	protein binding	cytoplasm; cytoskeleton; membrane	cell communication; cell differentiation; cell organization and biogenesis; development; regulation of biological process; transport	2.8
172	Q2IBD4-2	Isoform 2 of Cortactin-binding protein 2 OS=Rattus norvegicus GN=Cttnbp2 - [CTTB2_RAT]				2.1
173	F1LP64-2	Isoform 2 of E3 ubiquitin-protein ligase TRIP12 OS=Rattus norvegicus GN=Trip12 - [TRIPC_RAT]	catalytic activity; protein binding	nucleus; organelle lumen	cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus	3.1
174	Q5U2Y1-2	Isoform 2 of General transcription factor II-I OS=Rattus norvegicus GN=Gtf2i - [GTF2I_RAT]	DNA binding; protein binding	cytoplasm; nucleus; organelle lumen	cellular homeostasis; development; metabolic process; regulation of biological process	3.4
175	O88658-2	Isoform 2 of Kinesin-like protein KIF1B OS=Rattus norvegicus GN=Kif1b - [KIF1B_RAT]	catalytic activity; motor activity; nucleotide binding; protein binding	cytoplasm; cytoskeleton; membrane; mitochondrion	cell communication; cellular component movement; metabolic process; transport	3.1
176	Q8K4V4-2	Isoform 2 of Sorting nexin-27 OS=Rattus norvegicus GN=Snx27 - [SNX27_RAT]	protein binding	cytoplasm; cytosol; endosome; nucleus; organelle lumen	cell communication; development; regulation of biological process; response to stimulus; transport	3.0
177	P08644-2	Isoform 2B of GTPase KRas OS=Rattus norvegicus GN=Kras - [RASK_RAT]	catalytic activity; nucleotide binding; protein binding; transporter activity	cytoplasm; membrane; mitochondrion	cell communication; cell death; cell differentiation; cell organization and biogenesis; cell proliferation; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	2.6
178	Q68SB1-3	Isoform 3 of Double-stranded RNA-binding protein Staufen homolog 2 OS=Rattus norvegicus GN=Stau2 - [STAU2_RAT]	RNA binding	cytoplasm; cytoskeleton; endoplasmic reticulum; nucleus; organelle lumen	transport	2.8
179	Q9JHL4-3	Isoform 3 of Drebrin-like protein OS=Rattus norvegicus GN=Dbnl - [DBNL_RAT]	protein binding	cytoplasm; cytoskeleton; cytosol; Golgi; membrane	cell communication; cell differentiation; cell organization and biogenesis; development; regulation of biological process; response to stimulus; transport	4.7

180	P39052-3	Isoform 3 of Dynamin-2 OS=Rattus norvegicus GN=Dnm2 [DYN2_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; cytoskeleton; membrane; nucleus	metabolic process; transport	3.8
181	Q2TA68-3	Isoform 3 of Dynamin-like 120 kDa protein, mitochondrial OS=Rattus norvegicus GN=Opa1 - [OPA1_RAT]	catalytic activity; nucleotide binding			3.4
182	O35303-4	Isoform 4 of Dynamin-1-like protein OS=Rattus norvegicus GN=Dnm1l - [DNM1L_RAT]	catalytic activity; nucleotide binding			2.7
183	Q9R080-4	Isoform 4 of G-protein-signaling modulator 1 OS=Rattus norvegicus GN=Gpsm1 - [GPSM1_RAT]	enzyme regulator activity; protein binding	cytoplasm; cytosol; endoplasmic reticulum; Golgi; membrane; nucleus; organelle lumen	cell communication; cell differentiation; development; regulation of biological process; response to stimulus	3.1
184	Q03555-6	Isoform 5 of Gephyrin OS=Rattus norvegicus GN=Gphn - [GEPH_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding; structural molecule activity	cytoplasm; cytoskeleton; membrane	cell differentiation; cell organization and biogenesis; development; metabolic process; transport	2.1
185	P37285-3	Isoform B of Kinesin light chain 1 OS=Rattus norvegicus GN=Klc1 - [KLC1_RAT]	catalytic activity; motor activity; protein binding	cytoplasm; cytoskeleton; cytosol; membrane	cell organization and biogenesis; cellular component movement; transport	2.2
186	Q99P39-2	Isoform Cytoplasmic of Cysteine desulfurase, mitochondrial OS=Rattus norvegicus GN=Nfs1 - [NFS1_RAT]	catalytic activity		metabolic process	2.3
187	Q07266-2	Isoform E1 of Drebrin OS=Rattus norvegicus GN=Dbn1 - [DREB_RAT]	protein binding	cytoplasm; cytoskeleton; membrane	cell communication; cell differentiation; cell organization and biogenesis; cell proliferation; development	2.6
188	P08082-2	Isoform Non-brain of Clathrin light chain B OS=Rattus norvegicus GN=Cltb - [CLCB_RAT]	structural molecule activity; transporter activity	cytoplasm; Golgi; membrane	cell communication; cell organization and biogenesis; transport	8.4
189	P35213-2	Isoform Short of 14-3-3 protein beta/alpha OS=Rattus norvegicus GN=Ywhab - [1433B_RAT]	protein binding			3.7
190	Q03351-2	Isoform TRKC of NT-3 growth factor receptor OS=Rattus norvegicus GN=Ntrk3 - [NTRK3_RAT]	catalytic activity; nucleotide binding; protein binding; receptor activity; signal transducer activity	cytoplasm; Golgi; membrane	cell communication; cell death; cell differentiation; cell growth; cell organization and biogenesis; cell proliferation; cellular component movement; development; metabolic process; regulation of biological process; reproduction; response to stimulus	2.6
191	F1LS86	Isoleucine-tRNA synthetase (Predicted) OS=Rattus norvegicus GN=Iars PE=3 SV=2 - [F1LS86_RAT]	catalytic activity; nucleotide binding	cytoplasm; nucleus; organelle lumen	metabolic process	2.0
192	P97924	Kalirin OS=Rattus norvegicus GN=Kalrn PE=1 SV=3 - [KALRN_RAT]	catalytic activity; enzyme regulator activity; metal ion binding; nucleotide binding; protein binding	cytoplasm; cytoskeleton	cell communication; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus	2.2
193	F1M5N7	Kinesin family member 21B (Predicted) OS=Rattus norvegicus GN=Kif21b PE=3 SV=2 - [F1M5N7_RAT]	catalytic activity; motor activity; nucleotide binding; protein binding	cytoplasm; cytoskeleton; membrane; mitochondrion	cellular component movement	2.3
194	F1M8F2	Kinesin heavy chain isoform 5A OS=Rattus norvegicus GN=Kif5a PE=2 SV=1 - [F1M8F2_RAT]	catalytic activity; motor activity; nucleotide binding	cytoplasm; cytoskeleton; membrane; mitochondrion	cellular component movement	2.2
195	P56536	Kinesin heavy chain isoform 5C (Fragment) OS=Rattus norvegicus GN=Kif5c PE=1 SV=2 - [KIF5C_RAT]	catalytic activity; motor activity; nucleotide binding; protein binding	cytoplasm; cytoskeleton	cell differentiation; cell organization and biogenesis; cellular component movement; development; response to stimulus; transport	2.1
196	Q2PQA9	Kinesin-1 heavy chain OS=Rattus norvegicus GN=Kif5b PE=1 SV=1 - [KINH_RAT]	catalytic activity; motor activity; nucleotide binding; protein binding; transporter activity	chromosome; cytoplasm; cytoskeleton; membrane; nucleus; organelle lumen	cell differentiation; cell organization and biogenesis; cellular component movement; cellular homeostasis; metabolic process; regulation of biological process; reproduction; transport	2.4
197	F1M8L1	Kinesin-like protein KIF2A OS=Rattus norvegicus GN=Kif2a PE=2 SV=2 - [F1M8L1_RAT]				2.2
198	Q68FQ9	LanC lantibiotic synthetase component C-like 2 (Bacterial) OS=Rattus norvegicus GN=Lancl2 PE=2 SV=1 - [Q68FQ9_RAT]	catalytic activity	cytoplasm; cytoskeleton; cytosol; membrane; nucleus	cell communication; metabolic process; regulation of biological process; response to stimulus	3.0

199	Q6MG49	Large proline-rich protein BAG6 OS=Rattus norvegicus GN=Bag6 PE=2 SV=2 - [BAG6_RAT]	protein binding	cytoplasm; cytosol; nucleus	cell communication; cell death; cell differentiation; cell organization and biogenesis; cell proliferation; development; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	2.3
200	Q5XIN6	LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Rattus norvegicus GN=Letm1 PE=1 SV=1 - [LETM1_RAT]	metal ion binding	cytoplasm; membrane; mitochondrion	cell organization and biogenesis	2.9
201	F1LM33	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus GN=Lrpprc PE=4 SV=2 - [F1LM33_RAT]	DNA binding; protein binding; RNA binding	chromosome; cytoplasm; cytoskeleton; membrane; mitochondrion; nucleus; organelle lumen	cell organization and biogenesis; cellular component movement; metabolic process; regulation of biological process; transport	2.8
202	P0CC10	Leucine-rich repeat-containing protein 4B OS=Rattus norvegicus GN=Lrrc4b PE=1 SV=1 - [LRC4B_RAT]	protein binding	membrane	cell communication; cell organization and biogenesis; development; regulation of biological process	3.6
203	B3DM92	Lipid phosphate phosphatase-related protein type 3 OS=Rattus norvegicus GN=Lppr3 PE=2 SV=1 - [B3DM92_RAT]	catalytic activity	membrane	metabolic process	2.5
204	G3V864	Lipid phosphate phosphatase-related protein type 4 OS=Rattus norvegicus GN=Lppr4 PE=4 SV=1 - [G3V864_RAT]	catalytic activity	cell surface; membrane	cell differentiation; cell organization and biogenesis; development; metabolic process	2.4
205	B0BN63	LOC681996 protein OS=Rattus norvegicus GN=LOC681996 PE=2 SV=1 - [B0BN63_RAT]	enzyme regulator activity; protein binding	cytoplasm	metabolic process; regulation of biological process; response to stimulus	2.6
206	B5DEG8	LOC685144 protein OS=Rattus norvegicus GN=Sec24c PE=2 SV=1 - [B5DEG8_RAT]	metal ion binding	cytoplasm; membrane; nucleus; organelle lumen	transport	2.1
207	P18163	Long-chain-fatty-acid--CoA ligase 1 OS=Rattus norvegicus GN=Acsl1 PE=1 SV=1 - [ACSL1_RAT]	catalytic activity; nucleotide binding	cytoplasm; endoplasmic reticulum; membrane; mitochondrion	cell communication; metabolic process; regulation of biological process; response to stimulus; transport	2.6
208	Q1HAQ0	Lysophosphatidylcholine acyltransferase 1 OS=Rattus norvegicus GN=Lpcat1 PE=2 SV=2 - [PCAT1_RAT]	catalytic activity; metal ion binding	cytoplasm; endoplasmic reticulum; Golgi; membrane	development; metabolic process; regulation of biological process	2.7
209	O08873	MAP kinase-activating death domain protein OS=Rattus norvegicus GN=Madd PE=1 SV=1 - [MADD_RAT]	enzyme regulator activity	cytoplasm; membrane	cell communication; cell death; metabolic process; regulation of biological process; response to stimulus	2.9
210	F1M836	MAP/microtubule affinity-regulating kinase 3 OS=Rattus norvegicus GN=Mark3 PE=2 SV=1 - [F1M836_RAT]	catalytic activity; nucleotide binding; protein binding	membrane	metabolic process	3.0
211	Q9EPH2	MARCKS-related protein OS=Rattus norvegicus GN=Marcksl1 PE=2 SV=3 - [MRP_RAT]	protein binding	cytoplasm; membrane	cell proliferation; regulation of biological process; transport	3.0
212	F1M7H7	Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1 (Fragment) OS=Rattus norvegicus GN=Magi1 PE=4 SV=2 - [F1M7H7_RAT]				10.4
213	Q5U2N3	Membrane-associated phosphatidylinositol transfer protein 1 OS=Rattus norvegicus GN=Pitpnm1 PE=2 SV=1 - [PITM1_RAT]	metal ion binding	cytoplasm; endoplasmic reticulum; Golgi; membrane	transport	2.6
214	D3ZNY3	Methylmalonic aciduria (Cobalamin deficiency) cblA type (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Mmaa PE=4 SV=1 - [D3ZNY3_RAT]	catalytic activity; nucleotide binding			2.4
215	P34926	Microtubule-associated protein 1A OS=Rattus norvegicus GN=Map1a PE=1 SV=1 - [MAP1A_RAT]	catalytic activity; protein binding	cytoplasm; cytoskeleton; cytosol	cell organization and biogenesis; regulation of biological process	3.8
216	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=2 SV=1 - [F1LRL9_RAT]		cytoplasm; cytoskeleton; cytosol	cell differentiation; cell growth; cell organization and biogenesis; cellular component movement; development; regulation of biological process; transport	2.6
217	P0C5W1	Microtubule-associated protein 1S OS=Rattus norvegicus GN=Map1s PE=1 SV=1 - [MAP1S_RAT]	catalytic activity; DNA binding; protein binding	cytoplasm; cytoskeleton; cytosol; nucleus	cell death; cell differentiation; cell organization and biogenesis; development	4.5
218	F1MAQ5	Microtubule-associated protein OS=Rattus norvegicus GN=Map2 PE=2 SV=2 - [F1MAQ5_RAT]				2.2

219	Q810W7	Microtubule-associated serine/threonine-protein kinase 1 OS=Rattus norvegicus GN=Mast1 PE=2 SV=1 - [MAST1_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding	cytoplasm; cytoskeleton; membrane; nucleus	cell communication; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	3.1
220	R9PXR4	Mitochondrial import receptor subunit TOM70 OS=Rattus norvegicus GN=Tomm70a PE=4 SV=1 - [R9PXR4_RAT]				3.3
221	A1L1L6	Mitochondrial Rho GTPase OS=Rattus norvegicus GN=Rhot1 PE=2 SV=1 - [A1L1L6_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding	cytoplasm; membrane; mitochondrion	cell communication; cell death; cell organization and biogenesis; cellular component movement; cellular homeostasis; metabolic process; regulation of biological process; response to stimulus; transport	2.3
222	B5DFE0	Mpp6 protein OS=Rattus norvegicus GN=Mpp6 PE=2 SV=1 - [B5DFE0_RAT]	protein binding	membrane		2.3
223	B2GUZ3	Mthfd1l protein OS=Rattus norvegicus GN=Mthfd1l PE=2 SV=1 - [B2GUZ3_RAT]	catalytic activity; nucleotide binding		metabolic process	2.8
224	P51583	Multifunctional protein ADE2 OS=Rattus norvegicus GN=Paics PE=2 SV=3 - [PUR6_RAT]	catalytic activity; nucleotide binding; protein binding		metabolic process	3.4
225	Q64119	Myosin light polypeptide 6 OS=Rattus norvegicus GN=Myl6 PE=1 SV=3 - [MYL6_RAT]	catalytic activity; metal ion binding; motor activity; structural molecule activity	cytoskeleton	cellular component movement; development	4.4
226	D3ZA31	Myotubularin related protein 2 (Predicted), isoform CRA_b OS=Rattus norvegicus GN=Mtmr2 PE=4 SV=1 - [D3ZA31_RAT]	catalytic activity; protein binding	cytoplasm; cytoskeleton; cytosol; membrane; nucleus; vacuole	cell communication; cell differentiation; cell organization and biogenesis; cellular homeostasis; development; metabolic process; regulation of biological process; transport	2.8
227	P30009	Myristoylated alanine-rich C-kinase substrate OS=Rattus norvegicus GN=Marcks PE=1 SV=2 - [MARCS_RAT]	protein binding	cytoplasm; cytoskeleton; membrane; nucleus		3.0
228	P69060	N-acylneuraminate cytidylyltransferase OS=Rattus norvegicus GN=Cmas PE=2 SV=1 - [NEUA_RAT]	catalytic activity	nucleus	metabolic process	4.1
229	Q6MG60	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Rattus norvegicus GN=Ddah2 PE=1 SV=1 - [DDAH2_RAT]	catalytic activity	cytoplasm; mitochondrion	metabolic process	7.7
230	Q561S0	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Rattus norvegicus GN=Ndufa10 PE=1 SV=1 - [NDUAA_RAT]	catalytic activity; nucleotide binding	cytoplasm; membrane; mitochondrion; organelle lumen	metabolic process; response to stimulus; transport	4.6
231	Q66HF1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Rattus norvegicus GN=Ndufs1 PE=1 SV=1 - [NDUS1_RAT]	catalytic activity; metal ion binding	cytoplasm; membrane; mitochondrion	cell death; cell organization and biogenesis; cellular homeostasis; metabolic process; transport	2.6
232	G3V700	Nardilysin OS=Rattus norvegicus GN=Nrd1 PE=3 SV=1 - [G3V700_RAT]	catalytic activity; metal ion binding	cytoplasm; mitochondrion	metabolic process; regulation of biological process	3.5
233	F1LSE5	Neighbor of Brca1 gene 1, isoform CRA_a OS=Rattus norvegicus GN=LOC498369 PE=4 SV=2 - [F1LSE5_RAT]	metal ion binding; protein binding	cytoplasm; cytosol; endosome; vacuole	cell communication; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus	3.6
234	O35274	Neurabin-2 OS=Rattus norvegicus GN=Ppp1r9b PE=1 SV=1 - [NEB2_RAT]	protein binding	cytoplasm; cytoskeleton; membrane; nucleus; organelle lumen	cell communication; cell differentiation; cell growth; cell organization and biogenesis; cellular component movement; development; metabolic process; regulation of biological process; response to stimulus	2.3
235	O35095	Neurochondrin OS=Rattus norvegicus GN=Ncdn PE=1 SV=2 - [NCDN_RAT]	protein binding	cytoplasm; cytosol; nucleus	cell communication; cell differentiation; cell organization and biogenesis; development; regulation of biological process	5.0
236	P07936	Neuromodulin OS=Rattus norvegicus GN=Gap43 PE=1 SV=1 - [NEUM_RAT]	protein binding	cytoplasm; membrane	cell differentiation; cell organization and biogenesis; development; regulation of biological process; response to stimulus	2.2

237	P13084	Nucleophosmin OS=Rattus norvegicus GN=Npm1 PE=1 SV=1 - [NPM_RAT]	DNA binding; enzyme regulator activity; protein binding; RNA binding	cytoplasm; cytoskeleton; cytosol; nucleus; organelle lumen; ribosome	cell communication; cell death; cell growth; cell organization and biogenesis; cell proliferation; cellular homeostasis; metabolic process; regulation of biological process; response to stimulus; transport	3.8
238	A0JPJ7	Obg-like ATPase 1 OS=Rattus norvegicus GN=Ola1 PE=2 SV=1 - [OLA1_RAT]	catalytic activity; nucleotide binding; transporter activity	cytoplasm; membrane; nucleus; organelle lumen	metabolic process; transport	3.3
239	D4AE06	Peptidyl-prolyl cis-trans isomerase (Fragment) OS=Rattus norvegicus GN=Fkbp15 PE=2 SV=2 - [D4AE06_RAT]				2.3
240	Q62915	Peripheral plasma membrane protein CASK OS=Rattus norvegicus GN=Cask PE=1 SV=1 - [CSKP_RAT]	catalytic activity; nucleotide binding; protein binding; receptor activity; signal transducer activity	cytoplasm; cytosol; extracellular; membrane; nucleus; organelle lumen	cell organization and biogenesis; cell proliferation; metabolic process; regulation of biological process; response to stimulus; transport	3.0
241	D3ZEN5	Peroxiredoxin-5, mitochondrial (Fragment) OS=Rattus norvegicus GN=Prdx5 PE=2 SV=2 - [D3ZEN5_RAT]				2.6
242	P31044	Phosphatidylethanolamine-binding protein 1 OS=Rattus norvegicus GN=Pebp1 PE=1 SV=3 - [PEBP1_RAT]	enzyme regulator activity; nucleotide binding; protein binding	cell surface; cytoplasm; endoplasmic reticulum; extracellular; Golgi; membrane; mitochondrion	cell communication; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; reproduction; response to stimulus	2.4
243	Q5FVS6	Phosphatidylinositol 3-kinase regulatory subunit beta OS=Rattus norvegicus GN=Pik3r2 PE=2 SV=1 - [Q5FVS6_RAT]	catalytic activity; enzyme regulator activity; protein binding	cytoplasm; cytosol; membrane; mitochondrion	cell communication; metabolic process; regulation of biological process; response to stimulus	2.3
244	O88377	Phosphatidylinositol 5-phosphate 4-kinase type-2 beta OS=Rattus norvegicus GN=Pip4k2b PE=1 SV=1 - [PI42B_RAT]	catalytic activity; nucleotide binding	cytoplasm; endoplasmic reticulum; membrane; nucleus	metabolic process	2.8
245	F1LPG3	Phosphofurin acidic cluster sorting protein 1 OS=Rattus norvegicus GN=Pacs1 PE=2 SV=1 - [F1LPG3_RAT]	protein binding	cytoplasm; Golgi	cell organization and biogenesis; transport	2.3
246	F1M324	Phospholipase C-like 2 (Predicted) OS=Rattus norvegicus GN=Plcl2 PE=4 SV=2 - [F1M324_RAT]	catalytic activity; metal ion binding; protein binding; signal transducer activity	cytoplasm	cell communication; metabolic process; regulation of biological process; response to stimulus; transport	2.6
247	O08618	Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Rattus norvegicus GN=Prpsap2 PE=2 SV=1 - [KPRB_RAT]	catalytic activity; metal ion binding		metabolic process	3.6
248	G3V918	Phosphoribosylglycinamide formyltransferase, isoform CRA_a OS=Rattus norvegicus GN=Gart PE=3 SV=1 - [G3V918_RAT]	catalytic activity; metal ion binding; nucleotide binding	cytoplasm	development; metabolic process; response to stimulus	4.9
249	D3ZUF9	Pitrilysin metallepetidase 1 (Predicted) OS=Rattus norvegicus GN=Pitrm1 PE=3 SV=1 - [D3ZUF9_RAT]	catalytic activity; metal ion binding	cytoplasm; mitochondrion; nucleus; organelle lumen	metabolic process	3.1
250	Q6AYU5	Poly(RC) binding protein 2 OS=Rattus norvegicus GN=Pcbp2 PE=2 SV=1 - [Q6AYU5_RAT]	protein binding; RNA binding	cytoplasm; nucleus; organelle lumen	defense response; metabolic process; regulation of biological process; response to stimulus	2.4
251	D3ZZF8	Polyadenylate binding protein-interacting protein 1 (Predicted) OS=Rattus norvegicus GN=Paip1 PE=4 SV=2 - [D3ZZF8_RAT]	DNA binding; protein binding; RNA binding; translation regulator activity		metabolic process; regulation of biological process	7.5
252	Q9JKA7	Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 4 OS=Rattus norvegicus GN=Hcn4 PE=2 SV=1 - [HCN4_RAT]	nucleotide binding; protein binding; transporter activity	membrane	cell communication; development; regulation of biological process; transport	2.2
253	A1A5S1	Pre-mRNA-processing factor 6 OS=Rattus norvegicus GN=Prpf6 PE=2 SV=1 - [PRP6_RAT]	protein binding; RNA binding	nucleus; organelle lumen; spliceosomal complex	cell organization and biogenesis; metabolic process; regulation of biological process	2.5
254	Q9EPC6	Profilin-2 OS=Rattus norvegicus GN=Pfn2 PE=1 SV=3 - [PROF2_RAT]	protein binding	cytoplasm; cytoskeleton	cell communication; cell organization and biogenesis; regulation of biological process; transport	3.6
255	Q9QZA2	Programmed cell death 6-interacting protein OS=Rattus norvegicus GN=Pdcd6ip PE=1 SV=2 - [PDC6I_RAT]	protein binding	cytoplasm; cytoskeleton; cytosol	cell death; cell division; transport	2.8
256	O70196	Prolyl endopeptidase OS=Rattus norvegicus GN=Prep PE=1 SV=1 - [PPCE_RAT]	catalytic activity	cytoplasm; cytosol; nucleus	metabolic process	2.2

257	F1M8L5	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Rattus norvegicus GN=Pcca PE=2 SV=2 - [F1M8L5_RAT]				7.0
258	R9PXR7	Prostaglandin E synthase 3 (Fragment) OS=Rattus norvegicus GN=Ptges3 PE=4 SV=1 - [R9PXR7_RAT]				3.8
259	D3ZRN3	Protein Actbl2 OS=Rattus norvegicus GN=Actbl2 PE=3 SV=1 - [D3ZRN3_RAT]	nucleotide binding	cytoplasm; cytoskeleton		3.6
260	D3ZIE9	Protein Aldh18a1 OS=Rattus norvegicus GN=Aldh18a1 PE=4 SV=1 - [D3ZIE9_RAT]	catalytic activity	cytoplasm; mitochondrion	metabolic process	2.8
261	D3ZTP0	Protein Aldh1l2 OS=Rattus norvegicus GN=Aldh1l2 PE=3 SV=2 - [D3ZTP0_RAT]				3.1
262	F1M9N9	Protein Ank2 (Fragment) OS=Rattus norvegicus GN=Ank2 PE=2 SV=2 - [F1M9N9_RAT]				3.0
263	F1LM42	Protein Ank2 OS=Rattus norvegicus GN=Ank2 PE=2 SV=2 - [F1LM42_RAT]				3.0
264	F1LNM3	Protein Ank3 OS=Rattus norvegicus GN=Ank3 PE=2 SV=2 - [F1LNM3_RAT]				2.5
265	D4AE00	Protein Ap3b2 OS=Rattus norvegicus GN=Ap3b2 PE=4 SV=1 - [D4AE00_RAT]	transporter activity	cytoplasm; Golgi; membrane; nucleus; organelle lumen	cell communication; cellular component movement; transport	2.5
266	O70467	Protein arginine N-methyltransferase 3 OS=Rattus norvegicus GN=Prmt3 PE=1 SV=1 - [ANM3_RAT]	catalytic activity; metal ion binding	cytoplasm; cytosol; ribosome	metabolic process	2.2
267	F1LXQ7	Protein Arhgap21 (Fragment) OS=Rattus norvegicus GN=Arhgap21 PE=2 SV=2 - [F1LXQ7_RAT]				2.8
268	F1M2D4	Protein Arhgap23 OS=Rattus norvegicus GN=Arhgap23 PE=2 SV=2 - [F1M2D4_RAT]				3.1
269	D3ZYR0	Protein Arhgef12 OS=Rattus norvegicus GN=Arhgef12 PE=4 SV=2 - [D3ZYR0_RAT]				4.5
270	F1LT94	Protein Arhgef18 OS=Rattus norvegicus GN=Arhgef18 PE=4 SV=2 - [F1LT94_RAT]	enzyme regulator activity; protein binding	cytoplasm; membrane	cell communication; cell organization and biogenesis; regulation of biological process; response to stimulus	4.8
271	D3ZPP2	Protein Arl8a OS=Rattus norvegicus GN=Arl8a PE=3 SV=1 - [D3ZPP2_RAT]	nucleotide binding	cytoplasm; cytoskeleton; nucleus	cell communication; regulation of biological process; response to stimulus	2.7
272	F1MAF8	Protein Atg2b OS=Rattus norvegicus GN=Atg2b PE=4 SV=1 - [F1MAF8_RAT]		membrane		3.2
273	Q5U2P5	Protein C2cd2l OS=Rattus norvegicus GN=C2cd2l PE=2 SV=1 - [Q5U2P5_RAT]	protein binding	membrane		3.1
274	D3ZV15	Protein Cbl OS=Rattus norvegicus GN=Cbl PE=2 SV=1 - [D3ZV15_RAT]	catalytic activity; metal ion binding; protein binding; signal transducer activity	cytoplasm; cytosol; membrane; nucleus	cell communication; cell death; metabolic process; regulation of biological process; response to stimulus	3.5
275	D4A8V2	Protein Ccdc177 OS=Rattus norvegicus GN=Ccdc177 PE=4 SV=1 - [D4A8V2_RAT]	catalytic activity			3.2
276	F1M949	Protein Ckap5 OS=Rattus norvegicus GN=Ckap5 PE=2 SV=2 - [F1M949_RAT]	protein binding	cytoplasm; cytoskeleton	cell organization and biogenesis	2.1
277	D4A6H8	Protein Ctnna2 (Fragment) OS=Rattus norvegicus GN=Ctnna2 PE=4 SV=2 - [D4A6H8_RAT]				4.4
278	B2RZ68	Protein Dcaf7 OS=Rattus norvegicus GN=LOC100361861 PE=2 SV=1 - [B2RZ68_RAT]	protein binding	cytoplasm; nucleus; organelle lumen		2.6
279	F1MAB7	Protein Dgki OS=Rattus norvegicus GN=Dgki PE=2 SV=1 - [F1MAB7_RAT]	catalytic activity; enzyme regulator activity; protein binding	cytoplasm	cell communication; metabolic process; regulation of biological process; response to stimulus	2.7
280	F1LSC4	Protein Dhx57 OS=Rattus norvegicus GN=Dhx57 PE=2 SV=1 - [F1LSC4_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding			2.3

281	O88767	Protein DJ-1 OS=Rattus norvegicus GN=Park7 PE=1 SV=1 - [PARK7_RAT]	antioxidant activity; catalytic activity; protein binding; RNA binding	cytoplasm; cytosol; mitochondrion; nucleus	cell communication; cell death; cell organization and biogenesis; cellular homeostasis; defense response; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	13.7
282	D4AD15	Protein Eif4g1 OS=Rattus norvegicus GN=LOC680559 PE=2 SV=1 - [D4AD15_RAT]	DNA binding; enzyme regulator activity; protein binding; RNA binding	cytoplasm	development; metabolic process; regulation of biological process; response to stimulus	2.1
283	F1LZ53	Protein Exoc6b OS=Rattus norvegicus GN=Exoc6b PE=4 SV=2 - [F1LZ53_RAT]				2.2
284	D3ZT47	Protein Fam171a2 OS=Rattus norvegicus GN=Fam171a2 PE=4 SV=2 - [D3ZT47_RAT]		membrane		2.8
285	F1LQA6	Protein Fam40a OS=Rattus norvegicus GN=Strip1 PE=2 SV=1 - [F1LQA6_RAT]		membrane		2.4
286	D3ZQY4	Protein Fryl OS=Rattus norvegicus GN=Fryl PE=2 SV=1 - [D3ZQY4_RAT]		membrane		2.3
287	D3ZBJ3	Protein Gapvd1 OS=Rattus norvegicus GN=Gapvd1 PE=2 SV=2 - [D3ZBJ3_RAT]	enzyme regulator activity	membrane	cell communication; regulation of biological process; response to stimulus	5.1
288	F1LRI5	Protein Gcn1l1 OS=Rattus norvegicus GN=Gcn1l1 PE=2 SV=2 - [F1LRI5_RAT]				2.7
289	D3ZLS5	Protein Hectd1 OS=Rattus norvegicus GN=Hectd1 PE=4 SV=2 - [D3ZLS5_RAT]				3.6
290	F1M4Q8	Protein Hecw1 OS=Rattus norvegicus GN=Hecw1 PE=4 SV=2 - [F1M4Q8_RAT]	catalytic activity; protein binding	cytoplasm; nucleus; organelle lumen	metabolic process	2.3
291	F2Z3R2	Protein Hnrnpl OS=Rattus norvegicus GN=Hnrnpl PE=4 SV=1 - [F2Z3R2_RAT]	DNA binding; nucleotide binding; RNA binding	nucleus	metabolic process	2.1
292	D4ABT8	Protein Hnrnpul2 OS=Rattus norvegicus GN=Hnrnpul2 PE=4 SV=1 - [D4ABT8_RAT]	catalytic activity; nucleotide binding; protein binding	nucleus		2.1
293	M0R686	Protein Irgq OS=Rattus norvegicus GN=Irgq PE=4 SV=1 - [M0R686_RAT]				6.3
294	F1LNY5	Protein Kif1a OS=Rattus norvegicus GN=Kif1a PE=2 SV=2 - [F1LNY5_RAT]				2.6
295	D3ZSN6	Protein Kif21a (Fragment) OS=Rattus norvegicus GN=Kif21a PE=2 SV=2 - [D3ZSN6_RAT]				2.1
296	F1LMV8	Protein kinase C epsilon type OS=Rattus norvegicus GN=Prkce PE=2 SV=2 - [F1LMV8_RAT]				3.5
297	F1LW74	Protein LOC100360623 OS=Rattus norvegicus GN=LOC100360623 PE=4 SV=2 - [F1LW74_RAT]	enzyme regulator activity	cytoskeleton; membrane	cell communication; regulation of biological process; response to stimulus	2.9
298	M0R4G0	Protein LOC100910729 OS=Rattus norvegicus GN=LOC100910729 PE=4 SV=1 - [M0R4G0_RAT]				4.2
299	Q1RP74	Protein LOC100911774 OS=Rattus norvegicus GN=LOC100911774 PE=2 SV=1 - [Q1RP74_RAT]		cytoplasm; nucleus		4.2
300	D3ZFY8	Protein LOC100912618 OS=Rattus norvegicus GN=LOC100912618 PE=2 SV=1 - [D3ZFY8_RAT]	catalytic activity	cytoplasm	cell communication; metabolic process; regulation of biological process; response to stimulus	3.9
301	M0RBX9	Protein LOC683007 (Fragment) OS=Rattus norvegicus GN=LOC683007 PE=4 SV=1 - [M0RBX9_RAT]				2.6
302	M0R590	Protein LOC685186 OS=Rattus norvegicus GN=LOC685186 PE=3 SV=1 - [M0R590_RAT]	catalytic activity; nucleotide binding		metabolic process	3.2
303	F1LT49	Protein Lrrc47 OS=Rattus norvegicus GN=Lrrc47 PE=4 SV=2 - [F1LT49_RAT]	catalytic activity; protein binding; RNA binding			2.9
304	E9PSK7	Protein Mapk8ip3 OS=Rattus norvegicus GN=Mapk8ip3 PE=2 SV=2 - [E9PSK7_RAT]				2.3
305	D3Z941	Protein Mars OS=Rattus norvegicus GN=Mars PE=3 SV=1 - [D3Z941_RAT]	catalytic activity; metal ion binding; nucleotide binding	cytoplasm; mitochondrion	metabolic process	2.2
306	D3ZGN7	Protein Mical3 OS=Rattus norvegicus GN=Mical3 PE=4 SV=2 - [D3ZGN7_RAT]				2.4

307	F1M6E5	Protein Nacad OS=Rattus norvegicus GN=Nacad PE=4 SV=2 - [F1M6E5_RAT]				2.3
308	F1LPV0	Protein Nars OS=Rattus norvegicus GN=Nars PE=3 SV=2 - [F1LPV0_RAT]	catalytic activity; nucleotide binding	cytoplasm; mitochondrion	metabolic process	3.0
309	Q6JE36	Protein NDRG1 OS=Rattus norvegicus GN=Ndrg1 PE=1 SV=1 - [NDRG1_RAT]	protein binding	cytoplasm; cytoskeleton; cytosol; endosome; membrane; nucleus	cell communication; cell differentiation; cell organization and biogenesis; cellular	8.0
310	Q6AYR2	Protein NDRG3 OS=Rattus norvegicus GN=Ndrg3 PE=2 SV=1 - [NDRG3_RAT]	catalytic activity	cytoplasm	cell differentiation; development	13.9
311	D3ZJT2	Protein Nek9 OS=Rattus norvegicus GN=Nek9 PE=2 SV=2 - [D3ZJT2_RAT]				2.9
312	F1M9V7	Protein Npepps OS=Rattus norvegicus GN=Npepps PE=2 SV=1 - [F1M9V7_RAT]	catalytic activity; metal ion binding		metabolic process; response to stimulus	3.7
313	F1LS01	Protein Pcdh9 OS=Rattus norvegicus GN=Pcdh9 PE=2 SV=2 - [F1LS01_RAT]				2.4
314	F1LQJ7	Protein Pck2 OS=Rattus norvegicus GN=Pck2 PE=2 SV=2 - [F1LQJ7_RAT]				2.5
315	D4AB17	Protein Pfas OS=Rattus norvegicus GN=Pfas PE=4 SV=2 - [D4AB17_RAT]				4.6
316	F1LRW9	Protein Pi4ka OS=Rattus norvegicus GN=Pi4ka PE=2 SV=2 - [F1LRW9_RAT]				2.0
317	D3ZES7	Protein Plxna4a OS=Rattus norvegicus GN=Plxna4a PE=4 SV=1 - [D3ZES7_RAT]	protein binding; receptor activity; signal transducer activity	membrane	cell communication; cell differentiation; cell growth; cell organization and biogenesis; cellular component movement; development; regulation of biological process; response to stimulus	2.3
318	D3ZDX5	Protein Plxnb1 OS=Rattus norvegicus GN=Plxnb1 PE=4 SV=1 - [D3ZDX5_RAT]	enzyme regulator activity; protein binding; receptor activity	membrane	cell communication; cell differentiation; cell organization and biogenesis; cell proliferation; development; metabolic process; regulation of biological process; response to stimulus	2.8
319	F1LNI5	Protein Ppm1g OS=Rattus norvegicus GN=Ppm1g PE=2 SV=2 - [F1LNI5_RAT]				3.2
320	Q5XI34	Protein Ppp2r1a OS=Rattus norvegicus GN=Ppp2r1a PE=2 SV=1 - [Q5XI34_RAT]	catalytic activity; protein binding	chromosome; cytoplasm; cytosol	cell death; metabolic process; regulation of biological process	2.8
321	D3ZG37	Protein Ppp6r1 OS=Rattus norvegicus GN=Ppp6r1 PE=4 SV=1 - [D3ZG37_RAT]	protein binding	cytoplasm; nucleus; organelle lumen	metabolic process; regulation of biological process	2.4
322	F1M6T6	Protein Ppp6r2 (Fragment) OS=Rattus norvegicus GN=Ppp6r2 PE=4 SV=2 - [F1M6T6_RAT]		membrane		2.4
323	D4A657	Protein Prrc2c OS=Rattus norvegicus GN=RGD1307838 PE=2 SV=2 - [D4A657_RAT]				2.2
324	E9PSV5	Protein Psat1 OS=Rattus norvegicus GN=Psat1 PE=2 SV=2 - [E9PSV5_RAT]				2.8
325	F1LW77	Protein Rab33b OS=Rattus norvegicus GN=Rab33b PE=3 SV=2 - [F1LW77_RAT]	nucleotide binding	cytoplasm; Golgi; nucleus; organelle lumen	cell communication; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport	2.8
326	A1L1J8	Protein Rab5b OS=Rattus norvegicus GN=Rab5b PE=2 SV=1 - [A1L1J8_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; endosome; nucleus	cell communication; cell organization and biogenesis; regulation of biological process; response to stimulus; transport	4.6
327	B0BNK1	Protein Rab5c OS=Rattus norvegicus GN=Rab5c PE=2 SV=1 - [B0BNK1_RAT]	catalytic activity; nucleotide binding	cytoplasm; nucleus	cell communication; cell organization and biogenesis; regulation of biological process; response to stimulus; transport	4.1
328	F1MAA5	Protein Rangap1 OS=Rattus norvegicus GN=Rangap1 PE=4 SV=2 - [F1MAA5_RAT]	enzyme regulator activity	chromosome; cytoplasm	cell communication; regulation of biological process; response to stimulus; transport	2.6
329	D4ADX8	Protein Raph1 OS=Rattus norvegicus GN=Raph1 PE=4 SV=2 - [D4ADX8_RAT]				2.1

330	D3ZHK4	Protein Rb1cc1 OS=Rattus norvegicus GN=Rb1cc1 PE=4 SV=1 - [D3ZHK4_RAT]	catalytic activity; motor activity; protein binding	cytoplasm; cytoskeleton; membrane; nucleus	cell communication; cell death; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus	2.3
331	E9PT65	Protein Rdx OS=Rattus norvegicus GN=Rdx PE=2 SV=1 - [E9PT65_RAT]	protein binding	cytoplasm; cytoskeleton; Golgi; membrane; nucleus; organelle lumen	cell organization and biogenesis	2.6
332	Q3ZAU6	Protein Rnf14 OS=Rattus norvegicus GN=Rnf14 PE=2 SV=1 - [Q3ZAU6_RAT]	catalytic activity; metal ion binding; protein binding	cytoplasm; nucleus	cell communication; metabolic process; regulation of biological process; response to stimulus	5.9
333	F1M950	Protein Robo2 (Fragment) OS=Rattus norvegicus GN=Robo2 PE=2 SV=2 - [F1M950_RAT]				2.9
334	D3ZDU2	Protein Rptor OS=Rattus norvegicus GN=Rptor PE=4 SV=2 - [D3ZDU2_RAT]	catalytic activity; DNA binding; protein binding	cytoplasm; vacuole	cell communication; cell growth; cell organization and biogenesis; cell proliferation; metabolic process; regulation of biological process; response to stimulus	2.4
335	Q5BJU0	Protein Rras2 OS=Rattus norvegicus GN=Rras2 PE=2 SV=1 - [Q5BJU0_RAT]	catalytic activity; nucleotide binding	membrane	cell communication; cellular component movement; metabolic process; regulation of biological process; response to stimulus	3.0
336	Q5FVJ0	Protein RUFY3 OS=Rattus norvegicus GN=Rufy3 PE=1 SV=1 - [RUFY3_RAT]	metal ion binding; protein binding	cytoplasm; membrane	cell differentiation; cell organization and biogenesis; development; regulation of biological process	2.6
337	F1LRZ9	Protein Rundc3a OS=Rattus norvegicus GN=Rundc3a PE=2 SV=1 - [F1LRZ9_RAT]	enzyme regulator activity; protein binding	cytoplasm; cytosol; membrane	metabolic process; regulation of biological process	3.1
338	D3ZUM2	Protein Sarm1 OS=Rattus norvegicus GN=Sarm1 PE=4 SV=1 - [D3ZUM2_RAT]	protein binding	cytoplasm; cytoskeleton; membrane; mitochondrion	cell communication; cell death; regulation of biological process; response to stimulus	2.4
339	Q5U2R9	Protein Scfd2 OS=Rattus norvegicus GN=Scfd2 PE=2 SV=1 - [Q5U2R9_RAT]			transport	5.4
340	D3ZWS0	Protein Scrib OS=Rattus norvegicus GN=Scrib PE=4 SV=1 - [D3ZWS0_RAT]	protein binding	cytoplasm; membrane	cell communication; cell death; cell differentiation; cell proliferation; cellular component movement; development; metabolic process; regulation of biological process; response to stimulus; transport	3.3
341	D3ZN76	Protein Sec16a OS=Rattus norvegicus GN=Sec16a PE=2 SV=1 - [D3ZN76_RAT]		cytoplasm; cytosol; membrane; nucleus; organelle lumen	cell organization and biogenesis; metabolic process; transport	2.6
342	D4A2Z6	Protein Sec63 OS=Rattus norvegicus GN=Sec63 PE=4 SV=1 - [D4A2Z6_RAT]	protein binding; RNA binding; transporter activity	cytoplasm; nucleus; spliceosomal complex	development; metabolic process; transport	3.1
343	B5DFL9	Protein Sestd1 OS=Rattus norvegicus GN=Sestd1 PE=2 SV=1 - [B5DFL9_RAT]		membrane		2.9
344	F1LYJ9	Protein Soga1 (Fragment) OS=Rattus norvegicus GN=Soga1 PE=4 SV=2 - [F1LYJ9_RAT]				2.2
345	E9PSJ4	Protein Spag9 OS=Rattus norvegicus GN=Spag9 PE=2 SV=2 - [E9PSJ4_RAT]	protein binding	cytoplasm; membrane	cell communication; cell differentiation; cell organization and biogenesis; cellular component movement; development; metabolic process; regulation of biological process; response to stimulus; transport	4.2
346	F1LSV4	Protein Sptlc2 OS=Rattus norvegicus GN=Sptlc2 PE=2 SV=2 - [F1LSV4_RAT]				2.7
347	F1M287	Protein Srgap1 OS=Rattus norvegicus GN=Srgap1 PE=4 SV=2 - [F1M287_RAT]	enzyme regulator activity; protein binding		cell communication; cellular component movement; regulation of biological process; response to stimulus	2.5
348	F1M5M9	Protein Srgap3 OS=Rattus norvegicus GN=Srgap3 PE=2 SV=2 - [F1M5M9_RAT]	protein binding		cell communication; regulation of biological process; response to stimulus	2.7
349	Q9ET50	Protein Stau1 OS=Rattus norvegicus GN=Stau1 PE=2 SV=1 - [Q9ET50_RAT]	protein binding; RNA binding	cytoplasm		2.4
350	F1M6V8	Protein Strn4 OS=Rattus norvegicus GN=Strn4 PE=2 SV=1 - [F1M6V8_RAT]	protein binding			2.2

351	D4A4T0	Protein Stub1 OS=Rattus norvegicus GN=Stub1 PE=4 SV=1 - [D4A4T0_RAT]	catalytic activity; protein binding	cytoplasm; nucleus	cell communication; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	7.8
352	F1LM47	Protein Sucla2 OS=Rattus norvegicus GN=Sucla2 PE=2 SV=1 - [F1LM47_RAT]	catalytic activity; metal ion binding; nucleotide binding	cytoplasm; mitochondrion	metabolic process	3.0
353	G3V8T7	Protein Tdrkh OS=Rattus norvegicus GN=Tdrkh PE=4 SV=1 - [G3V8T7_RAT]	RNA binding	cytoplasm; mitochondrion		2.7
354	G3V852	Protein Tln1 OS=Rattus norvegicus GN=Tln1 PE=4 SV=1 - [G3V852_RAT]	protein binding; structural molecule activity	cytoskeleton; extracellular; membrane	cell organization and biogenesis	2.2
355	D3ZA84	Protein Tln2 OS=Rattus norvegicus GN=Tln2 PE=2 SV=2 - [D3ZA84_RAT]				2.7
356	Q52KJ9	Protein Tmx1 OS=Rattus norvegicus GN=Tmx1 PE=2 SV=1 - [Q52KJ9_RAT]	catalytic activity	cytoplasm; endoplasmic reticulum; membrane	cell death; cellular homeostasis; regulation of biological process	2.8
357	F1M9W9	Protein Trappc8 OS=Rattus norvegicus GN=Trappc8 PE=4 SV=2 - [F1M9W9_RAT]	protein binding			2.9
358	D3ZA17	Protein Trim46 OS=Rattus norvegicus GN=Trim46 PE=2 SV=2 - [D3ZA17_RAT]				2.0
359	D3ZTX1	Protein Trim67 OS=Rattus norvegicus GN=Trim67 PE=4 SV=1 - [D3ZTX1_RAT]	metal ion binding; protein binding	cytoplasm	cell communication; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus	2.2
360	F1M0Z1	Protein Trio OS=Rattus norvegicus GN=Trio PE=2 SV=2 - [F1M0Z1_RAT]	catalytic activity; enzyme regulator activity; nucleotide binding; protein binding	membrane	cell communication; regulation of biological process; response to stimulus	2.2
361	D3ZXP1	Protein Ttc28 (Fragment) OS=Rattus norvegicus GN=Ttc28 PE=4 SV=2 - [D3ZXP1_RAT]				2.3
362	B4F7C2	Protein Tubb4a OS=Rattus norvegicus GN=Tubb4a PE=2 SV=1 - [B4F7C2_RAT]	catalytic activity; nucleotide binding; structural molecule activity	cytoplasm; cytoskeleton; membrane	cell organization and biogenesis; cellular component movement; metabolic process	2.5
363	Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	catalytic activity; nucleotide binding; structural molecule activity	cytoplasm; cytoskeleton; membrane	cell organization and biogenesis; cellular component movement; metabolic process	2.6
364	D4A8H3	Protein Uba6 OS=Rattus norvegicus GN=Uba6 PE=4 SV=1 - [D4A8H3_RAT]	catalytic activity; nucleotide binding	cytoplasm	metabolic process	3.0
365	D3ZF89	Protein Ubap2 OS=Rattus norvegicus GN=Ubap2 PE=2 SV=2 - [D3ZF89_RAT]				3.5
366	F1M403	Protein Ube2o (Fragment) OS=Rattus norvegicus GN=Ube2o PE=2 SV=1 - [F1M403_RAT]	catalytic activity	membrane		3.5
367	F1M7B8	Protein Ube3a OS=Rattus norvegicus GN=Ube3a PE=4 SV=2 - [F1M7B8_RAT]	catalytic activity	cytoplasm; cytosol; membrane; nucleus	cell communication; development; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	2.5
368	F1M8V2	Protein Ube4b OS=Rattus norvegicus GN=Ube4b PE=2 SV=2 - [F1M8V2_RAT]				2.8
369	D4AA63	Protein Ubqln2 OS=Rattus norvegicus GN=Ubqln2 PE=4 SV=1 - [D4AA63_RAT]	protein binding	cytoplasm; membrane		2.4
370	E9PT04	Protein Vps39 OS=Rattus norvegicus GN=Vps39 PE=2 SV=1 - [E9PT04_RAT]	enzyme regulator activity; protein binding	cytoplasm; membrane; vacuole	transport	2.4
371	D4A7D8	Protein Wdfy3 OS=Rattus norvegicus GN=Wdfy3 PE=2 SV=2 - [D4A7D8_RAT]				2.4
372	G3V6Q3	Protein Wdr13 OS=Rattus norvegicus GN=Wdr13 PE=4 SV=2 - [G3V6Q3_RAT]				2.7
373	D3ZQ02	Protein Wdr37 OS=Rattus norvegicus GN=Wdr37 PE=2 SV=2 - [D3ZQ02_RAT]				2.6
374	G3V9M3	Protein Wdr47 OS=Rattus norvegicus GN=Wdr47 PE=4 SV=1 - [G3V9M3_RAT]	protein binding			2.6
375	D3ZMJ7	Protein Wnk2 OS=Rattus norvegicus GN=Wnk2 PE=4 SV=2 - [D3ZMJ7_RAT]	catalytic activity; nucleotide binding	cytoplasm	cell communication; cell proliferation; metabolic process; regulation of biological process; response to stimulus; transport	3.5

376	D4A7Z8	Protein Wnk3 OS=Rattus norvegicus GN=Wnk3 PE=4 SV=2 - [D4A7Z8_RAT]	catalytic activity; nucleotide binding	cytoplasm	cell death; cell organization and biogenesis; metabolic process; regulation of biological process; transport	3.1
377	D4A7Q6	Protein Zfp428 OS=Rattus norvegicus GN=Zfp428 PE=4 SV=2 - [D4A7Q6_RAT]	metal ion binding			4.2
378	F1M8P2	Protein Zyg11b (Fragment) OS=Rattus norvegicus GN=Zyg11b PE=4 SV=1 - [F1M8P2_RAT]	protein binding			3.3
379	G3V776	Proto-oncogene tyrosine-protein kinase Src OS=Rattus norvegicus GN=Src PE=4 SV=1 - [G3V776_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; cytoskeleton; cytosol; endosome; membrane; mitochondrion; nucleus; vacuole	cell communication; cell death; cell organization and biogenesis; cell proliferation; cellular component movement; development; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	2.3
380	Q6AY23	Pyrroline-5-carboxylate reductase 2 OS=Rattus norvegicus GN=Pycr2 PE=2 SV=1 - [P5CR2_RAT]	catalytic activity; nucleotide binding	cytoplasm	metabolic process	2.8
381	P11980	Pyruvate kinase PKM OS=Rattus norvegicus GN=Pkm PE=1 SV=3 - [KPYM_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding	cytoplasm; extracellular; membrane; mitochondrion; nucleus	cell death; development; metabolic process; response to stimulus	3.1
382	Q5RKJ9	RAB10, member RAS oncogene family OS=Rattus norvegicus GN=Rab10 PE=2 SV=1 - [Q5RKJ9_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; endoplasmic reticulum; endosome; Golgi; membrane; nucleus	cell communication; cell differentiation; cell division; cell organization and biogenesis; cell proliferation; development; metabolic process; regulation of biological process; response to stimulus; transport	3.4
383	F1LP59	Rab3 GTPase-activating protein catalytic subunit OS=Rattus norvegicus GN=RGD1306487 PE=2 SV=2 - [F1LP59_RAT]				2.9
384	D4ABP4	Rab3 GTPase-activating protein non-catalytic subunit (Fragment) OS=Rattus norvegicus GN=Rab3gap2 PE=2 SV=2 - [D4ABP4_RAT]				2.3
385	R9PXU5	RAF proto-oncogene serine/threonine-protein kinase (Fragment) OS=Rattus norvegicus GN=Raf1 PE=4 SV=1 - [R9PXU5_RAT]				3.9
386	F1M386	Rap guanine nucleotide exchange factor 2 OS=Rattus norvegicus GN=Rapgef2 PE=1 SV=2 - [RPGF2_RAT]	enzyme regulator activity; protein binding	membrane	cell communication; metabolic process; regulation of biological process; response to stimulus	2.5
387	Q6NYB7	Ras-related protein Rab-1A OS=Rattus norvegicus GN=Rab1A PE=1 SV=3 - [RAB1A_RAT]	catalytic activity; nucleotide binding	cytoplasm; endoplasmic reticulum; Golgi; membrane; nucleus	cell communication; regulation of biological process; response to stimulus; transport	3.6
388	Q6GQP4	Ras-related protein Rab-31 OS=Rattus norvegicus GN=Rab31 PE=1 SV=2 - [RAB31_RAT]	catalytic activity; nucleotide binding	cytoplasm; endosome; Golgi; membrane; nucleus	cell communication; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus; transport	2.5
389	Q5U316	Ras-related protein Rab-35 OS=Rattus norvegicus GN=Rab35 PE=2 SV=1 - [RAB35_RAT]	nucleotide binding	cytoplasm; endosome; extracellular; membrane; mitochondrion; nucleus	cell communication; cell division; regulation of biological process; response to stimulus; transport	3.2
390	P63012	Ras-related protein Rab-3A OS=Rattus norvegicus GN=Rab3a PE=1 SV=1 - [RAB3A_RAT]	catalytic activity; enzyme regulator activity; nucleotide binding; protein binding	cytoplasm; cytosol; membrane	cell communication; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus; transport	2.5
391	G3V7C6	RCG45400 OS=Rattus norvegicus GN=Tubb4b PE=3 SV=1 - [G3V7C6_RAT]	catalytic activity; nucleotide binding; structural molecule activity	cytoplasm; cytoskeleton	cell organization and biogenesis; cellular component movement; metabolic process	2.5
392	G3V963	RCG47487, isoform CRA_b OS=Rattus norvegicus GN=Tmem132a PE=4 SV=1 - [G3V963_RAT]		cytoplasm; endoplasmic reticulum; Golgi; membrane		2.4
393	G3V6L8	RCG61894, isoform CRA_a OS=Rattus norvegicus GN=Strn PE=4 SV=1 - [G3V6L8_RAT]	protein binding			3.2
394	Q03348	Receptor-type tyrosine-protein phosphatase alpha OS=Rattus norvegicus GN=Ptpra PE=2 SV=1 - [PTPRA_RAT]	catalytic activity; protein binding	membrane	cell communication; cell differentiation; development; metabolic process; regulation of biological process; response to stimulus	4.2

395	F1LQN3	Reticulon-4 OS=Rattus norvegicus GN=Rtn4 PE=2 SV=1 - [F1LQN3_RAT]		cytoplasm; endoplasmic reticulum; nucleus	cell differentiation; cell growth; cell organization and biogenesis; cellular component movement; development; regulation of biological process	3.0
396	P81128	Rho GTPase-activating protein 35 OS=Rattus norvegicus GN=Arhgap35 PE=1 SV=2 - [RHG35_RAT]	DNA binding; enzyme regulator activity; nucleotide binding; transporter activity	cytoplasm; cytoskeleton; membrane; nucleus	cell communication; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus; transport	3.2
397	Q5U2Q5	Ribonucleoside-diphosphate reductase OS=Rattus norvegicus GN=Rrm1 PE=2 SV=1 - [Q5U2Q5_RAT]	catalytic activity; nucleotide binding	cytoplasm; nucleus	cell organization and biogenesis; cell proliferation; development; metabolic process; reproduction; response to stimulus	4.3
398	D3Z8E0	Ribosomal protein S6 kinase OS=Rattus norvegicus GN=Rps6ka3 PE=3 SV=2 - [D3Z8E0_RAT]	catalytic activity; enzyme regulator activity; metal ion binding; nucleotide binding; protein binding	cytoplasm; ribosome	cell communication; cell death; defense response; metabolic process; regulation of biological process; response to stimulus	2.6
399	F1LQI2	Roundabout homolog 1 (Fragment) OS=Rattus norvegicus GN=Robo1 PE=2 SV=2 - [F1LQI2_RAT]				2.7
400	P60123	RuvB-like 1 OS=Rattus norvegicus GN=Ruvbl1 PE=1 SV=1 - [RUVB1_RAT]	catalytic activity; nucleotide binding	chromosome; cytoplasm; Golgi; nucleus; organelle lumen	cell division; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	6.3
401	Q6PEC4	S-phase kinase-associated protein 1 OS=Rattus norvegicus GN=Skp1 PE=2 SV=3 - [SKP1_RAT]	catalytic activity	cytoplasm; cytosol; nucleus	cell organization and biogenesis; metabolic process	3.7
402	Q6P799	Serine--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Sars PE=1 SV=3 - [SYSC_RAT]	catalytic activity; nucleotide binding	cytoplasm; mitochondrion	metabolic process	4.0
403	D3ZML2	Serine/threonine-protein kinase BRSK2 OS=Rattus norvegicus GN=Brsk2 PE=2 SV=1 - [BRSK2_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding	cytoplasm; cytoskeleton; endoplasmic reticulum; membrane; nucleus	cell communication; cell death; cell differentiation; cell division; cell organization and biogenesis; cellular homeostasis; development; metabolic process; regulation of biological process; response to stimulus; transport	2.4
404	E9PSS1	Serine/threonine-protein kinase DCLK2 OS=Rattus norvegicus GN=Dclk2 PE=2 SV=2 - [E9PSS1_RAT]				2.1
405	P35465	Serine/threonine-protein kinase PAK 1 OS=Rattus norvegicus GN=Pak1 PE=1 SV=3 - [PAK1_RAT]	catalytic activity; nucleotide binding; protein binding; signal transducer activity	cytoplasm; cytosol; Golgi; membrane; nucleus	cell communication; cell death; cell differentiation; cell organization and biogenesis; cell proliferation; development; metabolic process; regulation of biological process; response to stimulus; transport	3.2
406	Q64303	Serine/threonine-protein kinase PAK 2 OS=Rattus norvegicus GN=Pak2 PE=1 SV=1 - [PAK2_RAT]	catalytic activity; enzyme regulator activity; nucleotide binding; protein binding	cytoplasm; membrane; nucleus	cell communication; cell death; metabolic process; regulation of biological process; response to stimulus	3.1
407	Q62829	Serine/threonine-protein kinase PAK 3 OS=Rattus norvegicus GN=Pak3 PE=1 SV=1 - [PAK3_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding	cytoplasm	cell communication; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus	3.2
408	Q9JIH7	Serine/threonine-protein kinase WNK1 OS=Rattus norvegicus GN=Wnk1 PE=1 SV=2 - [WNK1_RAT]	catalytic activity; enzyme regulator activity; metal ion binding; nucleotide binding; protein binding	cytoplasm	cell communication; metabolic process; regulation of biological process; response to stimulus; transport	3.7
409	P63331	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Rattus norvegicus GN=Ppp2ca PE=1 SV=1 - [PP2AA_RAT]	catalytic activity; metal ion binding; protein binding	chromosome; cytoplasm; cytoskeleton; cytosol; membrane; nucleus	cell communication; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; reproduction; response to stimulus	2.1
410	P20651	Serine/threonine-protein phosphatase 2B catalytic subunit beta isoform OS=Rattus norvegicus GN=Ppp3cb PE=2 SV=1 - [PP2BB_RAT]	catalytic activity; metal ion binding; protein binding	cytoplasm; cytosol; membrane	cell communication; cell differentiation; cellular homeostasis; development; metabolic process; regulation of biological process; response to stimulus; transport	2.2
411	F1LRK9	Serine/threonine-protein phosphatase 4 regulatory subunit 1 (Fragment) OS=Rattus norvegicus GN=Ppp4r1 PE=2 SV=2 - [F1LRK9_RAT]	enzyme regulator activity		cell communication; regulation of biological process; response to stimulus	4.7

412	P53042	Serine/threonine-protein phosphatase 5 OS=Rattus norvegicus GN=Ppp5c PE=2 SV=1 - [PPP5_RAT]	catalytic activity; metal ion binding; protein binding; RNA binding; signal transducer activity	cytoplasm; cytosol; Golgi; nucleus	cell communication; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	4.3
413	Q6AYB5	Signal recognition particle 54 kDa protein OS=Rattus norvegicus GN=Srp54 PE=2 SV=1 - [SRP54_RAT]	catalytic activity; nucleotide binding; RNA binding	cytoplasm; nucleus; organelle lumen	metabolic process; response to stimulus; transport	2.4
414	D3ZZB2	Similar to peroxisome biogenesis factor 1 (Predicted) OS=Rattus norvegicus GN=Pex1 PE=4 SV=1 - [D3ZZB2_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; cytosol; membrane; nucleus; organelle lumen	cell organization and biogenesis; metabolic process; response to stimulus; transport	7.8
415	D4A208	SLIT-ROBO Rho GTPase-activating protein 2 OS=Rattus norvegicus GN=Srgap2 PE=1 SV=1 - [SRGP2_RAT]	enzyme regulator activity; protein binding	cytoplasm; cytoskeleton; cytosol; membrane; mitochondrion; nucleus	cell communication; cell death; cell differentiation; cell organization and biogenesis; cell proliferation; cellular component movement; development; metabolic process; regulation of biological process; response to stimulus	2.3
416	P06685	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Rattus norvegicus GN=Atp1a1 PE=1 SV=1 - [AT1A1_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding; transporter activity	cytoplasm; endoplasmic reticulum; endosome; Golgi; membrane	cellular component movement; cellular homeostasis; metabolic process; regulation of biological process; response to stimulus; transport	2.5
417	P06686	Sodium/potassium-transporting ATPase subunit alpha-2 OS=Rattus norvegicus GN=Atp1a2 PE=1 SV=1 - [AT1A2_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding; transporter activity	cytoplasm; endosome; membrane	cell communication; cellular component movement; cellular homeostasis; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	3.0
418	P06687	Sodium/potassium-transporting ATPase subunit alpha-3 OS=Rattus norvegicus GN=Atp1a3 PE=1 SV=2 - [AT1A3_RAT]	catalytic activity; metal ion binding; nucleotide binding; protein binding; transporter activity	cytoplasm; endoplasmic reticulum; Golgi; membrane; nucleus	cell communication; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	3.0
419	F1M820	Sorbin and SH3 domain-containing protein 1 (Fragment) OS=Rattus norvegicus GN=Sorbs1 PE=2 SV=1 - [F1M820_RAT]	protein binding	cytoplasm; cytoskeleton; membrane; nucleus		3.2
420	D4A8L3	Sphingomyelin phosphodiesterase 3 OS=Rattus norvegicus GN=Smpd3 PE=2 SV=1 - [D4A8L3_RAT]	catalytic activity	cytoplasm; Golgi; membrane	cell communication; metabolic process; regulation of biological process; response to stimulus; transport	3.1
421	Q02769	Squalene synthase OS=Rattus norvegicus GN=Fdft1 PE=2 SV=1 - [FDFT_RAT]	catalytic activity	cytoplasm; endoplasmic reticulum; membrane	metabolic process	2.2
422	Q66X93	Staphylococcal nuclease domain-containing protein 1 OS=Rattus norvegicus GN=Snd1 PE=2 SV=1 - [SND1_RAT]	catalytic activity	cytoplasm; mitochondrion; nucleus	metabolic process; regulation of biological process	3.2
423	F1M953	Stress-70 protein, mitochondrial OS=Rattus norvegicus GN=Hspa9 PE=2 SV=1 - [F1M953_RAT]	nucleotide binding; protein binding	cell surface; cytoplasm; mitochondrion; nucleus; organelle lumen	cell organization and biogenesis; metabolic process; response to stimulus; transport	5.0
424	O35814	Stress-induced-phosphoprotein 1 OS=Rattus norvegicus GN=Stip1 PE=1 SV=1 - [STIP1_RAT]	protein binding	cytoplasm; nucleus		3.9
425	Q3MIE4	Synaptic vesicle membrane protein VAT-1 homolog OS=Rattus norvegicus GN=Vat1 PE=1 SV=1 - [VAT1_RAT]	catalytic activity; metal ion binding; nucleotide binding	cytoplasm; membrane; mitochondrion	cell organization and biogenesis; metabolic process; regulation of biological process	2.6
426	Q62910	Synaptojanin-1 OS=Rattus norvegicus GN=Synj1 PE=1 SV=3 - [SYNJ1_RAT]	catalytic activity; nucleotide binding; protein binding; RNA binding	cytoplasm; membrane	cell communication; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus; transport	2.4
427	P28480	T-complex protein 1 subunit alpha OS=Rattus norvegicus GN=Tcp1 PE=1 SV=1 - [TCPA_RAT]	nucleotide binding; protein binding	chromosome; cytoplasm; cytoskeleton; cytosol; Golgi; membrane; nucleus; organelle lumen	cell differentiation; metabolic process; reproduction	5.2
428	Q5XIM9	T-complex protein 1 subunit beta OS=Rattus norvegicus GN=Cct2 PE=1 SV=3 - [TCPB_RAT]	nucleotide binding; protein binding	cytoplasm; cytoskeleton; cytosol; nucleus; organelle lumen	cell organization and biogenesis; metabolic process; reproduction	3.1
429	Q7TPB1	T-complex protein 1 subunit delta OS=Rattus norvegicus GN=Cct4 PE=1 SV=3 - [TCPD_RAT]	nucleotide binding; protein binding	cytoplasm; cytoskeleton; cytosol; nucleus; organelle lumen	metabolic process; reproduction	2.5
430	Q68FQ0	T-complex protein 1 subunit epsilon OS=Rattus norvegicus GN=Cct5 PE=1 SV=1 - [TCPE_RAT]	nucleotide binding; protein binding	cytoplasm; cytoskeleton; cytosol; nucleus; organelle lumen	metabolic process; reproduction; response to stimulus	5.9

431	Q6P502	T-complex protein 1 subunit gamma OS=Rattus norvegicus GN=Cct3 PE=1 SV=1 - [TCPG_RAT]	nucleotide binding; protein binding	cytoplasm; cytoskeleton; cytosol; membrane	metabolic process; reproduction	2.5
432	Q9QYU4	Thiomorpholine-carboxylate dehydrogenase OS=Rattus norvegicus GN=Crym PE=1 SV=1 - [CRYM_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; cytosol; membrane; mitochondrion; nucleus; organelle lumen	metabolic process; regulation of biological process; response to stimulus; transport	4.5
433	R9PXU4	Thioredoxin reductase 1, isoform CRA_b OS=Rattus norvegicus GN=Txnrd1 PE=4 SV=1 - [R9PXU4_RAT]				2.3
434	Q5XHY5	Threonine--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Tars PE=2 SV=1 - [SYTC_RAT]	catalytic activity; metal ion binding; nucleotide binding	cytoplasm; cytoskeleton	metabolic process	2.9
435	P83941	Transcription elongation factor B polypeptide 1 OS=Rattus norvegicus GN=Tceb1 PE=1 SV=1 - [ELOC_RAT]	catalytic activity; protein binding	cytoplasm; nucleus	metabolic process; regulation of biological process	3.9
436	O08629	Transcription intermediary factor 1-beta OS=Rattus norvegicus GN=Trim28 PE=1 SV=2 - [TIF1B_RAT]	catalytic activity; DNA binding; metal ion binding; protein binding	chromosome; nucleus; organelle lumen	cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus	2.1
437	P46462	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus GN=Vcp PE=1 SV=3 - [TERA_RAT]	catalytic activity; nucleotide binding; protein binding; RNA binding	chromosome; cytoplasm; cytosol; endoplasmic reticulum; nucleus; organelle lumen; proteasome	cell death; cell organization and biogenesis; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	7.4
438	Q63186	Translation initiation factor eIF-2B subunit delta OS=Rattus norvegicus GN=Eif2b4 PE=2 SV=1 - [EI2BD_RAT]	enzyme regulator activity; protein binding; RNA binding	cytoplasm	cell communication; cell differentiation; cellular homeostasis; development; metabolic process; regulation of biological process; reproduction; response to stimulus	3.4
439	M0R4U4	Triosephosphate isomerase (Fragment) OS=Rattus norvegicus PE=3 SV=1 - [M0R4U4_RAT]				3.4
440	Q63610	Tropomyosin alpha-3 chain OS=Rattus norvegicus GN=Tpm3 PE=1 SV=2 - [TPM3_RAT]	protein binding	cytoplasm; cytoskeleton	development	3.8
441	P68370	Tubulin alpha-1A chain OS=Rattus norvegicus GN=Tuba1a PE=1 SV=1 - [TBA1A_RAT]	catalytic activity; nucleotide binding; protein binding; structural molecule activity	cytoplasm; cytoskeleton	cell organization and biogenesis; cellular component movement; metabolic process	2.5
442	P85108	Tubulin beta-2A chain OS=Rattus norvegicus GN=Tubb2a PE=1 SV=1 - [TBB2A_RAT]	catalytic activity; nucleotide binding; structural molecule activity	cytoplasm; cytoskeleton; membrane	cell organization and biogenesis; cellular component movement; metabolic process	2.5
443	Q3KRE8	Tubulin beta-2B chain OS=Rattus norvegicus GN=Tubb2b PE=1 SV=1 - [TBB2B_RAT]	catalytic activity; nucleotide binding; structural molecule activity	cytoplasm; cytoskeleton; membrane	cell differentiation; cell organization and biogenesis; cellular component movement; development; metabolic process	2.5
444	Q4QRB4	Tubulin beta-3 chain OS=Rattus norvegicus GN=Tubb3 PE=1 SV=1 - [TBB3_RAT]	catalytic activity; nucleotide binding; structural molecule activity	cytoplasm; cytoskeleton; membrane	cell differentiation; cell organization and biogenesis; cellular component movement; development; metabolic process; response to stimulus	2.4
445	P69897	Tubulin beta-5 chain OS=Rattus norvegicus GN=Tubb5 PE=1 SV=1 - [TBB5_RAT]	catalytic activity; nucleotide binding; protein binding; structural molecule activity	cytoplasm; cytoskeleton; extracellular; membrane; nucleus	cell organization and biogenesis; cellular component movement; metabolic process	2.5
446	P32577	Tyrosine-protein kinase CSK OS=Rattus norvegicus GN=Csk PE=1 SV=1 - [CSK_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; cytoskeleton; Golgi; membrane	cell communication; cell differentiation; cell organization and biogenesis; cell proliferation; development; metabolic process; regulation of biological process; response to stimulus; transport	3.5
447	P41499	Tyrosine-protein phosphatase non-receptor type 11 OS=Rattus norvegicus GN=Ptpn11 PE=1 SV=4 - [PTN11_RAT]	catalytic activity; protein binding	cytoplasm; cytosol; mitochondrion; nucleus	cell communication; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	7.3
448	Q641Z2	Tyrosine-protein phosphatase non-receptor type 9 OS=Rattus norvegicus GN=Ptpn9 PE=2 SV=1 - [PTN9_RAT]	catalytic activity	cytoplasm	metabolic process	2.4
449	B2RZA9	Ube2l3 protein OS=Rattus norvegicus GN=Ube2l3 PE=2 SV=1 - [B2RZA9_RAT]	catalytic activity; nucleotide binding; protein binding	cytoplasm; nucleus	cell proliferation; metabolic process; regulation of biological process; response to stimulus	6.3

450	Q3KR59	Ubiquitin carboxyl-terminal hydrolase 10 OS=Rattus norvegicus GN=Usp10 PE=2 SV=1 - [UBP10_RAT]	catalytic activity; protein binding	cytoplasm; cytoskeleton; endosome; nucleus	cell communication; metabolic process; regulation of biological process; response to stimulus	3.6
451	Q00981	Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Rattus norvegicus GN=Uchl1 PE=1 SV=2 - [UCHL1_RAT]	catalytic activity; protein binding	cytoplasm; cytosol; endoplasmic reticulum; membrane; nucleus; organelle lumen	cell communication; cell differentiation; cell organization and biogenesis; cell proliferation; cellular component movement; development; metabolic process; regulation of biological process; response to stimulus; transport	22.5
452	D3ZVQ0	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus GN=LOC100911959 PE=3 SV=1 - [D3ZVQ0_RAT]	catalytic activity; metal ion binding; protein binding		metabolic process; regulation of biological process	6.0
453	M0RDN9	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus GN=Usp19 PE=3 SV=1 - [M0RDN9_RAT]				3.5
454	F1MAA1	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus GN=Usp47 PE=2 SV=1 - [F1MAA1_RAT]	catalytic activity; protein binding	cytoplasm	cell death; cell growth; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	3.0
455	F1LM09	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus GN=Usp7 PE=2 SV=2 - [F1LM09_RAT]	catalytic activity; protein binding		metabolic process	3.1
456	D3ZC84	Ubiquitin carboxyl-terminal hydrolase OS=Rattus norvegicus GN=Usp9x PE=3 SV=1 - [D3ZC84_RAT]	catalytic activity; protein binding	cytoplasm	cell communication; metabolic process; regulation of biological process; response to stimulus	2.3
457	F1M9N5	Ubiquitin conjugation factor E4 A OS=Rattus norvegicus GN=Ube4a PE=2 SV=1 - [F1M9N5_RAT]	catalytic activity	cytoplasm	metabolic process	4.4
458	B2RYG6	Ubiquitin thioesterase OTUB1 OS=Rattus norvegicus GN=Otub1 PE=1 SV=1 - [OTUB1_RAT]	catalytic activity; protein binding	cytoplasm	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	11.9
459	M0R5J4	Uncharacterized protein OS=Rattus norvegicus PE=3 SV=1 - [M0R5J4_RAT]	catalytic activity; metal ion binding	cytoplasm; cytosol	metabolic process	3.7
460	D3ZET9	Uncharacterized protein OS=Rattus norvegicus PE=4 SV=2 - [D3ZET9_RAT]		membrane		2.2
461	Q793F9	Vacuolar protein sorting-associated protein 4A OS=Rattus norvegicus GN=Vps4a PE=2 SV=1 - [VPS4A_RAT]	catalytic activity; nucleotide binding; protein binding; RNA binding	cytoplasm; endosome; membrane	cell division; metabolic process; transport	3.2
462	Q6MG21	Valine--tRNA ligase, mitochondrial OS=Rattus norvegicus GN=Vars2 PE=3 SV=1 - [SYVM_RAT]	catalytic activity; nucleotide binding	cytoplasm; mitochondrion	metabolic process; regulation of biological process	2.3
463	Q9Z270	Vesicle-associated membrane protein-associated protein A OS=Rattus norvegicus GN=Vapa PE=1 SV=3 - [VAPA_RAT]	protein binding; signal transducer activity; structural molecule activity	cytoplasm; cytoskeleton; endoplasmic reticulum; membrane	cell communication; cell death; cell differentiation; cell organization and biogenesis; development; regulation of biological process; response to stimulus	2.4
464	Q9Z269	Vesicle-associated membrane protein-associated protein B OS=Rattus norvegicus GN=Vapb PE=1 SV=3 - [VAPB_RAT]	protein binding; structural molecule activity	cytoplasm; endoplasmic reticulum; Golgi; membrane	cell communication; cellular homeostasis; metabolic process; regulation of biological process; reproduction; response to stimulus	2.4
465	F1LQ81	Vesicle-fusing ATPase (Fragment) OS=Rattus norvegicus GN=Nsf PE=2 SV=2 - [F1LQ81_RAT]				2.7
466	Q4KM74	Vesicle-trafficking protein SEC22b OS=Rattus norvegicus GN=Sec22b PE=1 SV=3 - [SC22B_RAT]	protein binding	cytoplasm; endoplasmic reticulum; Golgi; membrane	transport	2.6
467	Q5XI52	Vezatin OS=Rattus norvegicus GN=Vezt PE=2 SV=1 - [VEZA_RAT]	protein binding	cytoplasm; membrane; nucleus	development; transport	2.7
468	Q9Z2L0	Voltage-dependent anion-selective channel protein 1 OS=Rattus norvegicus GN=Vdac1 PE=1 SV=4 - [VDAC1_RAT]	nucleotide binding; protein binding; transporter activity	cytoplasm; membrane; mitochondrion; organelle lumen	cell communication; cell death; defense response; regulation of biological process; response to stimulus; transport	6.4
469	D4A929	WD repeat-containing protein 81 OS=Rattus norvegicus GN=Wdr81 PE=1 SV=1 - [WDR81_RAT]	catalytic activity; protein binding		metabolic process; regulation of biological process	2.7
470	O54975	Xaa-Pro aminopeptidase 1 OS=Rattus norvegicus GN=Xpnpep1 PE=1 SV=1 - [XPP1_RAT]	catalytic activity; metal ion binding; protein binding	cytoplasm; cytosol	metabolic process	4.0

Table S4

S-nitrosylated proteins in CysNO-treated neuronal nuclear extracts: biological process

GO: Biological Process	Number of hits annotated	% of total annotated proteins
metabolic process (GO:0008152)	293	63.01
primary metabolic process (GO:0044238)	270	58.06
cellular process (GO:0009987)	203	43.66
nucleobase-containing compound metabolic process (GO:0006139)	167	35.91
protein metabolic process (GO:0019538)	126	27.10
RNA metabolic process (GO:0016070)	107	23.01
cellular component organization or biogenesis (GO:0071840)	87	18.71
regulation of biological process (GO:0050789)	86	18.49
cellular component organization (GO:0016043)	71	15.27
transcription from RNA polymerase II promoter (GO:0006366)	61	13.12
transcription, DNA-dependent (GO:0006351)	61	13.12
cell cycle (GO:0007049)	58	12.47
translation (GO:0006412)	56	12.04
protein transport (GO:0015031)	48	10.32
intracellular protein transport (GO:0006886)	48	10.32
mRNA processing (GO:0006397)	44	9.46
nitrogen compound metabolic process (GO:0006807)	41	8.82
anatomical structure morphogenesis (GO:0009653)	34	7.31
organelle organization (GO:0006996)	32	6.88
cellular component morphogenesis (GO:0032989)	29	6.24
mRNA splicing, via spliceosome (GO:0000398)	29	6.24
regulation of translation (GO:0006417)	28	6.02
cellular component biogenesis (GO:0044085)	23	4.95
RNA splicing (GO:0008380)	23	4.95
RNA splicing, via transesterification reactions (GO:0000375)	23	4.95
mitosis (GO:0007067)	23	4.95
chromatin organization (GO:0006325)	20	4.30
protein folding (GO:0006457)	17	3.66
protein complex biogenesis (GO:0070271)	15	3.23
protein complex assembly (GO:0006461)	15	3.23
nuclear transport (GO:0051169)	14	3.01
RNA localization (GO:0006403)	11	2.37
regulation of carbohydrate metabolic process (GO:0006109)	6	1.29

Table S5

S-nitrosylated proteins involved in transcription, DNA-dependent (GO:0006351)

61 proteins (★=novel target)

	Hit Number	Uniprot ID	Description	Molecular Function
★	1	D4A0W4	B-cell leukemia/lymphoma 11B (Predicted), isoform CRA_a;Bcl11b;ortholog	zinc finger transcription factor(PC00218);nucleic acid binding(PC00244)
★	2	D3ZWU1	Bromodomain containing 3 (Predicted), isoform CRA_b;Brd3;ortholog	acetyltransferase(PC00220);chromatin/chromatin-binding protein(PC00038)
★	3	O09018	COUP transcription factor 2;Nr2f2;ortholog	nuclear hormone receptor(PC00218);receptor(PC00169);nucleic acid binding(PC00197)
★	4	P15337	Cyclic AMP-responsive element-binding protein 1;Creb1;ortholog	CREB transcription factor(PC00218);nucleic acid binding(PC00056)
★	5	D4A7Q9	General transcription factor IIIC, polypeptide 3, 102kDa (Predicted);Gtf3c3;ortholog	transcription factor(PC00218)
★	6	Q925G1	Hepatoma-derived growth factor-related protein 2;Hdgfrp2;ortholog	transcription cofactor(PC00218);growth factor(PC00217)
★	7	Q923W4	Hepatoma-derived growth factor-related protein 3;Hdgfrp3;ortholog	transcription cofactor(PC00218);growth factor(PC00217)
★	8	Q8CGX0	Insulin-like growth factor 2 mRNA-binding protein 1;Igf2bp1;ortholog	mRNA splicing factor(PC00171);ribonucleoprotein(PC00031);enzyme modulator(PC00147)
★	9	O70437	Mothers against decapentaplegic homolog 4;Smad4;ortholog	transcription factor(PC00218);nucleic acid binding(PC00171)
★	10	P70475	Myelin transcription factor 1-like protein;Myt1l;ortholog	zinc finger transcription factor(PC00218)
★	11	Q63689	Neurogenic differentiation factor 2;Neurod2;ortholog	basic helix-loop-helix transcription factor(PC00218);nuclease(PC00055)
★	12	Q812D1	PC4 and SFRS1-interacting protein;Psip1;ortholog	transcription cofactor(PC00218);growth factor(PC00217)
★	13	Q4V9H5	PHD finger protein 20-like protein 1;Phf20l1;ortholog	zinc finger transcription factor(PC00218)
★	14	P63004	Platelet-activating factor acetylhydrolase IB subunit alpha;Pafah1b1;ortholog	mRNA splicing factor(PC00171);esterase(PC00031);kinase inhibitor(PC00147)
★	15	Q6AY48	Poly(RC) binding protein 3;Pcbp3;ortholog	mRNA splicing factor(PC00171);ribonucleoprotein(PC00031);enzyme modulator(PC00147)
★	16	D4A2B0	Polymerase (DNA-directed), delta interacting protein 3 (Predicted), isoform CRA_a;Poldip3;ortholog	RNA binding protein(PC00171)
★	17	P20267	POU domain, class 3, transcription factor 1;Pou3f1;ortholog	homeobox transcription factor(PC00218)
★	18	D3ZSY3	Protein Bcl11a;Bcl11a;ortholog	zinc finger transcription factor(PC00218);nucleic acid binding(PC00244)
★	19	F1LPP8	Protein Chd3 (Fragment);Chd3;ortholog	DNA helicase(PC00171);helicase(PC00009)
★	20	D3ZVD8	Protein LOC100911205;Hdac6;ortholog	reductase(PC00176);nucleic acid binding(PC00198);deacetylase(PC00171)
★	21	F1M4H5	Protein Nova2 (Fragment);Nova2;ortholog	mRNA splicing factor(PC00171);ribonucleoprotein(PC00031);enzyme modulator(PC00147)
★	22	F2Z3S9	Protein Nr2f1;Nr2f1;ortholog	nuclear hormone receptor(PC00218);receptor(PC00169);nucleic acid binding(PC00197)
★	23	M0R3Z8	Protein Rbm15;Rbm15;ortholog	RNA binding protein(PC00171)
★	24	D3ZHD6	Protein Rbm15b;Rbm15b;ortholog	RNA binding protein(PC00171)
★	25	D3ZBP2	Protein Sin3a;Sin3a;ortholog	transcription factor(PC00218);chromatin/chromatin-binding protein(PC00171);deacetylase(PC00009)
★	26	E9PTG1	Protein Smarca2;Smarca2;ortholog	DNA helicase(PC00171);helicase(PC00009)
★	27	Q4KLI0	Protein Smarcb1;Smarcb1;ortholog	DNA binding protein(PC00171)
★	28	Q8CHJ4	Protein Yy1;Yy1;ortholog	zinc finger transcription factor(PC00218)
★	29	F1M0V0	Protein Zfp280d;Zfp280d;ortholog	centromere DNA-binding protein(PC00171)

★	30	D3ZQL4	Protein Zfp346;Zfp346;ortholog	zinc finger transcription factor(PC00218);nuclease(PC00244)
★	31	D3ZIF0	Protein Zfp512;Zfp512;ortholog	zinc finger transcription factor(PC00218)
★	32	D4A069	Protein Zmym4;Zmym4;ortholog	transcription factor(PC00218);kinase inhibitor(PC00095)
★	33	M0R6L7	Uncharacterized protein (Fragment);unassigned;ortholog	methyltransferase(PC00220)
★	34	O88553	Zinc finger protein 37;Zfp37;ortholog	KRAB box transcription factor(PC00218)
	35	Q5U2X0	CDKN2A-interacting protein;Cdkn2aip;ortholog	DNA binding protein(PC00171)
	36	O08837	Cell division cycle 5-like protein;Cdc5l;ortholog	transcription factor(PC00218);DNA binding protein(PC00171)
	37	Q4KLY4	E3 ubiquitin-protein ligase RING2;Rnf2;ortholog	ubiquitin-protein ligase(PC00142)
	38	Q5U2Y1	General transcription factor II-I;Gtf2i;ortholog	transcription factor(PC00218)
	39	P61980	Heterogeneous nuclear ribonucleoprotein K;Hnrnpk;ortholog	mRNA splicing factor(PC00171);ribonucleoprotein(PC00031);enzyme modulator(PC00147)
	40	Q4QQW4	Histone deacetylase 1;Hdac1;ortholog	reductase(PC00176);nucleic acid binding(PC00198);deacetylase(PC00171)
	41	F7ENH8	Histone deacetylase;Hdac2;ortholog	reductase(PC00176);nucleic acid binding(PC00198);deacetylase(PC00171)
	42	B2GV01	Metastasis-associated gene family, member 2;Mta2;ortholog	chromatin/chromatin-binding protein(PC00171);histone(PC00009)
	43	F7EY92	Methyl-CpG binding domain protein 3 (Predicted), isoform CRA_a;Mbd3;ortholog	DNA binding protein(PC00171)
	44	O35821	Myb-binding protein 1A;Mybbp1a;ortholog	transcription factor(PC00218);DNA-directed DNA polymerase(PC00171)
	45	P09414	Nuclear factor 1 A-type;Nfia;ortholog	transcription factor(PC00218);nucleic acid binding(PC00171)
	46	F2Z3R4	Nuclear factor 1;Nfix;ortholog	transcription factor(PC00218);nucleic acid binding(PC00171)
	47	Q6AYU5	Poly(RC) binding protein 2;Pcbp2;ortholog	mRNA splicing factor(PC00171);ribonucleoprotein(PC00031);enzyme modulator(PC00147)
	48	E9PST5	Protein Acin1;Acin1;ortholog	DNA helicase(PC00171);chromatin/chromatin-binding protein(PC00009);helicase(PC00011)
	49	D3ZGX8	Protein Brd4;Brd4;ortholog	acetyltransferase(PC00220);chromatin/chromatin-binding protein(PC00038)
	50	E9PU01	Protein Chd4;Chd4;ortholog	DNA helicase(PC00171);helicase(PC00009)
	51	G3V829	Protein Fubp3;Fubp3;ortholog	mRNA splicing factor(PC00171);ribonucleoprotein(PC00031);enzyme modulator(PC00147)
	52	D3ZVD8	Protein LOC100911205;Hdac6;ortholog	
	53	D3ZJ19	Protein Satb2;Satb2;ortholog	homeobox transcription factor(PC00218);nucleic acid binding(PC00116)
	54	D3ZJU5	Protein Smarcc1;Smarcc1;ortholog	transcription cofactor(PC00218);chromatin/chromatin-binding protein(PC00217)
	55	P62716	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform;Ppp2cb;ortholog	protein phosphatase(PC00181);protein phosphatase(PC00195);calcium-binding protein(PC00121)
	56	P63329	Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform;Ppp3ca;ortholog	protein phosphatase(PC00181);protein phosphatase(PC00195)
	57	P62138	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit;Ppp1ca;ortholog	protein phosphatase(PC00181);protein phosphatase(PC00195);calcium-binding protein(PC00121)
	58	P62142	Serine/threonine-protein phosphatase PP1-beta catalytic subunit;Ppp1cb;ortholog	protein phosphatase(PC00181);protein phosphatase(PC00195);calcium-binding protein(PC00121)
	59	P63088	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit;Ppp1cc;ortholog	protein phosphatase(PC00181);protein phosphatase(PC00195);calcium-binding protein(PC00121)
	60	Q66X93	Staphylococcal nuclease domain-containing protein 1;Snd1;ortholog	transcription cofactor(PC00218);nucleic acid binding(PC00217)
	61	Q9R1D1	Transcriptional repressor CTCF;Ctcf;ortholog	KRAB box transcription factor(PC00218)

Table S6

S-nitrosylated proteins involved in chromatin organization (GO:0006325)

20 proteins (★=novel target)

	Hit Number	Uniprot ID	Description	Molecular Function
★	1	D3ZWU1	Bromodomain containing 3 (Predicted), isoform CRA_b;Brd3;ortholog	acetyltransferase(PC00220);chromatin/chromatin-binding protein(PC00038)
★	2	Q91XJ0	Calcium-responsive transcription coactivator;Ss18l1;ortholog	chromatin/chromatin-binding protein(PC00171)
★	3	D4AA06	Nuclear receptor binding SET domain protein 1 (Predicted), isoform CRA_a;Nsd1;ortholog	methyltransferase(PC00220);DNA binding protein(PC00155)
★	4	F1LPP8	Protein Chd3 (Fragment);Chd3;ortholog	DNA helicase(PC00171);helicase(PC00009)
★	5	B5DFB2	Protein Rbbp4;Rbbp4;ortholog	receptor(PC00197)
★	6	D3ZBP2	Protein Sin3a;Sin3a;ortholog	transcription factor(PC00218);chromatin/chromatin-binding protein(PC00171);deacetylase(PC00009)
★	7	E9PTG1	Protein Smarca2;Smarca2;ortholog	DNA helicase(PC00171);helicase(PC00009)
★	8	Q4KLI0	Protein Smarcb1;Smarcb1;ortholog	DNA binding protein(PC00171)
★	9	D3ZBS9	Protein Smarcd1;Smarcd1;ortholog	chromatin/chromatin-binding protein(PC00171)
★	10	Q5U3Y2	Protein Smarcd3;Smarcd3;ortholog	chromatin/chromatin-binding protein(PC00171)
★	11	D4A9J4	Protein Whsc1;LOC686349;ortholog	
★	12	D4A9J4	Protein Whsc1;LOC686349;ortholog	methyltransferase(PC00220);DNA binding protein(PC00155)
★	13	D3ZK47	Protein Whsc1l1;Whsc1l1;ortholog	methyltransferase(PC00220);DNA binding protein(PC00155)
★	14	O54772	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2;Smarcd2;ortholog	chromatin/chromatin-binding protein(PC00171)
	15	Q9WUL0	DNA topoisomerase 1;Top1;ortholog	DNA topoisomerase(PC00171)
	16	Q4QQW4	Histone deacetylase 1;Hdac1;ortholog	reductase(PC00176);nucleic acid binding(PC00198);deacetylase(PC00171)
	17	F7ENH8	Histone deacetylase;Hdac2;ortholog	reductase(PC00176);nucleic acid binding(PC00198);deacetylase(PC00171)
	18	Q71UF4	Histone-binding protein RBBP7;Rbbp7;ortholog	receptor(PC00197)
	19	D3ZGX8	Protein Brd4;Brd4;ortholog	acetyltransferase(PC00220);chromatin/chromatin-binding protein(PC00038)
	20	E9PU01	Protein Chd4;Chd4;ortholog	DNA helicase(PC00171);helicase(PC00009)

Table S7

SNO-Proteins with associated SNO-peptides: CysNO-treated nuclear extracts

Hit Number	Uniprot ID	Description	Molecular Function	Cellular Component	SNO-site
1	P10687	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1 OS=Rattus norvegicus GN=Plcb1 PE=1 SV=1 - [PLCB1_RAT]	catalytic activity; signal transducer activity; enzyme regulator activity; metal ion binding; protein binding	nucleus; cytoplasm; cytosol; membrane	EVIEAIAECAFK
1	P10687	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1 OS=Rattus norvegicus GN=Plcb1 PE=1 SV=1 - [PLCB1_RAT]	catalytic activity; signal transducer activity; enzyme regulator activity; metal ion binding; protein binding	nucleus; cytoplasm; cytosol; membrane	KRVETALEACSLPSSR
1	P10687	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1 OS=Rattus norvegicus GN=Plcb1 PE=1 SV=1 - [PLCB1_RAT]	catalytic activity; signal transducer activity; enzyme regulator activity; metal ion binding; protein binding	nucleus; cytoplasm; cytosol; membrane	LTDVAEECQNNQLK
1	P10687	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-1 OS=Rattus norvegicus GN=Plcb1 PE=1 SV=1 - [PLCB1_RAT]	catalytic activity; signal transducer activity; enzyme regulator activity; metal ion binding; protein binding	nucleus; cytoplasm; cytosol; membrane	QVLLSGCR
4	P68511	14-3-3 protein eta OS=Rattus norvegicus GN=Ywhah PE=1 SV=2 - [1433F_RAT]	protein binding	cytoplasm; membrane	NCNDFQYESK
6	P68255	14-3-3 protein theta OS=Rattus norvegicus GN=Ywhaq PE=1 SV=1 - [1433T_RAT]	protein binding	cytoplasm; membrane	LAEQAERYDDMATCMK
6	P68255	14-3-3 protein theta OS=Rattus norvegicus GN=Ywhaq PE=1 SV=1 - [1433T_RAT]	protein binding	cytoplasm; membrane	SICTTVLELLDK
6	P68255	14-3-3 protein theta OS=Rattus norvegicus GN=Ywhaq PE=1 SV=1 - [1433T_RAT]	protein binding	cytoplasm; membrane	YDDMATCMK
6	P68255	14-3-3 protein theta OS=Rattus norvegicus GN=Ywhaq PE=1 SV=1 - [1433T_RAT]	protein binding	cytoplasm; membrane	YLAEVACGDDR
7	P63102	14-3-3 protein zeta/delta OS=Rattus norvegicus GN=Ywhaz PE=1 SV=1 - [1433Z_RAT]	protein binding; RNA binding	nucleus; cytoplasm; mitochondrion; vacuole	YDDMAACMK
8	B0BMW2	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Rattus norvegicus GN=Hsd17b10 PE=2 SV=1 - [B0BMW2_RAT]	nucleotide binding; catalytic activity; protein binding; RNA binding	mitochondrion; membrane; endoplasmic reticulum	LGGNCIFAPANVTSEK
12	P62859	40S ribosomal protein S28 OS=Rattus norvegicus GN=Rps28 PE=1 SV=1 - [RS28_RAT]	RNA binding; structural molecule activity	cytoplasm; ribosome	TGSQGQCTQVRVEFMDDTSR
13	P62909	40S ribosomal protein S3 OS=Rattus norvegicus GN=Rps3 PE=1 SV=1 - [RS3_RAT]	DNA binding; RNA binding; structural molecule activity; catalytic activity; protein binding	nucleus; cytoplasm; membrane; cytosol; ribosome	FIMESGAKGCEVVVSGK
13	P62909	40S ribosomal protein S3 OS=Rattus norvegicus GN=Rps3 PE=1 SV=1 - [RS3_RAT]	DNA binding; RNA binding; structural molecule activity; catalytic activity; protein binding	nucleus; cytoplasm; membrane; cytosol; ribosome	GLCAIAQAESLR
14	M0R6L4	40S ribosomal protein S3a OS=Rattus norvegicus GN=LOC100365839 PE=3 SV=1 - [M0R6L4_RAT]	structural molecule activity	nucleus; cytoplasm; cytosol; ribosome	ACQSIYPLHDVFVR
14	M0R6L4	40S ribosomal protein S3a OS=Rattus norvegicus GN=LOC100365839 PE=3 SV=1 - [M0R6L4_RAT]	structural molecule activity	nucleus; cytoplasm; cytosol; ribosome	LITEDVQGKNCLTNFHGMDLTR
14	M0R6L4	40S ribosomal protein S3a OS=Rattus norvegicus GN=LOC100365839 PE=3 SV=1 - [M0R6L4_RAT]	structural molecule activity	nucleus; cytoplasm; cytosol; ribosome	MCSMVK
14	M0R6L4	40S ribosomal protein S3a OS=Rattus norvegicus GN=LOC100365839 PE=3 SV=1 - [M0R6L4_RAT]	structural molecule activity	nucleus; cytoplasm; cytosol; ribosome	NCLTNFHGMDLTR

15	B0BN81	40S ribosomal protein S5 OS=Rattus norvegicus GN=Rps5 PE=2 SV=1 - [B0BN81_RAT]	RNA binding; structural molecule activity	ribosome; membrane	KAQCPIVER
15	B0BN81	40S ribosomal protein S5 OS=Rattus norvegicus GN=Rps5 PE=2 SV=1 - [B0BN81_RAT]	RNA binding; structural molecule activity	ribosome; membrane	TIAECLADELINAAK
15	B0BN81	40S ribosomal protein S5 OS=Rattus norvegicus GN=Rps5 PE=2 SV=1 - [B0BN81_RAT]	RNA binding; structural molecule activity	ribosome; membrane	VNQAIWLLCTGAR
16	P62243	40S ribosomal protein S8 OS=Rattus norvegicus GN=Rps8 PE=1 SV=2 - [RS8_RAT]	structural molecule activity; RNA binding	nucleus; cytoplasm; ribosome; membrane	TLVKNCIVLIDSTPYR
18	D4A914	5'-3' exoribonuclease 2 (Predicted), isoform CRA_c OS=Rattus norvegicus GN=Xrn2 PE=4 SV=2 - [D4A914_RAT]	DNA binding; catalytic activity; metal ion binding; RNA binding	nucleus; membrane	NSPGCQVASNPR
18	D4A914	5'-3' exoribonuclease 2 (Predicted), isoform CRA_c OS=Rattus norvegicus GN=Xrn2 PE=4 SV=2 - [D4A914_RAT]	DNA binding; catalytic activity; metal ion binding; RNA binding	nucleus; membrane	YYYQGCASWK
19	P63039	60 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspd1 PE=1 SV=1 - [CH60_RAT]	nucleotide binding; protein binding; RNA binding	cytoplasm; mitochondrion; membrane; organelle lumen; endosome; endoplasmic reticulum; Golgi; cytosol; cell surface	AAVEEGIVLGGGCALLR
19	P63039	60 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspd1 PE=1 SV=1 - [CH60_RAT]	nucleotide binding; protein binding; RNA binding	cytoplasm; mitochondrion; membrane; organelle lumen; endosome; endoplasmic reticulum; Golgi; cytosol; cell surface	CEFQDAYVLLSEK
19	P63039	60 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspd1 PE=1 SV=1 - [CH60_RAT]	nucleotide binding; protein binding; RNA binding	cytoplasm; mitochondrion; membrane; organelle lumen; endosome; endoplasmic reticulum; Golgi; cytosol; cell surface	CIPALDSLKPANEDQK
19	P63039	60 kDa heat shock protein, mitochondrial OS=Rattus norvegicus GN=Hspd1 PE=1 SV=1 - [CH60_RAT]	nucleotide binding; protein binding; RNA binding	cytoplasm; mitochondrion; membrane; organelle lumen; endosome; endoplasmic reticulum; Golgi; cytosol; cell surface	GQKCEFQDAYVLLSEK
20	P19945	60S acidic ribosomal protein P0 OS=Rattus norvegicus GN=Rplp0 PE=1 SV=2 - [RLA0_RAT]	structural molecule activity; RNA binding	nucleus; cytoplasm; ribosome; membrane	AGAIAPCEVTVPAQNTGLGPEK
20	P19945	60S acidic ribosomal protein P0 OS=Rattus norvegicus GN=Rplp0 PE=1 SV=2 - [RLA0_RAT]	structural molecule activity; RNA binding	nucleus; cytoplasm; ribosome; membrane	CFIVGADNVGSK
21	Q6PDV7	60S ribosomal protein L10 OS=Rattus norvegicus GN=Rpl10 PE=1 SV=3 - [RL10_RAT]	structural molecule activity; RNA binding	cytoplasm; endoplasmic reticulum; ribosome; membrane	MLSCAGADRLQTGMR
21	Q6PDV7	60S ribosomal protein L10 OS=Rattus norvegicus GN=Rpl10 PE=1 SV=3 - [RL10_RAT]	structural molecule activity; RNA binding	cytoplasm; endoplasmic reticulum; ribosome; membrane	RLIPDGCGVK
22	P62914	60S ribosomal protein L11 OS=Rattus norvegicus GN=Rpl11 PE=1 SV=2 - [RL11_RAT]	RNA binding; structural molecule activity	nucleus; ribosome; membrane	IAVHCTVR
23	F1LSW7	60S ribosomal protein L14 OS=Rattus norvegicus GN=Rpl14 PE=4 SV=1 - [F1LSW7_RAT]	structural molecule activity	ribosome	ALVDGPCTR
23	F1LSW7	60S ribosomal protein L14 OS=Rattus norvegicus GN=Rpl14 PE=4 SV=1 - [F1LSW7_RAT]	structural molecule activity	ribosome	CMQLTDFILK
24	P24049	60S ribosomal protein L17 OS=Rattus norvegicus GN=Rpl17 PE=2 SV=3 - [RL17_RAT]	structural molecule activity; RNA binding	nucleus; ribosome	INPYMSSPCHIEMILTEK
25	P62718	60S ribosomal protein L18a OS=Rattus norvegicus GN=Rpl18a PE=2 SV=1 - [RL18A_RAT]	structural molecule activity; RNA binding	ribosome; membrane	DLTTAGAVTQCYRDMGAR
25	P62718	60S ribosomal protein L18a OS=Rattus norvegicus GN=Rpl18a PE=2 SV=1 - [RL18A_RAT]	structural molecule activity; RNA binding	ribosome; membrane	KSSGEIVYCGQVFEK
25	P62718	60S ribosomal protein L18a OS=Rattus norvegicus GN=Rpl18a PE=2 SV=1 - [RL18A_RAT]	structural molecule activity; RNA binding	ribosome; membrane	VEEIAAGKCR
26	P62832	60S ribosomal protein L23 OS=Rattus norvegicus GN=Rpl23 PE=2 SV=1 - [RL23_RAT]	structural molecule activity; RNA binding	cytoplasm; ribosome; membrane	ECADLWPR
26	P62832	60S ribosomal protein L23 OS=Rattus norvegicus GN=Rpl23 PE=2 SV=1 - [RL23_RAT]	structural molecule activity; RNA binding	cytoplasm; ribosome; membrane	GSAITGPVAKECADLWPR
26	P62832	60S ribosomal protein L23 OS=Rattus norvegicus GN=Rpl23 PE=2 SV=1 - [RL23_RAT]	structural molecule activity; RNA binding	cytoplasm; ribosome; membrane	ISLGLPVGAVINCADNTGAK
27	P17077	60S ribosomal protein L9 OS=Rattus norvegicus GN=Rpl9 PE=1 SV=1 - [RL9_RAT]	structural molecule activity; RNA binding	nucleus; cytoplasm; ribosome; membrane	TGVACSVSQAQK

27	P17077	60S ribosomal protein L9 OS=Rattus norvegicus GN=Rpl9 PE=1 SV=1 - [RL9_RAT]	structural molecule activity; RNA binding	nucleus; cytoplasm; ribosome; membrane	TICSHVQNMIK
31	P17764	Acetyl-CoA acetyltransferase, mitochondrial OS=Rattus norvegicus GN=Acat1 PE=1 SV=1 - [THIL_RAT]	catalytic activity; protein binding; metal ion binding	mitochondrion; membrane; organelle lumen	IHMGNCAENTAK
31	P17764	Acetyl-CoA acetyltransferase, mitochondrial OS=Rattus norvegicus GN=Acat1 PE=1 SV=1 - [THIL_RAT]	catalytic activity; protein binding; metal ion binding	mitochondrion; membrane; organelle lumen	QATLGAGLPIATPCTTVNK
31	P17764	Acetyl-CoA acetyltransferase, mitochondrial OS=Rattus norvegicus GN=Acat1 PE=1 SV=1 - [THIL_RAT]	catalytic activity; protein binding; metal ion binding	mitochondrion; membrane; organelle lumen	VCASGMK
33	Q9ER34	Aconitate hydratase, mitochondrial OS=Rattus norvegicus GN=Aco2 PE=1 SV=2 - [ACON_RAT]	catalytic activity; metal ion binding; protein binding	nucleus; mitochondrion	DFAPGKPLNCIIK
33	Q9ER34	Aconitate hydratase, mitochondrial OS=Rattus norvegicus GN=Aco2 PE=1 SV=2 - [ACON_RAT]	catalytic activity; metal ion binding; protein binding	nucleus; mitochondrion	VAVPSTIHCDHLIEAQLGGEK
33	Q9ER34	Aconitate hydratase, mitochondrial OS=Rattus norvegicus GN=Aco2 PE=1 SV=2 - [ACON_RAT]	catalytic activity; metal ion binding; protein binding	nucleus; mitochondrion	VGLIGSCTNSSYEDMGR
34	G3V6Z3	Actin filament-associated protein 1 OS=Rattus norvegicus GN=Afap1 PE=4 SV=1 - [G3V6Z3_RAT]	protein binding	cytoplasm; cytoskeleton	DQQPQMELPLQGCSITYIPR
34	G3V6Z3	Actin filament-associated protein 1 OS=Rattus norvegicus GN=Afap1 PE=4 SV=1 - [G3V6Z3_RAT]	protein binding	cytoplasm; cytoskeleton	GCEVIPGLDSK
34	G3V6Z3	Actin filament-associated protein 1 OS=Rattus norvegicus GN=Afap1 PE=4 SV=1 - [G3V6Z3_RAT]	protein binding	cytoplasm; cytoskeleton	QTFCFMNR
34	G3V6Z3	Actin filament-associated protein 1 OS=Rattus norvegicus GN=Afap1 PE=4 SV=1 - [G3V6Z3_RAT]	protein binding	cytoplasm; cytoskeleton	RLEEECKQR
34	G3V6Z3	Actin filament-associated protein 1 OS=Rattus norvegicus GN=Afap1 PE=4 SV=1 - [G3V6Z3_RAT]	protein binding	cytoplasm; cytoskeleton	SQPSSSSSPCR
34	G3V6Z3	Actin filament-associated protein 1 OS=Rattus norvegicus GN=Afap1 PE=4 SV=1 - [G3V6Z3_RAT]	protein binding	cytoplasm; cytoskeleton	TLENSPISSCDTSDAEGPLPVNSAAVLK
35	Q4KM87	Actin-like 6A OS=Rattus norvegicus GN=Actl6a PE=2 SV=1 - [Q4KM87_RAT]	DNA binding; nucleotide binding; protein binding	nucleus; membrane	SPLAGDFITMQCR
36	P86173	Actin-like protein 6B OS=Rattus norvegicus GN=Actl6b PE=1 SV=2 - [ACL6B_RAT]	nucleotide binding	nucleus	SPLAGDFISMQCR
37	Q4V7C7	Actin-related protein 3 OS=Rattus norvegicus GN=Actr3 PE=1 SV=1 - [ARP3_RAT]	nucleotide binding; protein binding; structural molecule activity	membrane; cytoplasm; cytoskeleton	KDYEEIGPSICR
37	Q4V7C7	Actin-related protein 3 OS=Rattus norvegicus GN=Actr3 PE=1 SV=1 - [ARP3_RAT]	nucleotide binding; protein binding; structural molecule activity	membrane; cytoplasm; cytoskeleton	YSYVCPDLVK
39	V9GZ85	Actin, cytoplasmic 2 (Fragment) OS=Rattus norvegicus GN=LOC100361457 PE=3 SV=1 - [V9GZ85_RAT]			LCYVALDFEQEMATAASSSSLEK
39	V9GZ85	Actin, cytoplasmic 2 (Fragment) OS=Rattus norvegicus GN=LOC100361457 PE=3 SV=1 - [V9GZ85_RAT]			QEYDESGPSIVHRKCF
41	D3ZUY8	Adaptor protein complex AP-2, alpha 1 subunit (Predicted) OS=Rattus norvegicus GN=Ap2a1 PE=4 SV=1 - [D3ZUY8_RAT]	protein binding; transporter activity	membrane	AADLLYAMCDR
41	D3ZUY8	Adaptor protein complex AP-2, alpha 1 subunit (Predicted) OS=Rattus norvegicus GN=Ap2a1 PE=4 SV=1 - [D3ZUY8_RAT]	protein binding; transporter activity	membrane	ALQVGCLLR
41	D3ZUY8	Adaptor protein complex AP-2, alpha 1 subunit (Predicted) OS=Rattus norvegicus GN=Ap2a1 PE=4 SV=1 - [D3ZUY8_RAT]	protein binding; transporter activity	membrane	HLCELLAQQF
41	D3ZUY8	Adaptor protein complex AP-2, alpha 1 subunit (Predicted) OS=Rattus norvegicus GN=Ap2a1 PE=4 SV=1 - [D3ZUY8_RAT]	protein binding; transporter activity	membrane	LLQCYPPPEDAAVK
41	D3ZUY8	Adaptor protein complex AP-2, alpha 1 subunit (Predicted) OS=Rattus norvegicus GN=Ap2a1 PE=4 SV=1 - [D3ZUY8_RAT]	protein binding; transporter activity	membrane	LVECLETVLNK
41	D3ZUY8	Adaptor protein complex AP-2, alpha 1 subunit (Predicted) OS=Rattus norvegicus GN=Ap2a1 PE=4 SV=1 - [D3ZUY8_RAT]	protein binding; transporter activity	membrane	TCVSLAVSR

41	D3ZUY8	Adaptor protein complex AP-2, alpha 1 subunit (Predicted) OS=Rattus norvegicus GN=Ap2a1 PE=4 SV=1 - [D3ZUY8_RAT]	protein binding; transporter activity	membrane	TVFEALQAPACHENMVK
42	Q05962	ADP/ATP translocase 1 OS=Rattus norvegicus GN=Slc25a4 PE=1 SV=3 - [ADT1_RAT]	transporter activity; protein binding	nucleus; mitochondrion; membrane	KGADIMYTGTVDCWR
43	Q09073	ADP/ATP translocase 2 OS=Rattus norvegicus GN=Slc25a5 PE=1 SV=3 - [ADT2_RAT]	transporter activity; protein binding; RNA binding	nucleus; mitochondrion; membrane	AGAEREFKGLGDCLVK
43	Q09073	ADP/ATP translocase 2 OS=Rattus norvegicus GN=Slc25a5 PE=1 SV=3 - [ADT2_RAT]	transporter activity; protein binding; RNA binding	nucleus; mitochondrion; membrane	GLGDCLVKIYK
43	Q09073	ADP/ATP translocase 2 OS=Rattus norvegicus GN=Slc25a5 PE=1 SV=3 - [ADT2_RAT]	transporter activity; protein binding; RNA binding	nucleus; mitochondrion; membrane	GTDIMYTGTLDCWRK
43	Q09073	ADP/ATP translocase 2 OS=Rattus norvegicus GN=Slc25a5 PE=1 SV=3 - [ADT2_RAT]	transporter activity; protein binding; RNA binding	nucleus; mitochondrion; membrane	KGTDIMYTGTLDCWRK
44	Q9EQR2	Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Rattus norvegicus GN=Agps PE=2 SV=1 - [ADAS_RAT]	catalytic activity; nucleotide binding	mitochondrion; membrane	GVQFAPLSTCR
44	Q9EQR2	Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Rattus norvegicus GN=Agps PE=2 SV=1 - [ADAS_RAT]	catalytic activity; nucleotide binding	mitochondrion; membrane	IPDIVVWPTCHDDVVK
44	Q9EQR2	Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Rattus norvegicus GN=Agps PE=2 SV=1 - [ADAS_RAT]	catalytic activity; nucleotide binding	mitochondrion; membrane	IVNLACK
45	D3ZZ99	Alpha-adducin OS=Rattus norvegicus GN=Add1 PE=4 SV=2 - [D3ZZ99_RAT]	structural molecule activity; protein binding; RNA binding	nucleus; cytoskeleton; membrane	TAGPQSQVLCGVMMDR
45	D3ZZ99	Alpha-adducin OS=Rattus norvegicus GN=Add1 PE=4 SV=2 - [D3ZZ99_RAT]	structural molecule activity; protein binding; RNA binding	nucleus; cytoskeleton; membrane	YSDVEVPASVTGHSFASDGDSGTCSPLR
46	Q6MG11	Alpha-tubulin N-acetyltransferase 1 OS=Rattus norvegicus GN=Atat1 PE=3 SV=1 - [ATAT_RAT]	catalytic activity	cytoplasm; cytoskeleton; membrane	LCPPHPTAR
47	O70511	Ankyrin-3 OS=Rattus norvegicus GN=Ank3 PE=1 SV=3 - [ANK3_RAT]	structural molecule activity; protein binding	cytoplasm; vacuole; cytoskeleton; membrane; cell surface; endoplasmic reticulum	DCVSFTTNVSAR
47	O70511	Ankyrin-3 OS=Rattus norvegicus GN=Ank3 PE=1 SV=3 - [ANK3_RAT]	structural molecule activity; protein binding	cytoplasm; vacuole; cytoskeleton; membrane; cell surface; endoplasmic reticulum	DGLTPLHCGAR
47	O70511	Ankyrin-3 OS=Rattus norvegicus GN=Ank3 PE=1 SV=3 - [ANK3_RAT]	structural molecule activity; protein binding	cytoplasm; vacuole; cytoskeleton; membrane; cell surface; endoplasmic reticulum	GLPQTAVCNLNITLPAHK
47	O70511	Ankyrin-3 OS=Rattus norvegicus GN=Ank3 PE=1 SV=3 - [ANK3_RAT]	structural molecule activity; protein binding	cytoplasm; vacuole; cytoskeleton; membrane; cell surface; endoplasmic reticulum	LVIEDAPKPCVPVGMK
47	O70511	Ankyrin-3 OS=Rattus norvegicus GN=Ank3 PE=1 SV=3 - [ANK3_RAT]	structural molecule activity; protein binding	cytoplasm; vacuole; cytoskeleton; membrane; cell surface; endoplasmic reticulum	MVYHSPPGSECASER
47	O70511	Ankyrin-3 OS=Rattus norvegicus GN=Ank3 PE=1 SV=3 - [ANK3_RAT]	structural molecule activity; protein binding	cytoplasm; vacuole; cytoskeleton; membrane; cell surface; endoplasmic reticulum	VRDTSQEPCGR
49	P18484	AP-2 complex subunit alpha-2 OS=Rattus norvegicus GN=Ap2a2 PE=1 SV=3 - [AP2A2_RAT]	protein binding; transporter activity	membrane	LLQCYPPPDPAVR
50	P62944	AP-2 complex subunit beta OS=Rattus norvegicus GN=Ap2b1 PE=1 SV=1 - [AP2B1_RAT]	protein binding; transporter activity	membrane	CVSTLLDLIQTK
50	P62944	AP-2 complex subunit beta OS=Rattus norvegicus GN=Ap2b1 PE=1 SV=1 - [AP2B1_RAT]	protein binding; transporter activity	membrane	ECHLNADTVSSK
50	P62944	AP-2 complex subunit beta OS=Rattus norvegicus GN=Ap2b1 PE=1 SV=1 - [AP2B1_RAT]	protein binding; transporter activity	membrane	ITEYLCEPLR
50	P62944	AP-2 complex subunit beta OS=Rattus norvegicus GN=Ap2b1 PE=1 SV=1 - [AP2B1_RAT]	protein binding; transporter activity	membrane	TAAVCVAK
50	P62944	AP-2 complex subunit beta OS=Rattus norvegicus GN=Ap2b1 PE=1 SV=1 - [AP2B1_RAT]	protein binding; transporter activity	membrane	TMGCIRVDK
51	P84092	AP-2 complex subunit mu OS=Rattus norvegicus GN=Ap2m1 PE=1 SV=1 - [AP2M1_RAT]	protein binding	mitochondrion; membrane	IPTPLNTSGVQVICMK
51	P84092	AP-2 complex subunit mu OS=Rattus norvegicus GN=Ap2m1 PE=1 SV=1 - [AP2M1_RAT]	protein binding	mitochondrion; membrane	MCDVMAAYFGK

51	P84092	AP-2 complex subunit mu OS=Rattus norvegicus GN=Ap2m1 PE=1 SV=1 - [AP2M1_RAT]	protein binding	mitochondrion; membrane	SYLSGMPECK
53	P15178	Aspartate--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Dars PE=2 SV=1 - [SYDC_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	IGSCTQQDVELHVQK
53	P15178	Aspartate--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Dars PE=2 SV=1 - [SYDC_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	LEYCEALAMLR
53	P15178	Aspartate--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Dars PE=2 SV=1 - [SYDC_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	QCFLVLR
55	Q641Y8	ATP-dependent RNA helicase DDX1 OS=Rattus norvegicus GN=Ddx1 PE=2 SV=1 - [DDX1_RAT]	nucleotide binding; DNA binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; membrane	FLICTDVAAR
55	Q641Y8	ATP-dependent RNA helicase DDX1 OS=Rattus norvegicus GN=Ddx1 PE=2 SV=1 - [DDX1_RAT]	nucleotide binding; DNA binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; membrane	IDCDNLEQYFMQQGGGPDK
55	Q641Y8	ATP-dependent RNA helicase DDX1 OS=Rattus norvegicus GN=Ddx1 PE=2 SV=1 - [DDX1_RAT]	nucleotide binding; DNA binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; membrane	MDQAIIFCR
55	Q641Y8	ATP-dependent RNA helicase DDX1 OS=Rattus norvegicus GN=Ddx1 PE=2 SV=1 - [DDX1_RAT]	nucleotide binding; DNA binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; membrane	NQALFPACVLK
56	Q5U216	ATP-dependent RNA helicase DDX39A OS=Rattus norvegicus GN=Ddx39a PE=2 SV=1 - [DX39A_RAT]	nucleotide binding; catalytic activity; RNA binding	nucleus; cytoplasm; membrane	HFVLDECDK
56	Q5U216	ATP-dependent RNA helicase DDX39A OS=Rattus norvegicus GN=Ddx39a PE=2 SV=1 - [DX39A_RAT]	nucleotide binding; catalytic activity; RNA binding	nucleus; cytoplasm; membrane	NCPHVVVGTPGR
57	D4A0W4	B-cell leukemia/lymphoma 11B (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Bcl11b PE=4 SV=1 - [D4A0W4_RAT]	DNA binding; metal ion binding	nucleus	AGDAGDTGAGGCGDAGAPGAVNGR
57	D4A0W4	B-cell leukemia/lymphoma 11B (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Bcl11b PE=4 SV=1 - [D4A0W4_RAT]	DNA binding; metal ion binding	nucleus	RAGDAGDTGAGGCGDAGAPGAVNGR
58	B1H235	Banp protein OS=Rattus norvegicus GN=Banp PE=2 SV=1 - [B1H235_RAT]	protein binding	nucleus	CVVPQTTVILNNDR
58	B1H235	Banp protein OS=Rattus norvegicus GN=Banp PE=2 SV=1 - [B1H235_RAT]	protein binding	nucleus	LEINCQDPSIK
59	F8WFS9	Beta-adducin OS=Rattus norvegicus GN=Add2 PE=4 SV=1 - [F8WFS9_RAT]	protein binding; structural molecule activity; metal ion binding	cytoplasm; cytoskeleton; membrane	GVSCSEVTASSLIK
60	B5DFM8	Breast carcinoma amplified sequence 2 OS=Rattus norvegicus GN=Bcas2 PE=2 SV=1 - [B5DFM8_RAT]		nucleus; spliceosomal complex	IENLELMSQHGCNAWK
63	Q9EQH5	C-terminal-binding protein 2 OS=Rattus norvegicus GN=Ctbp2 PE=1 SV=2 - [CTBP2_RAT]	catalytic activity; protein binding; nucleotide binding	nucleus	DLATVAFCDAQSTQEIHEK
64	Q91XJ0	Calcium-responsive transcription coactivator OS=Rattus norvegicus GN=Ss18l1 PE=1 SV=1 - [CREST_RAT]	protein binding	chromosome; nucleus	TAECTQYQQILHR
65	G3V9G3	Calcium/calmodulin-dependent protein kinase II, beta, isoform CRA_a OS=Rattus norvegicus GN=Camk2b PE=4 SV=1 - [G3V9G3_RAT]	nucleotide binding; catalytic activity; protein binding	cytosol; membrane	LCTGHEYAAK
65	G3V9G3	Calcium/calmodulin-dependent protein kinase II, beta, isoform CRA_a OS=Rattus norvegicus GN=Camk2b PE=4 SV=1 - [G3V9G3_RAT]	nucleotide binding; catalytic activity; protein binding	cytosol; membrane	QETVECLKK
65	G3V9G3	Calcium/calmodulin-dependent protein kinase II, beta, isoform CRA_a OS=Rattus norvegicus GN=Camk2b PE=4 SV=1 - [G3V9G3_RAT]	nucleotide binding; catalytic activity; protein binding	cytosol; membrane	WQNVHFHCSGAPVAPLQ
66	P11275	Calcium/calmodulin-dependent protein kinase type II subunit alpha OS=Rattus norvegicus GN=Camk2a PE=1 SV=1 - [KCC2A_RAT]	nucleotide binding; catalytic activity; protein binding	nucleus; mitochondrion; membrane	QETVDCLK
66	P11275	Calcium/calmodulin-dependent protein kinase type II subunit alpha OS=Rattus norvegicus GN=Camk2a PE=1 SV=1 - [KCC2A_RAT]	nucleotide binding; catalytic activity; protein binding	nucleus; mitochondrion; membrane	STVASCMHR
70	P37397	Calponin-3 OS=Rattus norvegicus GN=Cnn3 PE=1 SV=1 - [CNN3_RAT]	protein binding	cytoplasm; cytoskeleton	CASQAGMTAYGTR
70	P37397	Calponin-3 OS=Rattus norvegicus GN=Cnn3 PE=1 SV=1 - [CNN3_RAT]	protein binding	cytoplasm; cytoskeleton	DGIILCELINK

71	P12369	cAMP-dependent protein kinase type II-beta regulatory subunit OS=Rattus norvegicus GN=Prkar2b PE=1 SV=3 - [KAP3_RAT]	nucleotide binding; enzyme regulator activity; protein binding; catalytic activity	cytoplasm; membrane	ASVCAEAYNPDEEEDDAESR
71	P12369	cAMP-dependent protein kinase type II-beta regulatory subunit OS=Rattus norvegicus GN=Prkar2b PE=1 SV=3 - [KAP3_RAT]	nucleotide binding; enzyme regulator activity; protein binding; catalytic activity	cytoplasm; membrane	CVGNYDNR
71	P12369	cAMP-dependent protein kinase type II-beta regulatory subunit OS=Rattus norvegicus GN=Prkar2b PE=1 SV=3 - [KAP3_RAT]	nucleotide binding; enzyme regulator activity; protein binding; catalytic activity	cytoplasm; membrane	LLGPCMEIMK
71	P12369	cAMP-dependent protein kinase type II-beta regulatory subunit OS=Rattus norvegicus GN=Prkar2b PE=1 SV=3 - [KAP3_RAT]	nucleotide binding; enzyme regulator activity; protein binding; catalytic activity	cytoplasm; membrane	RASVCAEAYNPDEEEDDAESR
72	Q5M9G3	Caprin-1 OS=Rattus norvegicus GN=Caprin1 PE=1 SV=2 - [CAPR1_RAT]	RNA binding	cytoplasm; cytosol; membrane	EKPVCGTTYK
74	Q704S8	Carnitine O-acetyltransferase OS=Rattus norvegicus GN=Crat PE=1 SV=1 - [CACP_RAT]	catalytic activity; protein binding	mitochondrion; membrane; endoplasmic reticulum	IYGQACATYESASLR
74	Q704S8	Carnitine O-acetyltransferase OS=Rattus norvegicus GN=Crat PE=1 SV=1 - [CACP_RAT]	catalytic activity; protein binding	mitochondrion; membrane; endoplasmic reticulum	SIFTVCLDK
75	Q9JJ76	Casein kinase 1 epsilon OS=Rattus norvegicus GN=Csnk1e PE=2 SV=1 - [Q9JJ76_RAT]	nucleotide binding; catalytic activity; RNA binding	nucleus; cytoplasm	MSTPIEVLCK
77	P04762	Catalase OS=Rattus norvegicus GN=Cat PE=1 SV=3 - [CATA_RAT]	catalytic activity; antioxidant activity; protein binding; metal ion binding; nucleotide binding	mitochondrion; vacuole; membrane; endoplasmic reticulum; Golgi; cytosol	LCENIANHLK
77	P04762	Catalase OS=Rattus norvegicus GN=Cat PE=1 SV=3 - [CATA_RAT]	catalytic activity; antioxidant activity; protein binding; metal ion binding; nucleotide binding	mitochondrion; vacuole; membrane; endoplasmic reticulum; Golgi; cytosol	LGPNYLQIPVNCPYR
77	P04762	Catalase OS=Rattus norvegicus GN=Cat PE=1 SV=3 - [CATA_RAT]	catalytic activity; antioxidant activity; protein binding; metal ion binding; nucleotide binding	mitochondrion; vacuole; membrane; endoplasmic reticulum; Golgi; cytosol	LVNANGEAVYCK
79	Q5U2X0	CDKN2A-interacting protein OS=Rattus norvegicus GN=Cdkn2aip PE=1 SV=1 - [CARF_RAT]	protein binding; RNA binding	nucleus; cytoplasm	SSQESIVCELR
79	Q5U2X0	CDKN2A-interacting protein OS=Rattus norvegicus GN=Cdkn2aip PE=1 SV=1 - [CARF_RAT]	protein binding; RNA binding	nucleus; cytoplasm	STSQSSESSVKFTCR
79	Q5U2X0	CDKN2A-interacting protein OS=Rattus norvegicus GN=Cdkn2aip PE=1 SV=1 - [CARF_RAT]	protein binding; RNA binding	nucleus; cytoplasm	SVCSQSSSNSSQVTSAGSGK
79	Q5U2X0	CDKN2A-interacting protein OS=Rattus norvegicus GN=Cdkn2aip PE=1 SV=1 - [CARF_RAT]	protein binding; RNA binding	nucleus; cytoplasm	SVYLGTGCGK
80	O08837	Cell division cycle 5-like protein OS=Rattus norvegicus GN=Cdc5l PE=1 SV=2 - [CDC5L_RAT]	DNA binding; RNA binding; protein binding	nucleus; spliceosomal complex; cytoplasm; membrane	RLECLKEDVQR
84	D4ACB8	Chaperonin subunit 8 (Theta) (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Cct8 PE=3 SV=1 - [D4ACB8_RAT]	nucleotide binding; protein binding	cytoplasm; cytosol; cytoskeleton	IAVYSCPFDGMITETK
84	D4ACB8	Chaperonin subunit 8 (Theta) (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Cct8 PE=3 SV=1 - [D4ACB8_RAT]	nucleotide binding; protein binding	cytoplasm; cytosol; cytoskeleton	NIQACKELAQTTR
84	D4ACB8	Chaperonin subunit 8 (Theta) (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Cct8 PE=3 SV=1 - [D4ACB8_RAT]	nucleotide binding; protein binding	cytoplasm; cytosol; cytoskeleton	QITSYGETCPGLEQYAIKK
86	Q5RJK5	Chromobox homolog 3 (HP1 gamma homolog, Drosophila) OS=Rattus norvegicus GN=LOC100360260 PE=2 SV=1 - [Q5RJK5_RAT]	DNA binding; protein binding	chromosome; nucleus	LTWHSCPEDEAQ
87	D3ZR50	Chromodomain-helicase-DNA-binding protein 5 OS=Rattus norvegicus GN=Chd5 PE=4 SV=1 - [D3ZR50_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding; metal ion binding	nucleus	AYHLVCLDPELEK
87	D3ZR50	Chromodomain-helicase-DNA-binding protein 5 OS=Rattus norvegicus GN=Chd5 PE=4 SV=1 - [D3ZR50_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding; metal ion binding	nucleus	LAEVECLAESHQHLSK
88	G3V936	Citrate synthase OS=Rattus norvegicus GN=Cs PE=3 SV=1 - [G3V936_RAT]	catalytic activity	mitochondrion; organelle lumen	GYSIPECQK

88	G3V936	Citrate synthase OS=Rattus norvegicus GN=Cs PE=3 SV=1 - [G3V936_RAT]	catalytic activity	mitochondrion; organelle lumen	LPCVAAK
89	P08082	Clathrin light chain B OS=Rattus norvegicus GN=Cltb PE=1 SV=1 - [CLCB_RAT]	structural molecule activity; transporter activity	cytoplasm; membrane	VAQLCDFNPK
90	D4A0H5	Cleavage and polyadenylation specific factor 1, 160kDa (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Cpsf1 PE=4 SV=1 - [D4A0H5_RAT]	RNA binding	nucleus	ADPTHWCLLVR
90	D4A0H5	Cleavage and polyadenylation specific factor 1, 160kDa (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Cpsf1 PE=4 SV=1 - [D4A0H5_RAT]	RNA binding	nucleus	AEGCSTEEGSGVR
90	D4A0H5	Cleavage and polyadenylation specific factor 1, 160kDa (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Cpsf1 PE=4 SV=1 - [D4A0H5_RAT]	RNA binding	nucleus	IELEEWEHVTCMK
90	D4A0H5	Cleavage and polyadenylation specific factor 1, 160kDa (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Cpsf1 PE=4 SV=1 - [D4A0H5_RAT]	RNA binding	nucleus	KKAEGCSTEEGSGVR
90	D4A0H5	Cleavage and polyadenylation specific factor 1, 160kDa (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Cpsf1 PE=4 SV=1 - [D4A0H5_RAT]	RNA binding	nucleus	VIALCLYR
90	D4A0H5	Cleavage and polyadenylation specific factor 1, 160kDa (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Cpsf1 PE=4 SV=1 - [D4A0H5_RAT]	RNA binding	nucleus	VYAVATSTNTPCTR
91	D3ZPL1	Cleavage and polyadenylation specific factor 6, 68kDa (Predicted), isoform CRA_b OS=Rattus norvegicus GN=Cpsf6 PE=4 SV=2 - [D3ZPL1_RAT]	nucleotide binding; RNA binding	nucleus; membrane	RELHGQNPVVTPCNK
93	Q5BJQ6	Cleavage stimulation factor subunit 1 OS=Rattus norvegicus GN=Cstf1 PE=2 SV=1 - [CSTF1_RAT]	protein binding; RNA binding	nucleus; cytoplasm	AHDGAEVCSAIFSK
94	Q99JD4	CLIP-associating protein 2 OS=Rattus norvegicus GN=Clasp2 PE=2 SV=1 - [CLAP2_RAT]	protein binding	chromosome; cytoplasm; Golgi; cytoskeleton; membrane	CASSNWSER
94	Q99JD4	CLIP-associating protein 2 OS=Rattus norvegicus GN=Clasp2 PE=2 SV=1 - [CLAP2_RAT]	protein binding	chromosome; cytoplasm; Golgi; cytoskeleton; membrane	EACITVAHLSTVLGNK
94	Q99JD4	CLIP-associating protein 2 OS=Rattus norvegicus GN=Clasp2 PE=2 SV=1 - [CLAP2_RAT]	protein binding	chromosome; cytoplasm; Golgi; cytoskeleton; membrane	KEDGDTVCSGPGMSDPR
94	Q99JD4	CLIP-associating protein 2 OS=Rattus norvegicus GN=Clasp2 PE=2 SV=1 - [CLAP2_RAT]	protein binding	chromosome; cytoplasm; Golgi; cytoskeleton; membrane	LIPLITSNCTSK
94	Q99JD4	CLIP-associating protein 2 OS=Rattus norvegicus GN=Clasp2 PE=2 SV=1 - [CLAP2_RAT]	protein binding	chromosome; cytoplasm; Golgi; cytoskeleton; membrane	RYESYGMHSDDDANSDASSACSER
94	Q99JD4	CLIP-associating protein 2 OS=Rattus norvegicus GN=Clasp2 PE=2 SV=1 - [CLAP2_RAT]	protein binding	chromosome; cytoplasm; Golgi; cytoskeleton; membrane	SAEEAASVLATSISPEQCIK
94	Q99JD4	CLIP-associating protein 2 OS=Rattus norvegicus GN=Clasp2 PE=2 SV=1 - [CLAP2_RAT]	protein binding	chromosome; cytoplasm; Golgi; cytoskeleton; membrane	VMATSGCAAIR
94	Q99JD4	CLIP-associating protein 2 OS=Rattus norvegicus GN=Clasp2 PE=2 SV=1 - [CLAP2_RAT]	protein binding	chromosome; cytoplasm; Golgi; cytoskeleton; membrane	YESYGMHSDDDANSDASSACSER
95	P45592	Cofilin-1 OS=Rattus norvegicus GN=Cfl1 PE=1 SV=3 - [COF1_RAT]	protein binding	nucleus; cytoplasm; cytoskeleton; membrane	AVLFCLSEDKK
95	P45592	Cofilin-1 OS=Rattus norvegicus GN=Cfl1 PE=1 SV=3 - [COF1_RAT]	protein binding	nucleus; cytoplasm; cytoskeleton; membrane	DRCTLAEK
95	P45592	Cofilin-1 OS=Rattus norvegicus GN=Cfl1 PE=1 SV=3 - [COF1_RAT]	protein binding	nucleus; cytoplasm; cytoskeleton; membrane	KAVLFCLSEDKK
95	P45592	Cofilin-1 OS=Rattus norvegicus GN=Cfl1 PE=1 SV=3 - [COF1_RAT]	protein binding	nucleus; cytoplasm; cytoskeleton; membrane	LTGIKHELQANCYEEVKDR
95	P45592	Cofilin-1 OS=Rattus norvegicus GN=Cfl1 PE=1 SV=3 - [COF1_RAT]	protein binding	nucleus; cytoplasm; cytoskeleton; membrane	MLPDKDCRYALYDATYETK
96	F1LMV9	Coronin (Fragment) OS=Rattus norvegicus GN=Coro2b PE=3 SV=2 - [F1LMV9_RAT]	protein binding	membrane	EHCFDGIPITK
96	F1LMV9	Coronin (Fragment) OS=Rattus norvegicus GN=Coro2b PE=3 SV=2 - [F1LMV9_RAT]	protein binding	membrane	VCGHQGNVLDIK

96	F1LMV9	Coronin (Fragment) OS=Rattus norvegicus GN=Coro2b PE=3 SV=2 - [F1LMV9_RAT]	protein binding	membrane	VLQEANCKNHR
97	G3V624	Coronin OS=Rattus norvegicus GN=Coro1c PE=3 SV=1 - [G3V624_RAT]	protein binding	cytoskeleton	KCEPIIMTVPR
97	G3V624	Coronin OS=Rattus norvegicus GN=Coro1c PE=3 SV=1 - [G3V624_RAT]	protein binding	cytoskeleton	KSDLICAPK
97	G3V624	Coronin OS=Rattus norvegicus GN=Coro1c PE=3 SV=1 - [G3V624_RAT]	protein binding	cytoskeleton	NDQCYDDIR
97	G3V624	Coronin OS=Rattus norvegicus GN=Coro1c PE=3 SV=1 - [G3V624_RAT]	protein binding	cytoskeleton	NGSLICTASK
97	G3V624	Coronin OS=Rattus norvegicus GN=Coro1c PE=3 SV=1 - [G3V624_RAT]	protein binding	cytoskeleton	RGLDVNKCEIAR
97	G3V624	Coronin OS=Rattus norvegicus GN=Coro1c PE=3 SV=1 - [G3V624_RAT]	protein binding	cytoskeleton	SDLICAPK
97	G3V624	Coronin OS=Rattus norvegicus GN=Coro1c PE=3 SV=1 - [G3V624_RAT]	protein binding	cytoskeleton	SIKDTICNQDER
97	G3V624	Coronin OS=Rattus norvegicus GN=Coro1c PE=3 SV=1 - [G3V624_RAT]	protein binding	cytoskeleton	VTWDSSFCAVNPR
98	Q91ZN1	Coronin-1A OS=Rattus norvegicus GN=Coro1a PE=1 SV=3 - [COR1A_RAT]	protein binding; RNA binding	nucleus; cytoplasm; endosome; cytoskeleton; membrane	ADQCYEDVR
99	O09018	COUP transcription factor 2 OS=Rattus norvegicus GN=Nr2f2 PE=1 SV=1 - [COT2_RAT]	DNA binding; receptor activity; signal transducer activity; metal ion binding; protein binding	nucleus	NLSYTCR
100	P63155	Crooked neck-like protein 1 OS=Rattus norvegicus GN=Crnkl1 PE=2 SV=1 - [CRNL1_RAT]	RNA binding; protein binding	nucleus; spliceosomal complex	FLEFGPENCTSWIK
101	Q4QQT3	CUGBP Elav-like family member 1 OS=Rattus norvegicus GN=Celf1 PE=2 SV=1 - [CELF1_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; membrane	AMHQAQTMEGCSSPMVVK
101	Q4QQT3	CUGBP Elav-like family member 1 OS=Rattus norvegicus GN=Celf1 PE=2 SV=1 - [CELF1_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; membrane	CTENDIR
101	Q4QQT3	CUGBP Elav-like family member 1 OS=Rattus norvegicus GN=Celf1 PE=2 SV=1 - [CELF1_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; membrane	GCAFVTFTTR
101	Q4QQT3	CUGBP Elav-like family member 1 OS=Rattus norvegicus GN=Celf1 PE=2 SV=1 - [CELF1_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; membrane	VMFSSFGQIEECR
102	Z4YNP1	CUGBP Elav-like family member 2 OS=Rattus norvegicus GN=Celf2 PE=4 SV=1 - [Z4YNP1_RAT]	nucleotide binding; RNA binding		AMHQSQTMEGCSSPIVVK
102	Z4YNP1	CUGBP Elav-like family member 2 OS=Rattus norvegicus GN=Celf2 PE=4 SV=1 - [Z4YNP1_RAT]	nucleotide binding; RNA binding		CNENDIR
102	Z4YNP1	CUGBP Elav-like family member 2 OS=Rattus norvegicus GN=Celf2 PE=4 SV=1 - [Z4YNP1_RAT]	nucleotide binding; RNA binding		VMFSPFGQIEECR
103	B1WBY1	Cul1 protein OS=Rattus norvegicus GN=Cul1 PE=2 SV=1 - [B1WBY1_RAT]	protein binding		DCLFRPLNK
103	B1WBY1	Cul1 protein OS=Rattus norvegicus GN=Cul1 PE=2 SV=1 - [B1WBY1_RAT]	protein binding		GELVTNCFK
103	B1WBY1	Cul1 protein OS=Rattus norvegicus GN=Cul1 PE=2 SV=1 - [B1WBY1_RAT]	protein binding		KCEQVLIEK
103	B1WBY1	Cul1 protein OS=Rattus norvegicus GN=Cul1 PE=2 SV=1 - [B1WBY1_RAT]	protein binding		QACGFEYTSK
104	P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	protein binding	nucleus; cytoplasm; membrane	AAAKCLDAVVSTR
104	P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	protein binding	nucleus; cytoplasm; membrane	CVAALTR
104	P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	protein binding	nucleus; cytoplasm; membrane	FCNVDDDELR

104	P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	protein binding	nucleus; cytoplasm; membrane	LSTLCPSAVLQR
104	P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	protein binding	nucleus; cytoplasm; membrane	LVEPLRATCTTK
104	P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	protein binding	nucleus; cytoplasm; membrane	NCIGDFLK
104	P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	protein binding	nucleus; cytoplasm; membrane	NVVAECLGK
104	P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	protein binding	nucleus; cytoplasm; membrane	TVIGELPPASSGSALAANVCKK
104	P97536	Cullin-associated NEDD8-dissociated protein 1 OS=Rattus norvegicus GN=Cand1 PE=1 SV=1 - [CAND1_RAT]	protein binding	nucleus; cytoplasm; membrane	TYIQCIAAISR
106	Q5M963	Cytidine monophosphate N-acetylneuraminic acid synthetase OS=Rattus norvegicus GN=Cmas PE=2 SV=1 - [Q5M963_RAT]	catalytic activity	nucleus; membrane	AGLSAVPADACSR
106	Q5M963	Cytidine monophosphate N-acetylneuraminic acid synthetase OS=Rattus norvegicus GN=Cmas PE=2 SV=1 - [Q5M963_RAT]	catalytic activity	nucleus; membrane	EVAYLGNEVSDEECLKR
107	Q68FY0	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Rattus norvegicus GN=Uqcrc1 PE=1 SV=1 - [QCR1_RAT]	catalytic activity; metal ion binding; protein binding	mitochondrion; membrane	LCTSATESEVTR
107	Q68FY0	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Rattus norvegicus GN=Uqcrc1 PE=1 SV=1 - [QCR1_RAT]	catalytic activity; metal ion binding; protein binding	mitochondrion; membrane	NALISHLDGTTPVCEDIGR
107	Q68FY0	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Rattus norvegicus GN=Uqcrc1 PE=1 SV=1 - [QCR1_RAT]	catalytic activity; metal ion binding; protein binding	mitochondrion; membrane	YFYDQCPAVAGYGPIEQLSDYNR
112	D3ZU74	Cytoplasmic dynein 1 intermediate chain 2 OS=Rattus norvegicus GN=Dync1i2 PE=4 SV=1 - [D3ZU74_RAT]	catalytic activity; motor activity; protein binding		TTPEYVFHCQSAVMSATFAK
114	D4A8H8	Cytoplasmic FMR1 interacting protein 1 (Predicted) OS=Rattus norvegicus GN=Cyfip1 PE=4 SV=1 - [D4A8H8_RAT]	protein binding	cytoplasm	CFQPPIHQSLASS
114	D4A8H8	Cytoplasmic FMR1 interacting protein 1 (Predicted) OS=Rattus norvegicus GN=Cyfip1 PE=4 SV=1 - [D4A8H8_RAT]	protein binding	cytoplasm	CNEQPNRVEIYEK
114	D4A8H8	Cytoplasmic FMR1 interacting protein 1 (Predicted) OS=Rattus norvegicus GN=Cyfip1 PE=4 SV=1 - [D4A8H8_RAT]	protein binding	cytoplasm	DCPDNAEEYER
114	D4A8H8	Cytoplasmic FMR1 interacting protein 1 (Predicted) OS=Rattus norvegicus GN=Cyfip1 PE=4 SV=1 - [D4A8H8_RAT]	protein binding	cytoplasm	TVCDWETGHEPFNDPALR
114	D4A8H8	Cytoplasmic FMR1 interacting protein 1 (Predicted) OS=Rattus norvegicus GN=Cyfip1 PE=4 SV=1 - [D4A8H8_RAT]	protein binding	cytoplasm	YSNKDCPDNAEEYER
116	Q4KLZ3	DAZ associated protein 1 OS=Rattus norvegicus GN=Dazap1 PE=2 SV=1 - [Q4KLZ3_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm	DPNCVGTVLASRPHTLDGR
116	Q4KLZ3	DAZ associated protein 1 OS=Rattus norvegicus GN=Dazap1 PE=2 SV=1 - [Q4KLZ3_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm	IFVGGIPHNCGETELR
116	Q4KLZ3	DAZ associated protein 1 OS=Rattus norvegicus GN=Dazap1 PE=2 SV=1 - [Q4KLZ3_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm	NIDPKPCTPR

116	Q4KLZ3	DAZ associated protein 1 OS=Rattus norvegicus GN=Dazap1 PE=2 SV=1 - [Q4KLZ3_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm	SYFSQYGEVVDCVIMK
117	A0A096MIX2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a OS=Rattus norvegicus GN=Ddx17 PE=4 SV=1 - [A0A096MIX2_RAT]	catalytic activity; nucleotide binding; protein binding; RNA binding	nucleus; membrane	CTYLVLDEADR
117	A0A096MIX2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a OS=Rattus norvegicus GN=Ddx17 PE=4 SV=1 - [A0A096MIX2_RAT]	catalytic activity; nucleotide binding; protein binding; RNA binding	nucleus; membrane	DGWPAMCIHGDK
117	A0A096MIX2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a OS=Rattus norvegicus GN=Ddx17 PE=4 SV=1 - [A0A096MIX2_RAT]	catalytic activity; nucleotide binding; protein binding; RNA binding	nucleus; membrane	ELAQQVQQVADDYGKCSR
117	A0A096MIX2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a OS=Rattus norvegicus GN=Ddx17 PE=4 SV=1 - [A0A096MIX2_RAT]	catalytic activity; nucleotide binding; protein binding; RNA binding	nucleus; membrane	RCDDLTR
117	A0A096MIX2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a OS=Rattus norvegicus GN=Ddx17 PE=4 SV=1 - [A0A096MIX2_RAT]	catalytic activity; nucleotide binding; protein binding; RNA binding	nucleus; membrane	RCTYLVLDEADR
117	A0A096MIX2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a OS=Rattus norvegicus GN=Ddx17 PE=4 SV=1 - [A0A096MIX2_RAT]	catalytic activity; nucleotide binding; protein binding; RNA binding	nucleus; membrane	TTSSANNPNLMYQDECDRRLR
118	G3V9M1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23 (Predicted), isoform CRA_b OS=Rattus norvegicus GN=Ddx23 PE=3 SV=1 - [G3V9M1_RAT]	nucleotide binding; DNA binding; catalytic activity; RNA binding	nucleus; mitochondrion; membrane; spliceosomal complex	MGYNACTLHGGK
119	Q6AYI1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 OS=Rattus norvegicus GN=Ddx5 PE=1 SV=1 - [Q6AYI1_RAT]	nucleotide binding; catalytic activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	CDELTR
119	Q6AYI1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 OS=Rattus norvegicus GN=Ddx5 PE=1 SV=1 - [Q6AYI1_RAT]	nucleotide binding; catalytic activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	LIDFLECGKTNLR
119	Q6AYI1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5 OS=Rattus norvegicus GN=Ddx5 PE=1 SV=1 - [Q6AYI1_RAT]	nucleotide binding; catalytic activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	RCDELTRK
121	D3ZD97	DEAH (Asp-Glu-Ala-His) box polypeptide 15 (Predicted), isoform CRA_b OS=Rattus norvegicus GN=Dhx15 PE=4 SV=1 - [D3ZD97_RAT]	nucleotide binding; RNA binding; catalytic activity	nucleus; spliceosomal complex; cytoplasm	IAPQYYDMSNFPQCEAK
121	D3ZD97	DEAH (Asp-Glu-Ala-His) box polypeptide 15 (Predicted), isoform CRA_b OS=Rattus norvegicus GN=Dhx15 PE=4 SV=1 - [D3ZD97_RAT]	nucleotide binding; RNA binding; catalytic activity	nucleus; spliceosomal complex; cytoplasm	TCTDIKPEWLVK
121	D3ZD97	DEAH (Asp-Glu-Ala-His) box polypeptide 15 (Predicted), isoform CRA_b OS=Rattus norvegicus GN=Dhx15 PE=4 SV=1 - [D3ZD97_RAT]	nucleotide binding; RNA binding; catalytic activity	nucleus; spliceosomal complex; cytoplasm	TTQIPQWCVEYMR
122	D4A9D6	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (Predicted) OS=Rattus norvegicus GN=Dhx9 PE=4 SV=1 - [D4A9D6_RAT]	nucleotide binding; protein binding; RNA binding; catalytic activity	nucleus; cytoplasm; membrane	AAECNIVVTQPR
122	D4A9D6	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (Predicted) OS=Rattus norvegicus GN=Dhx9 PE=4 SV=1 - [D4A9D6_RAT]	nucleotide binding; protein binding; RNA binding; catalytic activity	nucleus; cytoplasm; membrane	GEEPGKSCGYSVR
122	D4A9D6	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (Predicted) OS=Rattus norvegicus GN=Dhx9 PE=4 SV=1 - [D4A9D6_RAT]	nucleotide binding; protein binding; RNA binding; catalytic activity	nucleus; cytoplasm; membrane	LAAQSCALSLVR
122	D4A9D6	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (Predicted) OS=Rattus norvegicus GN=Dhx9 PE=4 SV=1 - [D4A9D6_RAT]	nucleotide binding; protein binding; RNA binding; catalytic activity	nucleus; cytoplasm; membrane	LQISHEAAACITALR
122	D4A9D6	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (Predicted) OS=Rattus norvegicus GN=Dhx9 PE=4 SV=1 - [D4A9D6_RAT]	nucleotide binding; protein binding; RNA binding; catalytic activity	nucleus; cytoplasm; membrane	MSGEEAEIRFCEQK
122	D4A9D6	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (Predicted) OS=Rattus norvegicus GN=Dhx9 PE=4 SV=1 - [D4A9D6_RAT]	nucleotide binding; protein binding; RNA binding; catalytic activity	nucleus; cytoplasm; membrane	NFLYAWCGK

122	D4A9D6	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (Predicted) OS=Rattus norvegicus GN=Dhx9 PE=4 SV=1 - [D4A9D6_RAT]	nucleotide binding; protein binding; RNA binding; catalytic activity	nucleus; cytoplasm; membrane	QKFMCEVR
122	D4A9D6	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (Predicted) OS=Rattus norvegicus GN=Dhx9 PE=4 SV=1 - [D4A9D6_RAT]	nucleotide binding; protein binding; RNA binding; catalytic activity	nucleus; cytoplasm; membrane	SSVNCPFSSQDMK
122	D4A9D6	DEAH (Asp-Glu-Ala-His) box polypeptide 9 (Predicted) OS=Rattus norvegicus GN=Dhx9 PE=4 SV=1 - [D4A9D6_RAT]	nucleotide binding; protein binding; RNA binding; catalytic activity	nucleus; cytoplasm; membrane	VAYERGEEPGKSCGYSVR
123	Q7M0E3	Destrin OS=Rattus norvegicus GN=Dstn PE=1 SV=3 - [DEST_RAT]	protein binding	cytoplasm; cytoskeleton	AVIFCLSADKK
123	Q7M0E3	Destrin OS=Rattus norvegicus GN=Dstn PE=1 SV=3 - [DEST_RAT]	protein binding	cytoplasm; cytoskeleton	CIVVEEGK
123	Q7M0E3	Destrin OS=Rattus norvegicus GN=Dstn PE=1 SV=3 - [DEST_RAT]	protein binding	cytoplasm; cytoskeleton	HFVGMLPEKDCR
123	Q7M0E3	Destrin OS=Rattus norvegicus GN=Dstn PE=1 SV=3 - [DEST_RAT]	protein binding	cytoplasm; cytoskeleton	VRKCSTPEEIK
124	G3V9K8	Developmentally regulated RNA-binding protein 1 OS=Rattus norvegicus GN=Rbm45 PE=4 SV=1 - [G3V9K8_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm	AMEEMHGQCLGPNDTKPIK
124	G3V9K8	Developmentally regulated RNA-binding protein 1 OS=Rattus norvegicus GN=Rbm45 PE=4 SV=1 - [G3V9K8_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm	VYGDIEYCSVIK
124	G3V9K8	Developmentally regulated RNA-binding protein 1 OS=Rattus norvegicus GN=Rbm45 PE=4 SV=1 - [G3V9K8_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm	YLKPSQAAQAIENCDR
126	Q62950	Dihydropyrimidinase-related protein 1 OS=Rattus norvegicus GN=Crmp1 PE=1 SV=1 - [DPYL1_RAT]	catalytic activity; protein binding	cytoplasm; cytoskeleton	INCPVYITK
126	Q62950	Dihydropyrimidinase-related protein 1 OS=Rattus norvegicus GN=Crmp1 PE=1 SV=1 - [DPYL1_RAT]	catalytic activity; protein binding	cytoplasm; cytoskeleton	STVEYNIFEGMECHGSPLVVISQGK
127	P47942	Dihydropyrimidinase-related protein 2 OS=Rattus norvegicus GN=Dpysl2 PE=1 SV=1 - [DPYL2_RAT]	protein binding; catalytic activity	cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	GLYDGPVCEVSVTPKTVTPASSAK
127	P47942	Dihydropyrimidinase-related protein 2 OS=Rattus norvegicus GN=Dpysl2 PE=1 SV=1 - [DPYL2_RAT]	protein binding; catalytic activity	cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	SITIANQTNCPLYVTK
127	P47942	Dihydropyrimidinase-related protein 2 OS=Rattus norvegicus GN=Dpysl2 PE=1 SV=1 - [DPYL2_RAT]	protein binding; catalytic activity	cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	THNSALEYNIFEGMECR
128	Q62952	Dihydropyrimidinase-related protein 3 OS=Rattus norvegicus GN=Dpysl3 PE=1 SV=2 - [DPYL3_RAT]	catalytic activity; protein binding	cytoplasm; cytosol	AITVASQTNCPLYVTK
128	Q62952	Dihydropyrimidinase-related protein 3 OS=Rattus norvegicus GN=Dpysl3 PE=1 SV=2 - [DPYL3_RAT]	catalytic activity; protein binding	cytoplasm; cytosol	FIPCSPFSDYVYK
128	Q62952	Dihydropyrimidinase-related protein 3 OS=Rattus norvegicus GN=Dpysl3 PE=1 SV=2 - [DPYL3_RAT]	catalytic activity; protein binding	cytoplasm; cytosol	GAPLVVICQGK
129	Q62951	Dihydropyrimidinase-related protein 4 (Fragment) OS=Rattus norvegicus GN=Dpysl4 PE=1 SV=1 - [DPYL4_RAT]	catalytic activity; protein binding	cytoplasm	LQMPVLGMTPADDFCQGTK
129	Q62951	Dihydropyrimidinase-related protein 4 (Fragment) OS=Rattus norvegicus GN=Dpysl4 PE=1 SV=1 - [DPYL4_RAT]	catalytic activity; protein binding	cytoplasm	QANCPLYITK
130	Q9JHU0	Dihydropyrimidinase-related protein 5 OS=Rattus norvegicus GN=Dpysl5 PE=1 SV=1 - [DPYL5_RAT]	protein binding; catalytic activity	cytoplasm	CHGVPLVTISR
130	Q9JHU0	Dihydropyrimidinase-related protein 5 OS=Rattus norvegicus GN=Dpysl5 PE=1 SV=1 - [DPYL5_RAT]	protein binding; catalytic activity	cytoplasm	DSELYQVFHACR
130	Q9JHU0	Dihydropyrimidinase-related protein 5 OS=Rattus norvegicus GN=Dpysl5 PE=1 SV=1 - [DPYL5_RAT]	protein binding; catalytic activity	cytoplasm	THCPIYLVNVSSISAGDVIAAAK
130	Q9JHU0	Dihydropyrimidinase-related protein 5 OS=Rattus norvegicus GN=Dpysl5 PE=1 SV=1 - [DPYL5_RAT]	protein binding; catalytic activity	cytoplasm	VVNDDCTHEADVYIENGIIQQVGR

130	Q9JHU0	Dihydropyrimidinase-related protein 5 OS=Rattus norvegicus GN=Dpysl5 PE=1 SV=1 - [DPYL5_RAT]	protein binding; catalytic activity	cytoplasm	VVYENGVFMCAEGTGK
131	Q6P730	Disabled homolog 2-interacting protein OS=Rattus norvegicus GN=Dab2ip PE=1 SV=1 - [DAB2P_RAT]	enzyme regulator activity; protein binding	cytoplasm; membrane	ALYESDENCEVDPSK
132	D4ABM3	Dishevelled associated activator of morphogenesis 1 (Predicted) OS=Rattus norvegicus GN=Daam1 PE=4 SV=1 - [D4ABM3_RAT]	protein binding	cytoplasm; membrane	AQNCNILLSR
132	D4ABM3	Dishevelled associated activator of morphogenesis 1 (Predicted) OS=Rattus norvegicus GN=Daam1 PE=4 SV=1 - [D4ABM3_RAT]	protein binding	cytoplasm; membrane	IHTSLIGCIK
134	Q9WUL0	DNA topoisomerase 1 OS=Rattus norvegicus GN=Top1 PE=2 SV=1 - [TOP1_RAT]	DNA binding; catalytic activity; nucleotide binding; protein binding; RNA binding	chromosome; nucleus; cytoplasm	AVAILCNHQR
134	Q9WUL0	DNA topoisomerase 1 OS=Rattus norvegicus GN=Top1 PE=2 SV=1 - [TOP1_RAT]	DNA binding; catalytic activity; nucleotide binding; protein binding; RNA binding	chromosome; nucleus; cytoplasm	CDFTQMSQYFK
134	Q9WUL0	DNA topoisomerase 1 OS=Rattus norvegicus GN=Top1 PE=2 SV=1 - [TOP1_RAT]	DNA binding; catalytic activity; nucleotide binding; protein binding; RNA binding	chromosome; nucleus; cytoplasm	EYGFCVMDNHR
134	Q9WUL0	DNA topoisomerase 1 OS=Rattus norvegicus GN=Top1 PE=2 SV=1 - [TOP1_RAT]	DNA binding; catalytic activity; nucleotide binding; protein binding; RNA binding	chromosome; nucleus; cytoplasm	ITVAWCK
134	Q9WUL0	DNA topoisomerase 1 OS=Rattus norvegicus GN=Top1 PE=2 SV=1 - [TOP1_RAT]	DNA binding; catalytic activity; nucleotide binding; protein binding; RNA binding	chromosome; nucleus; cytoplasm	RIMPEDIIINCSK
135	F1M7A0	DNA topoisomerase 2 (Fragment) OS=Rattus norvegicus GN=Top2a PE=3 SV=2 - [F1M7A0_RAT]	nucleotide binding; metal ion binding; DNA binding; catalytic activity; protein binding	chromosome; nucleus	LCNIFSTK
136	P43138	DNA-(apurinic or apyrimidinic site) lyase OS=Rattus norvegicus GN=Apex1 PE=1 SV=2 - [APEX1_RAT]	DNA binding; RNA binding; catalytic activity; protein binding; metal ion binding	nucleus; cytoplasm; mitochondrion; endoplasmic reticulum	EEAPDILCLQETK
136	P43138	DNA-(apurinic or apyrimidinic site) lyase OS=Rattus norvegicus GN=Apex1 PE=1 SV=2 - [APEX1_RAT]	DNA binding; RNA binding; catalytic activity; protein binding; metal ion binding	nucleus; cytoplasm; mitochondrion; endoplasmic reticulum	ICSWNVDGLR
137	P07153	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Rattus norvegicus GN=Rpn1 PE=2 SV=1 - [RPN1_RAT]	catalytic activity; RNA binding	endoplasmic reticulum; membrane	LKTEGSDLCDRVSEMQK
137	P07153	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Rattus norvegicus GN=Rpn1 PE=2 SV=1 - [RPN1_RAT]	catalytic activity; RNA binding	endoplasmic reticulum; membrane	TEGSDLCDRVSEMQK
137	P07153	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Rattus norvegicus GN=Rpn1 PE=2 SV=1 - [RPN1_RAT]	catalytic activity; RNA binding	endoplasmic reticulum; membrane	VACITEQVLTLVNK
138	Q07266	Drebrin OS=Rattus norvegicus GN=Dbn1 PE=1 SV=3 - [DREB_RAT]	protein binding	cytoplasm; membrane; cytoskeleton	LDGEEVCKEAK
138	Q07266	Drebrin OS=Rattus norvegicus GN=Dbn1 PE=1 SV=3 - [DREB_RAT]	protein binding	cytoplasm; membrane; cytoskeleton	TPNLSSSLPCSHLDSHR
138	Q07266	Drebrin OS=Rattus norvegicus GN=Dbn1 PE=1 SV=3 - [DREB_RAT]	protein binding	cytoplasm; membrane; cytoskeleton	VAAAPQVWAGCAEEPPR
138	Q07266	Drebrin OS=Rattus norvegicus GN=Dbn1 PE=1 SV=3 - [DREB_RAT]	protein binding	cytoplasm; membrane; cytoskeleton	VMYGFCSVK
144	A0A0A0MY48	Dynamin-2 OS=Rattus norvegicus GN=Dnm2 PE=4 SV=1 - [A0A0A0MY48_RAT]			TEYAEFLHCK
146	D4AAL9	Dynamin-3 OS=Rattus norvegicus GN=Dnm3 PE=3 SV=2 - [D4AAL9_RAT]	nucleotide binding; catalytic activity		AEYAEFLHCK
146	D4AAL9	Dynamin-3 OS=Rattus norvegicus GN=Dnm3 PE=3 SV=2 - [D4AAL9_RAT]	nucleotide binding; catalytic activity		LCEETER
146	D4AAL9	Dynamin-3 OS=Rattus norvegicus GN=Dnm3 PE=3 SV=2 - [D4AAL9_RAT]	nucleotide binding; catalytic activity		SLELACDSQEDVDSWK
148	P63170	Dynein light chain 1, cytoplasmic OS=Rattus norvegicus GN=Dynll1 PE=1 SV=1 - [DYL1_RAT]	catalytic activity; motor activity; enzyme regulator activity; protein binding	chromosome; nucleus; cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	KAVIKNADMSEEMQQDSVECATQALEK
149	Q78P75	Dynein light chain 2, cytoplasmic OS=Rattus norvegicus GN=Dynll2 PE=1 SV=1 - [DYL2_RAT]	catalytic activity; motor activity; protein binding	nucleus; cytoplasm; cytoskeleton; membrane	NADMSEDMQQDAVDCATQAMEK

150	Q9Z336	Dynein light chain Tctex-type 1 OS=Rattus norvegicus GN=Dynlt1 PE=1 SV=1 - [DYLT1_RAT]	catalytic activity; motor activity; protein binding	cytoplasm; Golgi; cytoskeleton	YIVTCVIMQK
152	F1LP64	E3 ubiquitin-protein ligase TRIP12 OS=Rattus norvegicus GN=Trip12 PE=2 SV=1 - [TRIPC_RAT]	catalytic activity; protein binding	nucleus; cytoplasm	AGCSTITDSSSAASTSSSSSAVASASSTVPAGAR
152	F1LP64	E3 ubiquitin-protein ligase TRIP12 OS=Rattus norvegicus GN=Trip12 PE=2 SV=1 - [TRIPC_RAT]	catalytic activity; protein binding	nucleus; cytoplasm	EDEESSKDCVGGK
152	F1LP64	E3 ubiquitin-protein ligase TRIP12 OS=Rattus norvegicus GN=Trip12 PE=2 SV=1 - [TRIPC_RAT]	catalytic activity; protein binding	nucleus; cytoplasm	MNNCLSQMEQFPVK
152	F1LP64	E3 ubiquitin-protein ligase TRIP12 OS=Rattus norvegicus GN=Trip12 PE=2 SV=1 - [TRIPC_RAT]	catalytic activity; protein binding	nucleus; cytoplasm	SCSSSSAVIVPQPEDPDR
152	F1LP64	E3 ubiquitin-protein ligase TRIP12 OS=Rattus norvegicus GN=Trip12 PE=2 SV=1 - [TRIPC_RAT]	catalytic activity; protein binding	nucleus; cytoplasm	TCPFFFPFDTR
153	O09032	ELAV-like protein 4 OS=Rattus norvegicus GN=Elavl4 PE=1 SV=1 - [ELAV4_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; cytosol; cytoskeleton; membrane; ribosome	LMSGPVPPSACPPR
153	O09032	ELAV-like protein 4 OS=Rattus norvegicus GN=Elavl4 PE=1 SV=1 - [ELAV4_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; cytosol; cytoskeleton; membrane; ribosome	NCPSPMQTGAATDDSK
155	G3V6U4	ELAV-like protein OS=Rattus norvegicus GN=Elavl2 PE=3 SV=2 - [G3V6U4_RAT]	nucleotide binding; RNA binding		SLFGSIGEIESCK
156	Q76IJ9	ELAV-like protein OS=Rattus norvegicus GN=Elavl3 PE=2 SV=1 - [Q76IJ9_RAT]	nucleotide binding; RNA binding		SLFGSIGDIESCK
157	F1LPE9	ELKS/Rab6-interacting/CAST family member 1 OS=Rattus norvegicus GN=Erc1 PE=4 SV=1 - [F1LPE9_RAT]	protein binding	cytoplasm	TGEPCVAELTEENFQR
158	M0R757	Elongation factor 1-alpha OS=Rattus norvegicus GN=LOC100360413 PE=3 SV=1 - [M0R757_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; membrane	KDGSASGTTLLEALDCILPPTRPTDKPLR
158	M0R757	Elongation factor 1-alpha OS=Rattus norvegicus GN=LOC100360413 PE=3 SV=1 - [M0R757_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; membrane	NMITGTSQADCAVLIVAAGVGEFEAGISK
158	M0R757	Elongation factor 1-alpha OS=Rattus norvegicus GN=LOC100360413 PE=3 SV=1 - [M0R757_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; membrane	SGDAAIVDMVPGKPMCVESFSDYPPLGR
159	Q68FR9	Elongation factor 1-delta OS=Rattus norvegicus GN=Eef1d PE=1 SV=2 - [EF1D_RAT]	DNA binding; RNA binding; signal transducer activity	nucleus; cytoplasm	LQIQCVVEDDK
160	Q68FR6	Elongation factor 1-gamma OS=Rattus norvegicus GN=Eef1g PE=1 SV=3 - [EF1G_RAT]	RNA binding; protein binding	nucleus; membrane	AILGEVKLCEK
160	Q68FR6	Elongation factor 1-gamma OS=Rattus norvegicus GN=Eef1g PE=1 SV=3 - [EF1G_RAT]	RNA binding; protein binding	nucleus; membrane	KAAAPAPEEEMDECEQALAAEPK
161	P05197	Elongation factor 2 OS=Rattus norvegicus GN=Eef2 PE=1 SV=4 - [EF2_RAT]	nucleotide binding; RNA binding; catalytic activity; translation regulator activity; protein binding	nucleus; cytoplasm; membrane	CLYASVLTAQPR
161	P05197	Elongation factor 2 OS=Rattus norvegicus GN=Eef2 PE=1 SV=4 - [EF2_RAT]	nucleotide binding; RNA binding; catalytic activity; translation regulator activity; protein binding	nucleus; cytoplasm; membrane	DLEEDHACIPIKK
161	P05197	Elongation factor 2 OS=Rattus norvegicus GN=Eef2 PE=1 SV=4 - [EF2_RAT]	nucleotide binding; RNA binding; catalytic activity; translation regulator activity; protein binding	nucleus; cytoplasm; membrane	EGALCEENMR
161	P05197	Elongation factor 2 OS=Rattus norvegicus GN=Eef2 PE=1 SV=4 - [EF2_RAT]	nucleotide binding; RNA binding; catalytic activity; translation regulator activity; protein binding	nucleus; cytoplasm; membrane	ETVSEESNVLCLSK
161	P05197	Elongation factor 2 OS=Rattus norvegicus GN=Eef2 PE=1 SV=4 - [EF2_RAT]	nucleotide binding; RNA binding; catalytic activity; translation regulator activity; protein binding	nucleus; cytoplasm; membrane	IWCFGPDGTGPNILTDITK
161	P05197	Elongation factor 2 OS=Rattus norvegicus GN=Eef2 PE=1 SV=4 - [EF2_RAT]	nucleotide binding; RNA binding; catalytic activity; translation regulator activity; protein binding	nucleus; cytoplasm; membrane	STLTDSLVCK
161	P05197	Elongation factor 2 OS=Rattus norvegicus GN=Eef2 PE=1 SV=4 - [EF2_RAT]	nucleotide binding; RNA binding; catalytic activity; translation regulator activity; protein binding	nucleus; cytoplasm; membrane	YRCELLYEGPPDDEAAMGIK
162	P85834	Elongation factor Tu, mitochondrial OS=Rattus norvegicus GN=Tufm PE=1 SV=1 - [EFTU_RAT]	nucleotide binding; RNA binding; catalytic activity	mitochondrion; membrane	GEETPVIVGSALCALEQR
162	P85834	Elongation factor Tu, mitochondrial OS=Rattus norvegicus GN=Tufm PE=1 SV=1 - [EFTU_RAT]	nucleotide binding; RNA binding; catalytic activity	mitochondrion; membrane	KGDECELLGHNK
164	A0A0A0MY09	Endoplasmin OS=Rattus norvegicus GN=Hsp90b1 PE=4 SV=1 - [A0A0A0MY09_RAT]			LTESPCALVASQYGWSGNMER
165	Q5XIC0	Enoyl-CoA delta isomerase 2, mitochondrial OS=Rattus norvegicus GN=Eci2 PE=1 SV=1 - [ECI2_RAT]	catalytic activity; protein binding	nucleus; mitochondrion; organelle lumen; membrane	LHAVNEEECTTLR

166	Q66HT2	Epidermal Langerhans cell protein LCP1 OS=Rattus norvegicus GN=Tox4 PE=2 SV=1 - [Q66HT2_RAT]	DNA binding; protein binding	chromosome; nucleus	SGCENPPVISK
167	P56571	ES1 protein homolog, mitochondrial OS=Rattus norvegicus PE=1 SV=2 - [ES1_RAT]		mitochondrion	NLSTFAVDGKDCK
171	P81795	Eukaryotic translation initiation factor 2 subunit 3 OS=Rattus norvegicus GN=Eif2s3 PE=1 SV=2 - [IF2G_RAT]	nucleotide binding; RNA binding; catalytic activity		IVLTNPVCTEVGEK
171	P81795	Eukaryotic translation initiation factor 2 subunit 3 OS=Rattus norvegicus GN=Eif2s3 PE=1 SV=2 - [IF2G_RAT]	nucleotide binding; RNA binding; catalytic activity		SCGSSTPDEFPTDIPGTK
171	P81795	Eukaryotic translation initiation factor 2 subunit 3 OS=Rattus norvegicus GN=Eif2s3 PE=1 SV=2 - [IF2G_RAT]	nucleotide binding; RNA binding; catalytic activity		SFDVNKPGCEVDDLKGGVAGGSILK
172	Q6P685	Eukaryotic translation initiation factor 2, subunit 2 (Beta) OS=Rattus norvegicus GN=Eif2s2 PE=2 SV=1 - [Q6P685_RAT]	RNA binding; protein binding		CSVASIK
172	Q6P685	Eukaryotic translation initiation factor 2, subunit 2 (Beta) OS=Rattus norvegicus GN=Eif2s2 PE=2 SV=1 - [Q6P685_RAT]	RNA binding; protein binding		TSFVNFTDICK
173	B5DFC8	Eukaryotic translation initiation factor 3 subunit C OS=Rattus norvegicus GN=Eif3c PE=2 SV=1 - [EIF3C_RAT]	RNA binding; protein binding	cytoplasm	GCILTLVER
173	B5DFC8	Eukaryotic translation initiation factor 3 subunit C OS=Rattus norvegicus GN=Eif3c PE=2 SV=1 - [EIF3C_RAT]	RNA binding; protein binding	cytoplasm	GTTEEICQIYLR
173	B5DFC8	Eukaryotic translation initiation factor 3 subunit C OS=Rattus norvegicus GN=Eif3c PE=2 SV=1 - [EIF3C_RAT]	RNA binding; protein binding	cytoplasm	TCHSFIINEK
174	Q5RK09	Eukaryotic translation initiation factor 3 subunit G OS=Rattus norvegicus GN=Eif3g PE=2 SV=1 - [EIF3G_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm	EDLNCQEEEDPMNK
177	Q3T1J1	Eukaryotic translation initiation factor 5A-1 OS=Rattus norvegicus GN=Eif5a PE=1 SV=3 - [IF5A1_RAT]	RNA binding; protein binding	nucleus; cytoplasm; endoplasmic reticulum; membrane	KYEDICPSTHNMDVPNIK
177	Q3T1J1	Eukaryotic translation initiation factor 5A-1 OS=Rattus norvegicus GN=Eif5a PE=1 SV=3 - [IF5A1_RAT]	RNA binding; protein binding	nucleus; cytoplasm; endoplasmic reticulum; membrane	YEDICPSTHNMDVPNIK
179	Q5XI32	F-actin-capping protein subunit beta OS=Rattus norvegicus GN=Capzb PE=1 SV=1 - [CAPZB_RAT]	protein binding	cytoplasm; cytoskeleton; membrane	DETVSDCSPHIANIGR
179	Q5XI32	F-actin-capping protein subunit beta OS=Rattus norvegicus GN=Capzb PE=1 SV=1 - [CAPZB_RAT]	protein binding	cytoplasm; cytoskeleton; membrane	DYLLCDYNR
179	Q5XI32	F-actin-capping protein subunit beta OS=Rattus norvegicus GN=Capzb PE=1 SV=1 - [CAPZB_RAT]	protein binding	cytoplasm; cytoskeleton; membrane	GCWDSIHVVEVQEK
179	Q5XI32	F-actin-capping protein subunit beta OS=Rattus norvegicus GN=Capzb PE=1 SV=1 - [CAPZB_RAT]	protein binding	cytoplasm; cytoskeleton; membrane	QMEKDETVSDCSPHIANIGR
180	B5DF95	Family with sequence similarity 164, member A OS=Rattus norvegicus GN=Zc2hc1a PE=2 SV=1 - [B5DF95_RAT]			HINFCK
181	M0R961	Far upstream element-binding protein 2 OS=Rattus norvegicus GN=Khsrp PE=4 SV=1 - [M0R961_RAT]	DNA binding; RNA binding; protein binding	nucleus; cytoplasm; membrane	CGLVIGR
181	M0R961	Far upstream element-binding protein 2 OS=Rattus norvegicus GN=Khsrp PE=4 SV=1 - [M0R961_RAT]	DNA binding; RNA binding; protein binding	nucleus; cytoplasm; membrane	IQQDSGCKVQISPDSGGLPER
181	M0R961	Far upstream element-binding protein 2 OS=Rattus norvegicus GN=Khsrp PE=4 SV=1 - [M0R961_RAT]	DNA binding; RNA binding; protein binding	nucleus; cytoplasm; membrane	VQQACEMVMDILR
182	P85845	Fascin OS=Rattus norvegicus GN=Fscn1 PE=1 SV=2 - [FSCN1_RAT]	protein binding; RNA binding	cytoplasm; cytosol; cytoskeleton; membrane	DGNVTCER
182	P85845	Fascin OS=Rattus norvegicus GN=Fscn1 PE=1 SV=2 - [FSCN1_RAT]	protein binding; RNA binding	cytoplasm; cytosol; cytoskeleton; membrane	GEHGFIGCR

182	P85845	Fascin OS=Rattus norvegicus GN=Fscn1 PE=1 SV=2 - [FSCN1_RAT]	protein binding; RNA binding	cytoplasm; cytosol; cytoskeleton; membrane	KQIWTLEQPPDEAGSAAVCLR
182	P85845	Fascin OS=Rattus norvegicus GN=Fscn1 PE=1 SV=2 - [FSCN1_RAT]	protein binding; RNA binding	cytoplasm; cytosol; cytoskeleton; membrane	LSCFAQSVSPAEK
182	P85845	Fascin OS=Rattus norvegicus GN=Fscn1 PE=1 SV=2 - [FSCN1_RAT]	protein binding; RNA binding	cytoplasm; cytosol; cytoskeleton; membrane	QIWTLEQPPDEAGSAAVCLR
182	P85845	Fascin OS=Rattus norvegicus GN=Fscn1 PE=1 SV=2 - [FSCN1_RAT]	protein binding; RNA binding	cytoplasm; cytosol; cytoskeleton; membrane	VAFRDCEGR
182	P85845	Fascin OS=Rattus norvegicus GN=Fscn1 PE=1 SV=2 - [FSCN1_RAT]	protein binding; RNA binding	cytoplasm; cytosol; cytoskeleton; membrane	YFGGTEDRLSCFAQSVSPAEK
183	C0JPT7	Filamin alpha OS=Rattus norvegicus GN=Flna PE=2 SV=1 - [C0JPT7_RAT]	protein binding; signal transducer activity; RNA binding	nucleus; cytoplasm; cytosol; membrane; cytoskeleton	AHVVPCFDASK
183	C0JPT7	Filamin alpha OS=Rattus norvegicus GN=Flna PE=2 SV=1 - [C0JPT7_RAT]	protein binding; signal transducer activity; RNA binding	nucleus; cytoplasm; cytosol; membrane; cytoskeleton	APSVANVGSHCDLSLK
183	C0JPT7	Filamin alpha OS=Rattus norvegicus GN=Flna PE=2 SV=1 - [C0JPT7_RAT]	protein binding; signal transducer activity; RNA binding	nucleus; cytoplasm; cytosol; membrane; cytoskeleton	CSGPGLER
183	C0JPT7	Filamin alpha OS=Rattus norvegicus GN=Flna PE=2 SV=1 - [C0JPT7_RAT]	protein binding; signal transducer activity; RNA binding	nucleus; cytoplasm; cytosol; membrane; cytoskeleton	DNGNGTYSCSYVPR
183	C0JPT7	Filamin alpha OS=Rattus norvegicus GN=Flna PE=2 SV=1 - [C0JPT7_RAT]	protein binding; signal transducer activity; RNA binding	nucleus; cytoplasm; cytosol; membrane; cytoskeleton	IVSPSGAAVPCKVEPGLGADNSVVR
183	C0JPT7	Filamin alpha OS=Rattus norvegicus GN=Flna PE=2 SV=1 - [C0JPT7_RAT]	protein binding; signal transducer activity; RNA binding	nucleus; cytoplasm; cytosol; membrane; cytoskeleton	LQVEPAVDTSGVQCYGPGIEGQGVFR
183	C0JPT7	Filamin alpha OS=Rattus norvegicus GN=Flna PE=2 SV=1 - [C0JPT7_RAT]	protein binding; signal transducer activity; RNA binding	nucleus; cytoplasm; cytosol; membrane; cytoskeleton	SNFTVDCSK
183	C0JPT7	Filamin alpha OS=Rattus norvegicus GN=Flna PE=2 SV=1 - [C0JPT7_RAT]	protein binding; signal transducer activity; RNA binding	nucleus; cytoplasm; cytosol; membrane; cytoskeleton	THEAEIVEGENHTYCIR
183	C0JPT7	Filamin alpha OS=Rattus norvegicus GN=Flna PE=2 SV=1 - [C0JPT7_RAT]	protein binding; signal transducer activity; RNA binding	nucleus; cytoplasm; cytosol; membrane; cytoskeleton	TPCEEILVK
183	C0JPT7	Filamin alpha OS=Rattus norvegicus GN=Flna PE=2 SV=1 - [C0JPT7_RAT]	protein binding; signal transducer activity; RNA binding	nucleus; cytoplasm; cytosol; membrane; cytoskeleton	VANPSGNLTDTYVQDCGDGTYK
183	C0JPT7	Filamin alpha OS=Rattus norvegicus GN=Flna PE=2 SV=1 - [C0JPT7_RAT]	protein binding; signal transducer activity; RNA binding	nucleus; cytoplasm; cytosol; membrane; cytoskeleton	VDINTEDLEDGTCR
183	C0JPT7	Filamin alpha OS=Rattus norvegicus GN=Flna PE=2 SV=1 - [C0JPT7_RAT]	protein binding; signal transducer activity; RNA binding	nucleus; cytoplasm; cytosol; membrane; cytoskeleton	VHSPSGALEECYVTEIDQDK
184	Q5RKI5	Flightless I homolog (Drosophila) OS=Rattus norvegicus GN=Flii PE=2 SV=1 - [Q5RKI5_RAT]	protein binding	nucleus; cytoplasm	ACQVYIQHTR
184	Q5RKI5	Flightless I homolog (Drosophila) OS=Rattus norvegicus GN=Flii PE=2 SV=1 - [Q5RKI5_RAT]	protein binding	nucleus; cytoplasm	ACSAIHAVNLR
184	Q5RKI5	Flightless I homolog (Drosophila) OS=Rattus norvegicus GN=Flii PE=2 SV=1 - [Q5RKI5_RAT]	protein binding	nucleus; cytoplasm	NQLTSLPSAICK
184	Q5RKI5	Flightless I homolog (Drosophila) OS=Rattus norvegicus GN=Flii PE=2 SV=1 - [Q5RKI5_RAT]	protein binding	nucleus; cytoplasm	NYLGAECR
184	Q5RKI5	Flightless I homolog (Drosophila) OS=Rattus norvegicus GN=Flii PE=2 SV=1 - [Q5RKI5_RAT]	protein binding	nucleus; cytoplasm	TGLCYLPEELAALQK
184	Q5RKI5	Flightless I homolog (Drosophila) OS=Rattus norvegicus GN=Flii PE=2 SV=1 - [Q5RKI5_RAT]	protein binding	nucleus; cytoplasm	VPECLYTLPNLHR
190	F1LNV7	General transcription factor 3C polypeptide 1 OS=Rattus norvegicus GN=Gtf3c1 PE=4 SV=1 - [F1LNV7_RAT]		nucleus	ADAELCADKEEHFELDREPTPGR
190	F1LNV7	General transcription factor 3C polypeptide 1 OS=Rattus norvegicus GN=Gtf3c1 PE=4 SV=1 - [F1LNV7_RAT]		nucleus	CTMVEAFSR
190	F1LNV7	General transcription factor 3C polypeptide 1 OS=Rattus norvegicus GN=Gtf3c1 PE=4 SV=1 - [F1LNV7_RAT]		nucleus	FPTTVCTESFQFYDR
190	F1LNV7	General transcription factor 3C polypeptide 1 OS=Rattus norvegicus GN=Gtf3c1 PE=4 SV=1 - [F1LNV7_RAT]		nucleus	GLESLGCIQK
190	F1LNV7	General transcription factor 3C polypeptide 1 OS=Rattus norvegicus GN=Gtf3c1 PE=4 SV=1 - [F1LNV7_RAT]		nucleus	KCAMLEYTTGSR

190	F1LNV7	General transcription factor 3C polypeptide 1 OS=Rattus norvegicus GN=Gtf3c1 PE=4 SV=1 - [F1LNV7_RAT]		nucleus	LNMPVCK
190	F1LNV7	General transcription factor 3C polypeptide 1 OS=Rattus norvegicus GN=Gtf3c1 PE=4 SV=1 - [F1LNV7_RAT]		nucleus	LREELGLCER
190	F1LNV7	General transcription factor 3C polypeptide 1 OS=Rattus norvegicus GN=Gtf3c1 PE=4 SV=1 - [F1LNV7_RAT]		nucleus	NLNPNDSIVVNSCQVK
190	F1LNV7	General transcription factor 3C polypeptide 1 OS=Rattus norvegicus GN=Gtf3c1 PE=4 SV=1 - [F1LNV7_RAT]		nucleus	RPYCSIQSPETDAEEATR
190	F1LNV7	General transcription factor 3C polypeptide 1 OS=Rattus norvegicus GN=Gtf3c1 PE=4 SV=1 - [F1LNV7_RAT]		nucleus	VCLAEVYQDK
191	Q5U2Y1	General transcription factor II-I OS=Rattus norvegicus GN=Gtf2i PE=2 SV=2 - [GTF2I_RAT]	DNA binding; protein binding	nucleus; cytoplasm; membrane	VMAADADRPMLSPGGSCGPIK
192	D4A7Q9	General transcription factor IIIC, polypeptide 3, 102kDa (Predicted) OS=Rattus norvegicus GN=Gtf3c3 PE=4 SV=1 - [D4A7Q9_RAT]	protein binding		AAETVTCSIPDSVPIDITVK
192	D4A7Q9	General transcription factor IIIC, polypeptide 3, 102kDa (Predicted) OS=Rattus norvegicus GN=Gtf3c3 PE=4 SV=1 - [D4A7Q9_RAT]	protein binding		AQVCLISSSK
192	D4A7Q9	General transcription factor IIIC, polypeptide 3, 102kDa (Predicted) OS=Rattus norvegicus GN=Gtf3c3 PE=4 SV=1 - [D4A7Q9_RAT]	protein binding		GPCQESFYNLGR
194	M0R660	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus GN=RGD1565368 PE=3 SV=1 - [M0R660_RAT]	catalytic activity; nucleotide binding	cytoplasm; membrane	VPTPNVSVVDLTCRLEKPAK
197	P18266	Glycogen synthase kinase-3 beta OS=Rattus norvegicus GN=Gsk3b PE=1 SV=1 - [GSK3B_RAT]	nucleotide binding; protein binding; catalytic activity	nucleus; cytoplasm; cytosol; membrane	GEPNVSYICSR
197	P18266	Glycogen synthase kinase-3 beta OS=Rattus norvegicus GN=Gsk3b PE=1 SV=1 - [GSK3B_RAT]	nucleotide binding; protein binding; catalytic activity	nucleus; cytoplasm; cytosol; membrane	KLDHCNIVR
197	P18266	Glycogen synthase kinase-3 beta OS=Rattus norvegicus GN=Gsk3b PE=1 SV=1 - [GSK3B_RAT]	nucleotide binding; protein binding; catalytic activity	nucleus; cytoplasm; cytosol; membrane	LCDFGSAK
197	P18266	Glycogen synthase kinase-3 beta OS=Rattus norvegicus GN=Gsk3b PE=1 SV=1 - [GSK3B_RAT]	nucleotide binding; protein binding; catalytic activity	nucleus; cytoplasm; cytosol; membrane	LCDSGELVAIK
197	P18266	Glycogen synthase kinase-3 beta OS=Rattus norvegicus GN=Gsk3b PE=1 SV=1 - [GSK3B_RAT]	nucleotide binding; protein binding; catalytic activity	nucleus; cytoplasm; cytosol; membrane	LTPLEACAHSFFDELRDPNVK
197	P18266	Glycogen synthase kinase-3 beta OS=Rattus norvegicus GN=Gsk3b PE=1 SV=1 - [GSK3B_RAT]	nucleotide binding; protein binding; catalytic activity	nucleus; cytoplasm; cytosol; membrane	TPPEAIALCSR
197	P18266	Glycogen synthase kinase-3 beta OS=Rattus norvegicus GN=Gsk3b PE=1 SV=1 - [GSK3B_RAT]	nucleotide binding; protein binding; catalytic activity	nucleus; cytoplasm; cytosol; membrane	TTSFAESCKPVQQPSAFGSMK
198	M0R4R4	Growth arrest-specific protein 7 (Fragment) OS=Rattus norvegicus GN=Gas7 PE=4 SV=1 - [M0R4R4_RAT]	protein binding		CVDLYNQAQSK
198	M0R4R4	Growth arrest-specific protein 7 (Fragment) OS=Rattus norvegicus GN=Gas7 PE=4 SV=1 - [M0R4R4_RAT]	protein binding		QHLCQYTQLR
198	M0R4R4	Growth arrest-specific protein 7 (Fragment) OS=Rattus norvegicus GN=Gas7 PE=4 SV=1 - [M0R4R4_RAT]	protein binding		YYVNTTTNETTWECPSSSSGISASPGPHR
200	D4AE68	Guanine nucleotide binding protein, alpha q polypeptide, isoform CRA_a OS=Rattus norvegicus GN=Gnaq PE=4 SV=2 - [D4AE68_RAT]	nucleotide binding; protein binding; catalytic activity; signal transducer activity; enzyme regulator activity; metal ion binding	membrane; cytosol	SLWNDPGIQECYDR
201	P10824	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Rattus norvegicus GN=Gnai1 PE=1 SV=3 - [GNAI1_RAT]	nucleotide binding; protein binding; catalytic activity; signal transducer activity; enzyme regulator activity; metal ion binding	nucleus; cytoplasm; membrane; Golgi; cytoskeleton	DSGVQACFNR
201	P10824	Guanine nucleotide-binding protein G(i) subunit alpha-1 OS=Rattus norvegicus GN=Gnai1 PE=1 SV=3 - [GNAI1_RAT]	nucleotide binding; protein binding; catalytic activity; signal transducer activity; enzyme regulator activity; metal ion binding	nucleus; cytoplasm; membrane; Golgi; cytoskeleton	IIHEAGYSEEECKQYK
202	P04897	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Rattus norvegicus GN=Gnai2 PE=1 SV=3 - [GNAI2_RAT]	nucleotide binding; protein binding; catalytic activity; signal transducer activity; metal ion binding	nucleus; cytoplasm; cytosol; cytoskeleton; membrane	IIHEDGYSEEECR

202	P04897	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Rattus norvegicus GN=Gnai2 PE=1 SV=3 - [GNAI2_RAT]	nucleotide binding; protein binding; catalytic activity; signal transducer activity; metal ion binding	nucleus; cytoplasm; cytosol; cytoskeleton; membrane	ITQSPLTICFPEYTGANK
203	P54311	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Rattus norvegicus GN=Gnb1 PE=1 SV=4 - [GBB1_RAT]	protein binding; catalytic activity; signal transducer activity	membrane	KACADATLSQITNNIDPVGR
203	P54311	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Rattus norvegicus GN=Gnb1 PE=1 SV=4 - [GBB1_RAT]	protein binding; catalytic activity; signal transducer activity	membrane	LFVSGACDASAK
204	P54313	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Rattus norvegicus GN=Gnb2 PE=1 SV=4 - [GBB2_RAT]	signal transducer activity; protein binding	cytoplasm; membrane	KACGDSTLTQITAGLDPVGR
204	P54313	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Rattus norvegicus GN=Gnb2 PE=1 SV=4 - [GBB2_RAT]	signal transducer activity; protein binding	cytoplasm; membrane	TFVSGACDASIK
205	P08753	Guanine nucleotide-binding protein G(k) subunit alpha OS=Rattus norvegicus GN=Gnai3 PE=1 SV=3 - [GNAI3_RAT]	nucleotide binding; catalytic activity; signal transducer activity; protein binding; metal ion binding	membrane; cytoplasm; Golgi; cytoskeleton	DGGVQACFSR
205	P08753	Guanine nucleotide-binding protein G(k) subunit alpha OS=Rattus norvegicus GN=Gnai3 PE=1 SV=3 - [GNAI3_RAT]	nucleotide binding; catalytic activity; signal transducer activity; protein binding; metal ion binding	membrane; cytoplasm; Golgi; cytoskeleton	EVYTHFTCATDTK
205	P08753	Guanine nucleotide-binding protein G(k) subunit alpha OS=Rattus norvegicus GN=Gnai3 PE=1 SV=3 - [GNAI3_RAT]	nucleotide binding; catalytic activity; signal transducer activity; protein binding; metal ion binding	membrane; cytoplasm; Golgi; cytoskeleton	IIHEDGYSEDECKQYK
205	P08753	Guanine nucleotide-binding protein G(k) subunit alpha OS=Rattus norvegicus GN=Gnai3 PE=1 SV=3 - [GNAI3_RAT]	nucleotide binding; catalytic activity; signal transducer activity; protein binding; metal ion binding	membrane; cytoplasm; Golgi; cytoskeleton	NNLKECGLY
207	P63095	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Rattus norvegicus GN=Gnas PE=1 SV=1 - [GNAS2_RAT]	nucleotide binding; protein binding; catalytic activity; signal transducer activity; metal ion binding	extracellular; nucleus; cytoplasm; endosome; cytosol; membrane	VFNDCRDIIQR
209	P63245	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Rattus norvegicus GN=Gnb2l1 PE=1 SV=3 - [GBLP_RAT]	protein binding; enzyme regulator activity; RNA binding	nucleus; cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	FSPNSSNPIIVSCGWDK
209	P63245	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Rattus norvegicus GN=Gnb2l1 PE=1 SV=3 - [GBLP_RAT]	protein binding; enzyme regulator activity; RNA binding	nucleus; cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	LWNTLGVCK
209	P63245	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Rattus norvegicus GN=Gnb2l1 PE=1 SV=3 - [GBLP_RAT]	protein binding; enzyme regulator activity; RNA binding	nucleus; cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	TNHIGHTGYLNTVTVSPDGSLCASGGK
209	P63245	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Rattus norvegicus GN=Gnb2l1 PE=1 SV=3 - [GBLP_RAT]	protein binding; enzyme regulator activity; RNA binding	nucleus; cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	VWNLANCK
209	P63245	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Rattus norvegicus GN=Gnb2l1 PE=1 SV=3 - [GBLP_RAT]	protein binding; enzyme regulator activity; RNA binding	nucleus; cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	YTVQDESHSEWVSCVR
209	P63245	Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Rattus norvegicus GN=Gnb2l1 PE=1 SV=3 - [GBLP_RAT]	protein binding; enzyme regulator activity; RNA binding	nucleus; cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	YWLCAATGPSIK
210	Q811S9	Guanine nucleotide-binding protein-like 3 OS=Rattus norvegicus GN=Gnl3 PE=1 SV=1 - [GNL3_RAT]	nucleotide binding; catalytic activity; protein binding; RNA binding	nucleus; membrane	LLGGFQQSCGK
212	F1LRV4	Heat shock 70 kDa protein 4 OS=Rattus norvegicus GN=Hspa4 PE=3 SV=1 - [F1LRV4_RAT]	nucleotide binding	nucleus; mitochondrion	KPVVDCVVSVPSFYTDAER
212	F1LRV4	Heat shock 70 kDa protein 4 OS=Rattus norvegicus GN=Hspa4 PE=3 SV=1 - [F1LRV4_RAT]	nucleotide binding	nucleus; mitochondrion	SVMDATQIAGLNCLR
212	F1LRV4	Heat shock 70 kDa protein 4 OS=Rattus norvegicus GN=Hspa4 PE=3 SV=1 - [F1LRV4_RAT]	nucleotide binding	nucleus; mitochondrion	WNSPAEEGSSDCEVFPK

213	D3ZC55	Heat shock 70kDa protein 12A (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Hspa12a PE=4 SV=1 - [D3ZC55_RAT]			EPECIHVMR
215	P82995	Heat shock protein HSP 90-alpha OS=Rattus norvegicus GN=Hsp90aa1 PE=1 SV=3 - [HS90A_RAT]	nucleotide binding; RNA binding; protein binding; catalytic activity; enzyme regulator activity	nucleus; cytoplasm; mitochondrion; cytosol; membrane; cell surface	YYTSASGDEMVSLKDYCTR
216	P34058	Heat shock protein HSP 90-beta OS=Rattus norvegicus GN=Hsp90ab1 PE=1 SV=4 - [HS90B_RAT]	nucleotide binding; RNA binding; protein binding	cytoplasm; mitochondrion; cytosol; cell surface; membrane	CLELFSELAEDKENYKK
219	Q6P747	Heterochromatin protein 1-binding protein 3 OS=Rattus norvegicus GN=Hp1bp3 PE=2 SV=1 - [HP1B3_RAT]	DNA binding; protein binding	chromosome; nucleus	TCSTTALK
220	Q6URK4	Heterogeneous nuclear ribonucleoprotein A3 OS=Rattus norvegicus GN=Hnrnpa3 PE=1 SV=1 - [ROA3_RAT]	nucleotide binding; RNA binding; transporter activity	nucleus; spliceosomal complex; cytoplasm	WGTLTDCVVMRDPQTK
220	Q6URK4	Heterogeneous nuclear ribonucleoprotein A3 OS=Rattus norvegicus GN=Hnrnpa3 PE=1 SV=1 - [ROA3_RAT]	nucleotide binding; RNA binding; transporter activity	nucleus; spliceosomal complex; cytoplasm	YHTINGHNCEVKK
222	Q3SWU3	Heterogeneous nuclear ribonucleoprotein D-like OS=Rattus norvegicus GN=Hnrnpdl PE=2 SV=1 - [HNRDL_RAT]	nucleotide binding; DNA binding; RNA binding	nucleus; cytoplasm	FGEVVDCTIKTDPVTGR
222	Q3SWU3	Heterogeneous nuclear ribonucleoprotein D-like OS=Rattus norvegicus GN=Hnrnpdl PE=2 SV=1 - [HNRDL_RAT]	nucleotide binding; DNA binding; RNA binding	nucleus; cytoplasm	GFCFITYTDEEPVKK
222	Q3SWU3	Heterogeneous nuclear ribonucleoprotein D-like OS=Rattus norvegicus GN=Hnrnpdl PE=2 SV=1 - [HNRDL_RAT]	nucleotide binding; DNA binding; RNA binding	nucleus; cytoplasm	YHQIGSGKCEIK
223	G3V6A4	Heterogeneous nuclear ribonucleoprotein D, isoform CRA_b OS=Rattus norvegicus GN=Hnrpd PE=4 SV=1 - [G3V6A4_RAT]	nucleotide binding; RNA binding; DNA binding	nucleus; cytosol	FGDVVDCTLK
223	G3V6A4	Heterogeneous nuclear ribonucleoprotein D, isoform CRA_b OS=Rattus norvegicus GN=Hnrpd PE=4 SV=1 - [G3V6A4_RAT]	nucleotide binding; RNA binding; DNA binding	nucleus; cytosol	GFCFITFKEEEPVKK
224	Q794E4	Heterogeneous nuclear ribonucleoprotein F OS=Rattus norvegicus GN=Hnrnpf PE=1 SV=3 - [HNRPF_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex; cytoplasm; membrane	DLSYCLSGMYDHR
224	Q794E4	Heterogeneous nuclear ribonucleoprotein F OS=Rattus norvegicus GN=Hnrnpf PE=1 SV=3 - [HNRPF_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex; cytoplasm; membrane	YGDSEFTVQSTTGHCVHMR
225	G3V9Q3	Heterogeneous nuclear ribonucleoprotein H OS=Rattus norvegicus GN=Hnrnph1 PE=4 SV=1 - [G3V9Q3_RAT]	nucleotide binding; RNA binding	nucleus; spliceosomal complex; cytoplasm; cytoskeleton; membrane	FFSDCKIQNGAQGIR
225	G3V9Q3	Heterogeneous nuclear ribonucleoprotein H OS=Rattus norvegicus GN=Hnrnph1 PE=4 SV=1 - [G3V9Q3_RAT]	nucleotide binding; RNA binding	nucleus; spliceosomal complex; cytoplasm; cytoskeleton; membrane	GLPWSCSADEVQR
226	Q6AY09	Heterogeneous nuclear ribonucleoprotein H2 OS=Rattus norvegicus GN=Hnrnph2 PE=1 SV=1 - [HNRH2_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm; cytoskeleton; membrane	GLPWSCSAEEVMR
226	Q6AY09	Heterogeneous nuclear ribonucleoprotein H2 OS=Rattus norvegicus GN=Hnrnph2 PE=1 SV=1 - [HNRH2_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm; cytoskeleton; membrane	YGDGGSSFQSTTGHCVHMR
227	P61980	Heterogeneous nuclear ribonucleoprotein K OS=Rattus norvegicus GN=Hnrnpk PE=1 SV=1 - [HNRPK_RAT]	DNA binding; RNA binding	nucleus; spliceosomal complex; cytoplasm; membrane	GSDFDCELR
228	F1LV13	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus GN=Hnrnpm PE=4 SV=1 - [F1LV13_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex; membrane	ACQIFVR
228	F1LV13	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus GN=Hnrnpm PE=4 SV=1 - [F1LV13_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex; membrane	DKFNECGHVLYADIK
228	F1LV13	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus GN=Hnrnpm PE=4 SV=1 - [F1LV13_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex; membrane	GCAVVEFK
228	F1LV13	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus GN=Hnrnpm PE=4 SV=1 - [F1LV13_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex; membrane	GCGVVKFESPEVAER
228	F1LV13	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus GN=Hnrnpm PE=4 SV=1 - [F1LV13_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex; membrane	KACQIFVR
228	F1LV13	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus GN=Hnrnpm PE=4 SV=1 - [F1LV13_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex; membrane	MEEESGAPCVPSGNGAPVPK
228	F1LV13	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus GN=Hnrnpm PE=4 SV=1 - [F1LV13_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex; membrane	SKGCGVVKFESPEVAER

228	F1LV13	Heterogeneous nuclear ribonucleoprotein M OS=Rattus norvegicus GN=Hnrnpm PE=4 SV=1 - [F1LV13_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex; membrane	SRGCAVVEFK
230	Q566E4	Heterogeneous nuclear ribonucleoprotein R OS=Rattus norvegicus GN=Hnrnpr PE=2 SV=1 - [Q566E4_RAT]	nucleotide binding; RNA binding	nucleus; spliceosomal complex	GYAFITFCGK
230	Q566E4	Heterogeneous nuclear ribonucleoprotein R OS=Rattus norvegicus GN=Hnrnpr PE=2 SV=1 - [Q566E4_RAT]	nucleotide binding; RNA binding	nucleus; spliceosomal complex	LCDSYEIRPGK
231	Q6IMY8	Heterogeneous nuclear ribonucleoprotein U OS=Rattus norvegicus GN=Hnrnpu PE=2 SV=1 - [Q6IMY8_RAT]	DNA binding; transporter activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	APQCLGKFIEIAAR
231	Q6IMY8	Heterogeneous nuclear ribonucleoprotein U OS=Rattus norvegicus GN=Hnrnpu PE=2 SV=1 - [Q6IMY8_RAT]	DNA binding; transporter activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	AVVVCPKDEDYKQR
231	Q6IMY8	Heterogeneous nuclear ribonucleoprotein U OS=Rattus norvegicus GN=Hnrnpu PE=2 SV=1 - [Q6IMY8_RAT]	DNA binding; transporter activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	DCEVVMMIGLPGAGK
231	Q6IMY8	Heterogeneous nuclear ribonucleoprotein U OS=Rattus norvegicus GN=Hnrnpu PE=2 SV=1 - [Q6IMY8_RAT]	DNA binding; transporter activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	EKPYFPIPEDCTFIQNVPLEDR
231	Q6IMY8	Heterogeneous nuclear ribonucleoprotein U OS=Rattus norvegicus GN=Hnrnpu PE=2 SV=1 - [Q6IMY8_RAT]	DNA binding; transporter activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	GKVCFEMK
231	Q6IMY8	Heterogeneous nuclear ribonucleoprotein U OS=Rattus norvegicus GN=Hnrnpu PE=2 SV=1 - [Q6IMY8_RAT]	DNA binding; transporter activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	GNFTLPEVAECFDEITYVELQKEEAQK
231	Q6IMY8	Heterogeneous nuclear ribonucleoprotein U OS=Rattus norvegicus GN=Hnrnpu PE=2 SV=1 - [Q6IMY8_RAT]	DNA binding; transporter activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	GPEEKKDCEVVMMIGLPGAGK
231	Q6IMY8	Heterogeneous nuclear ribonucleoprotein U OS=Rattus norvegicus GN=Hnrnpu PE=2 SV=1 - [Q6IMY8_RAT]	DNA binding; transporter activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	KAVVVCPKDEDYK
231	Q6IMY8	Heterogeneous nuclear ribonucleoprotein U OS=Rattus norvegicus GN=Hnrnpu PE=2 SV=1 - [Q6IMY8_RAT]	DNA binding; transporter activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	KDCEVVMMIGLPGAGK
231	Q6IMY8	Heterogeneous nuclear ribonucleoprotein U OS=Rattus norvegicus GN=Hnrnpu PE=2 SV=1 - [Q6IMY8_RAT]	DNA binding; transporter activity; protein binding; RNA binding	nucleus; membrane; spliceosomal complex	MCLFAGFQR
233	P05708	Hexokinase-1 OS=Rattus norvegicus GN=Hk1 PE=1 SV=4 - [HXK1_RAT]	nucleotide binding; catalytic activity; protein binding	nucleus; mitochondrion; membrane; cytosol	AILQQLGLNSTCDDSILVK
233	P05708	Hexokinase-1 OS=Rattus norvegicus GN=Hk1 PE=1 SV=4 - [HXK1_RAT]	nucleotide binding; catalytic activity; protein binding	nucleus; mitochondrion; membrane; cytosol	CTVSFLLSEDGSGK
233	P05708	Hexokinase-1 OS=Rattus norvegicus GN=Hk1 PE=1 SV=4 - [HXK1_RAT]	nucleotide binding; catalytic activity; protein binding	nucleus; mitochondrion; membrane; cytosol	RAAQLCGAGMAAVVEK
234	P27881	Hexokinase-2 OS=Rattus norvegicus GN=Hk2 PE=1 SV=1 - [HXK2_RAT]	nucleotide binding; catalytic activity	mitochondrion; membrane; cytosol	ASGCEGEDVVTLLK
234	P27881	Hexokinase-2 OS=Rattus norvegicus GN=Hk2 PE=1 SV=1 - [HXK2_RAT]	nucleotide binding; catalytic activity	mitochondrion; membrane; cytosol	HLGLESTCDDSIIVK
234	P27881	Hexokinase-2 OS=Rattus norvegicus GN=Hk2 PE=1 SV=1 - [HXK2_RAT]	nucleotide binding; catalytic activity	mitochondrion; membrane; cytosol	ICQIVSTR
234	P27881	Hexokinase-2 OS=Rattus norvegicus GN=Hk2 PE=1 SV=1 - [HXK2_RAT]	nucleotide binding; catalytic activity	mitochondrion; membrane; cytosol	LGLNPLQEDCVATHR
234	P27881	Hexokinase-2 OS=Rattus norvegicus GN=Hk2 PE=1 SV=1 - [HXK2_RAT]	nucleotide binding; catalytic activity	mitochondrion; membrane; cytosol	MLPTYVCATPDGTEK
234	P27881	Hexokinase-2 OS=Rattus norvegicus GN=Hk2 PE=1 SV=1 - [HXK2_RAT]	nucleotide binding; catalytic activity	mitochondrion; membrane; cytosol	RLVPDCDVR
237	F7ENH8	Histone deacetylase OS=Rattus norvegicus GN=Hdac2 PE=3 SV=1 - [F7ENH8_RAT]	DNA binding; protein binding; catalytic activity; RNA binding	chromosome; nucleus; cytoplasm	CVEVVK
237	F7ENH8	Histone deacetylase OS=Rattus norvegicus GN=Hdac2 PE=3 SV=1 - [F7ENH8_RAT]	DNA binding; protein binding; catalytic activity; RNA binding	chromosome; nucleus; cytoplasm	IACDEEFSDSEDEGEGGRR
237	F7ENH8	Histone deacetylase OS=Rattus norvegicus GN=Hdac2 PE=3 SV=1 - [F7ENH8_RAT]	DNA binding; protein binding; catalytic activity; RNA binding	chromosome; nucleus; cytoplasm	LGCFNLTVK
237	F7ENH8	Histone deacetylase OS=Rattus norvegicus GN=Hdac2 PE=3 SV=1 - [F7ENH8_RAT]	DNA binding; protein binding; catalytic activity; RNA binding	chromosome; nucleus; cytoplasm	VMEMYQPSAVVLQCGADSLSGDR
238	Q71UF4	Histone-binding protein RBBP7 OS=Rattus norvegicus GN=Rbbp7 PE=2 SV=1 - [RBBP7_RAT]	RNA binding; protein binding	nucleus	HPAKPDPSGECNPDLR
238	Q71UF4	Histone-binding protein RBBP7 OS=Rattus norvegicus GN=Rbbp7 PE=2 SV=1 - [RBBP7_RAT]	RNA binding; protein binding	nucleus	VHIPNDDAQFDASHCDSDKGEFGGFGSVTGK

239	D4A9J4	Histone-lysine N-methyltransferase OS=Rattus norvegicus GN=LOC686349 PE=4 SV=2 - [D4A9J4_RAT]	protein binding; catalytic activity; metal ion binding; DNA binding	nucleus; membrane	KGDSAAQFLVFCQK
239	D4A9J4	Histone-lysine N-methyltransferase OS=Rattus norvegicus GN=LOC686349 PE=4 SV=2 - [D4A9J4_RAT]	protein binding; catalytic activity; metal ion binding; DNA binding	nucleus; membrane	NLSDACKPLK
239	D4A9J4	Histone-lysine N-methyltransferase OS=Rattus norvegicus GN=LOC686349 PE=4 SV=2 - [D4A9J4_RAT]	protein binding; catalytic activity; metal ion binding; DNA binding	nucleus; membrane	SLVAFEGEEQFEKLCQESAK
239	D4A9J4	Histone-lysine N-methyltransferase OS=Rattus norvegicus GN=LOC686349 PE=4 SV=2 - [D4A9J4_RAT]	protein binding; catalytic activity; metal ion binding; DNA binding	nucleus; membrane	WWPAEVCHPK
240	D4AA06	Histone-lysine N-methyltransferase OS=Rattus norvegicus GN=Nsd1 PE=4 SV=1 - [D4AA06_RAT]	protein binding; catalytic activity; metal ion binding	nucleus	GDCSSGSPVGTSK
240	D4AA06	Histone-lysine N-methyltransferase OS=Rattus norvegicus GN=Nsd1 PE=4 SV=1 - [D4AA06_RAT]	protein binding; catalytic activity; metal ion binding	nucleus	TPDRGDCSSGSPVGTSK
240	D4AA06	Histone-lysine N-methyltransferase OS=Rattus norvegicus GN=Nsd1 PE=4 SV=1 - [D4AA06_RAT]	protein binding; catalytic activity; metal ion binding	nucleus	WEASVGLAEQCDVPR
241	D3ZK47	Histone-lysine N-methyltransferase OS=Rattus norvegicus GN=Whsc1l1 PE=4 SV=1 - [D3ZK47_RAT]	protein binding; catalytic activity; metal ion binding	nucleus	ASTDVETASCTYR
241	D3ZK47	Histone-lysine N-methyltransferase OS=Rattus norvegicus GN=Whsc1l1 PE=4 SV=1 - [D3ZK47_RAT]	protein binding; catalytic activity; metal ion binding	nucleus	GASEISDSCKPLK
241	D3ZK47	Histone-lysine N-methyltransferase OS=Rattus norvegicus GN=Whsc1l1 PE=4 SV=1 - [D3ZK47_RAT]	protein binding; catalytic activity; metal ion binding	nucleus	HFHPECLGLAAVPEGR
244	G3V8Y8	Huntingtin interacting protein 1, isoform CRA_a OS=Rattus norvegicus GN=Hip1 PE=4 SV=1 - [G3V8Y8_RAT]	protein binding	cytoplasm; Golgi	ADTTAIANCLGK
244	G3V8Y8	Huntingtin interacting protein 1, isoform CRA_a OS=Rattus norvegicus GN=Hip1 PE=4 SV=1 - [G3V8Y8_RAT]	protein binding	cytoplasm; Golgi	APPESADSLTEACR
244	G3V8Y8	Huntingtin interacting protein 1, isoform CRA_a OS=Rattus norvegicus GN=Hip1 PE=4 SV=1 - [G3V8Y8_RAT]	protein binding	cytoplasm; Golgi	LAGAQDSMCQQIK
244	G3V8Y8	Huntingtin interacting protein 1, isoform CRA_a OS=Rattus norvegicus GN=Hip1 PE=4 SV=1 - [G3V8Y8_RAT]	protein binding	cytoplasm; Golgi	QATDDCEFLR
244	G3V8Y8	Huntingtin interacting protein 1, isoform CRA_a OS=Rattus norvegicus GN=Hip1 PE=4 SV=1 - [G3V8Y8_RAT]	protein binding	cytoplasm; Golgi	SVSVTTAGQCR
244	G3V8Y8	Huntingtin interacting protein 1, isoform CRA_a OS=Rattus norvegicus GN=Hip1 PE=4 SV=1 - [G3V8Y8_RAT]	protein binding	cytoplasm; Golgi	TCILGTHHEK
244	G3V8Y8	Huntingtin interacting protein 1, isoform CRA_a OS=Rattus norvegicus GN=Hip1 PE=4 SV=1 - [G3V8Y8_RAT]	protein binding	cytoplasm; Golgi	VNSVSSCLEQLEK
245	F2Z3Q8	Importin subunit beta-1 OS=Rattus norvegicus GN=Kpnb1 PE=4 SV=1 - [F2Z3Q8_RAT]	protein binding; transporter activity	cytoplasm; membrane	ESCLEAYTGIVQGLK
245	F2Z3Q8	Importin subunit beta-1 OS=Rattus norvegicus GN=Kpnb1 PE=4 SV=1 - [F2Z3Q8_RAT]	protein binding; transporter activity	cytoplasm; membrane	QDENDDDDDWNPCK
246	Q8CGX0	Insulin-like growth factor 2 mRNA-binding protein 1 OS=Rattus norvegicus GN=Igf2bp1 PE=1 SV=1 - [IF2B1_RAT]	nucleotide binding; RNA binding; translation regulator activity	nucleus; cytoplasm; membrane	SGYAFVDCPDEHWAMK
247	G3V7J2	Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Rattus norvegicus GN=Prkra PE=4 SV=1 - [G3V7J2_RAT]	RNA binding; protein binding; catalytic activity	cytoplasm; membrane	NIPVYECER
247	G3V7J2	Interferon-inducible double-stranded RNA-dependent protein kinase activator A OS=Rattus norvegicus GN=Prkra PE=4 SV=1 - [G3V7J2_RAT]	RNA binding; protein binding; catalytic activity	cytoplasm; membrane	VTVGDITCTGEGTSK
249	Q9JIL3	Interleukin enhancer-binding factor 3 OS=Rattus norvegicus GN=Ilf3 PE=1 SV=2 - [ILF3_RAT]	DNA binding; RNA binding; protein binding	nucleus; cytoplasm; mitochondrion; membrane	CLAALASLR

250	F1LNF7	Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Rattus norvegicus GN=Idh3a PE=3 SV=1 - [F1LNF7_RAT]	metal ion binding; catalytic activity; nucleotide binding	mitochondrion	EVAENCKDIK
250	F1LNF7	Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Rattus norvegicus GN=Idh3a PE=3 SV=1 - [F1LNF7_RAT]	metal ion binding; catalytic activity; nucleotide binding	mitochondrion	IEAACFATIK
251	P56574	Isocitrate dehydrogenase [NADP], mitochondrial OS=Rattus norvegicus GN=Idh2 PE=1 SV=2 - [IDHP_RAT]	metal ion binding; catalytic activity; nucleotide binding	mitochondrion; membrane	CATITPDEAR
251	P56574	Isocitrate dehydrogenase [NADP], mitochondrial OS=Rattus norvegicus GN=Idh2 PE=1 SV=2 - [IDHP_RAT]	metal ion binding; catalytic activity; nucleotide binding	mitochondrion; membrane	DLAGCIHGLSNVK
251	P56574	Isocitrate dehydrogenase [NADP], mitochondrial OS=Rattus norvegicus GN=Idh2 PE=1 SV=2 - [IDHP_RAT]	metal ion binding; catalytic activity; nucleotide binding	mitochondrion; membrane	FAQTLEKVCVQTVESGAMTK
251	P56574	Isocitrate dehydrogenase [NADP], mitochondrial OS=Rattus norvegicus GN=Idh2 PE=1 SV=2 - [IDHP_RAT]	metal ion binding; catalytic activity; nucleotide binding	mitochondrion; membrane	SSGGFVWACK
251	P56574	Isocitrate dehydrogenase [NADP], mitochondrial OS=Rattus norvegicus GN=Idh2 PE=1 SV=2 - [IDHP_RAT]	metal ion binding; catalytic activity; nucleotide binding	mitochondrion; membrane	VCVQTVESGAMTK
253	Q91V33	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Rattus norvegicus GN=Khdrbs1 PE=1 SV=1 - [KHDR1_RAT]	RNA binding; protein binding	nucleus; cytoplasm; membrane	SCSKDPSGAHPSVR
254	D3ZHG2	Kinesin light chain 1 OS=Rattus norvegicus GN=Klc1 PE=4 SV=2 - [D3ZHG2_RAT]	catalytic activity; motor activity; protein binding		EFGSVDDENKPIWMHAEEREECK
254	D3ZHG2	Kinesin light chain 1 OS=Rattus norvegicus GN=Klc1 PE=4 SV=2 - [D3ZHG2_RAT]	catalytic activity; motor activity; protein binding		LCQENQWLRDELANTQQK
255	Q2PQA9	Kinesin-1 heavy chain OS=Rattus norvegicus GN=Kif5b PE=1 SV=1 - [KINH_RAT]	nucleotide binding; catalytic activity; motor activity; protein binding; transporter activity	nucleus; cytoplasm; cytoskeleton; membrane	ELAACQLR
255	Q2PQA9	Kinesin-1 heavy chain OS=Rattus norvegicus GN=Kif5b PE=1 SV=1 - [KINH_RAT]	nucleotide binding; catalytic activity; motor activity; protein binding; transporter activity	nucleus; cytoplasm; cytoskeleton; membrane	FVCSPDEVMDTIDEGK
255	Q2PQA9	Kinesin-1 heavy chain OS=Rattus norvegicus GN=Kif5b PE=1 SV=1 - [KINH_RAT]	nucleotide binding; catalytic activity; motor activity; protein binding; transporter activity	nucleus; cytoplasm; cytoskeleton; membrane	KMEENEKELAACQLR
255	Q2PQA9	Kinesin-1 heavy chain OS=Rattus norvegicus GN=Kif5b PE=1 SV=1 - [KINH_RAT]	nucleotide binding; catalytic activity; motor activity; protein binding; transporter activity	nucleus; cytoplasm; cytoskeleton; membrane	VFQSSTSQEQVYNDCAKK
256	F1M8L1	Kinesin-like protein OS=Rattus norvegicus GN=Kif2a PE=3 SV=2 - [F1M8L1_RAT]	nucleotide binding; catalytic activity; motor activity; protein binding		AQDVDATNPNYEIMCMIR
256	F1M8L1	Kinesin-like protein OS=Rattus norvegicus GN=Kif2a PE=3 SV=2 - [F1M8L1_RAT]	nucleotide binding; catalytic activity; motor activity; protein binding		CVEDVLK
256	F1M8L1	Kinesin-like protein OS=Rattus norvegicus GN=Kif2a PE=3 SV=2 - [F1M8L1_RAT]	nucleotide binding; catalytic activity; motor activity; protein binding		GMATCFAYGQTGSGK
256	F1M8L1	Kinesin-like protein OS=Rattus norvegicus GN=Kif2a PE=3 SV=2 - [F1M8L1_RAT]	nucleotide binding; catalytic activity; motor activity; protein binding		LIDIGNSCR
258	Q62733	Lamina-associated polypeptide 2, isoform beta OS=Rattus norvegicus GN=Tmpo PE=1 SV=3 - [LAP2_RAT]	DNA binding; protein binding	chromosome; nucleus; membrane	EMFPYEASTPTGISASCR
259	F1LM33	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus GN=Lrpprc PE=4 SV=2 - [F1LM33_RAT]	DNA binding; RNA binding; protein binding	chromosome; nucleus; membrane; cytoplasm; mitochondrion; cytoskeleton	AALQENKCLPK
259	F1LM33	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus GN=Lrpprc PE=4 SV=2 - [F1LM33_RAT]	DNA binding; RNA binding; protein binding	chromosome; nucleus; membrane; cytoplasm; mitochondrion; cytoskeleton	CIANNQVETLEK
259	F1LM33	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus GN=Lrpprc PE=4 SV=2 - [F1LM33_RAT]	DNA binding; RNA binding; protein binding	chromosome; nucleus; membrane; cytoplasm; mitochondrion; cytoskeleton	DDLPAALEASIACHEK

259	F1LM33	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus GN=Lrpprc PE=4 SV=2 - [F1LM33_RAT]	DNA binding; RNA binding; protein binding	chromosome; nucleus; membrane; cytoplasm; mitochondrion; cytoskeleton	HCVTMDTPAEK
259	F1LM33	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus GN=Lrpprc PE=4 SV=2 - [F1LM33_RAT]	DNA binding; RNA binding; protein binding	chromosome; nucleus; membrane; cytoplasm; mitochondrion; cytoskeleton	IHDVLCK
259	F1LM33	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus GN=Lrpprc PE=4 SV=2 - [F1LM33_RAT]	DNA binding; RNA binding; protein binding	chromosome; nucleus; membrane; cytoplasm; mitochondrion; cytoskeleton	LFECDRDQMYYNLLK
259	F1LM33	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus GN=Lrpprc PE=4 SV=2 - [F1LM33_RAT]	DNA binding; RNA binding; protein binding	chromosome; nucleus; membrane; cytoplasm; mitochondrion; cytoskeleton	LIAAYCSVGDIEGASK
259	F1LM33	Leucine-rich PPR motif-containing protein, mitochondrial OS=Rattus norvegicus GN=Lrpprc PE=4 SV=2 - [F1LM33_RAT]	DNA binding; RNA binding; protein binding	chromosome; nucleus; membrane; cytoplasm; mitochondrion; cytoskeleton	SCGSLLPELSLAER
260	Q5RJR8	Leucine-rich repeat-containing protein 59 OS=Rattus norvegicus GN=Lrrc59 PE=1 SV=1 - [LRC59_RAT]	protein binding; RNA binding	nucleus; endoplasmic reticulum; membrane	ATVLDLSCNK
260	Q5RJR8	Leucine-rich repeat-containing protein 59 OS=Rattus norvegicus GN=Lrrc59 PE=1 SV=1 - [LRC59_RAT]	protein binding; RNA binding	nucleus; endoplasmic reticulum; membrane	LSTLPSDFCGLTHLVK
260	Q5RJR8	Leucine-rich repeat-containing protein 59 OS=Rattus norvegicus GN=Lrrc59 PE=1 SV=1 - [LRC59_RAT]	protein binding; RNA binding	nucleus; endoplasmic reticulum; membrane	VAGDCLDEK
262	O35547	Long-chain-fatty-acid--CoA ligase 4 OS=Rattus norvegicus GN=Acsl4 PE=1 SV=1 - [ACSL4_RAT]	nucleotide binding; catalytic activity	cytoplasm; mitochondrion; endoplasmic reticulum; membrane	AALLDINCVK
262	O35547	Long-chain-fatty-acid--CoA ligase 4 OS=Rattus norvegicus GN=Acsl4 PE=1 SV=1 - [ACSL4_RAT]	nucleotide binding; catalytic activity	cytoplasm; mitochondrion; endoplasmic reticulum; membrane	GYDAPLCNLILFK
262	O35547	Long-chain-fatty-acid--CoA ligase 4 OS=Rattus norvegicus GN=Acsl4 PE=1 SV=1 - [ACSL4_RAT]	nucleotide binding; catalytic activity	cytoplasm; mitochondrion; endoplasmic reticulum; membrane	WINYLEVNCR
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	DSKHEELMLGDPCLK
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	EAPCILIYIPDGHTK
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	ELNHCLSLR
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	ERPAAAVSAPCAAAEDAAILYSR
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	GNAACQEHLR
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	HEELMLGDPCLK
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	IDMSSNNGCMRDPTLYR
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	INDAVECLLSLK
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	LGVENCYFPIFVSQGALEK
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	LNQWCNVVR
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	LSSCDVLTSAIK
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	MCEIVFEDPKTPGEK
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	QFAYQCSWGLTTR
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	SCQFVAVR
263	Q6TXE9	LRRGT00050 OS=Rattus norvegicus GN=Eprs PE=2 SV=1 - [Q6TXE9_RAT]	nucleotide binding; catalytic activity; RNA binding	cytoplasm; membrane	VACQGEVVRK

264	Q6TUH4	LRRGT00070 OS=Rattus norvegicus GN=Thoc1 PE=2 SV=1 - [Q6TUH4_RAT]	DNA binding; RNA binding; protein binding	nucleus; cytoplasm	QIECDSEDMK
265	D3ZJH9	Malic enzyme OS=Rattus norvegicus GN=Me2 PE=3 SV=1 - [D3ZJH9_RAT]	catalytic activity; metal ion binding; nucleotide binding	mitochondrion	CLFASGSPFEPVR
267	P43244	Matrin-3 OS=Rattus norvegicus GN=Matr3 PE=1 SV=2 - [MATR3_RAT]	nucleotide binding; RNA binding; metal ion binding	nucleus; cytoplasm; membrane	CRDDSFFGETSHNYHK
267	P43244	Matrin-3 OS=Rattus norvegicus GN=Matr3 PE=1 SV=2 - [MATR3_RAT]	nucleotide binding; RNA binding; metal ion binding	nucleus; cytoplasm; membrane	CVKVDLSEK
267	P43244	Matrin-3 OS=Rattus norvegicus GN=Matr3 PE=1 SV=2 - [MATR3_RAT]	nucleotide binding; RNA binding; metal ion binding	nucleus; cytoplasm; membrane	EDAMAMVDHCLKK
267	P43244	Matrin-3 OS=Rattus norvegicus GN=Matr3 PE=1 SV=2 - [MATR3_RAT]	nucleotide binding; RNA binding; metal ion binding	nucleus; cytoplasm; membrane	LCSLFYTNEEVAK
267	P43244	Matrin-3 OS=Rattus norvegicus GN=Matr3 PE=1 SV=2 - [MATR3_RAT]	nucleotide binding; RNA binding; metal ion binding	nucleus; cytoplasm; membrane	NTHCSSLPHYQK
268	Q5XIU9	Membrane-associated progesterone receptor component 2 OS=Rattus norvegicus GN=Pgrmc2 PE=2 SV=1 - [PGRC2_RAT]		membrane	RGLCSGPGAGEESPAATLPR
269	B2GV01	Metastasis-associated gene family, member 2 OS=Rattus norvegicus GN=Mta2 PE=2 SV=1 - [B2GV01_RAT]	DNA binding; protein binding; catalytic activity; metal ion binding	nucleus; membrane	ALDCSSSIR
269	B2GV01	Metastasis-associated gene family, member 2 OS=Rattus norvegicus GN=Mta2 PE=2 SV=1 - [B2GV01_RAT]	DNA binding; protein binding; catalytic activity; metal ion binding	nucleus; membrane	AMSTLVPQGGPVLCR
270	D3ZE72	Methionine aminopeptidase 1 OS=Rattus norvegicus GN=Metap1 PE=3 SV=1 - [D3ZE72_RAT]	catalytic activity; metal ion binding	nucleus; cytoplasm; ribosome	AGVTTEEIDHAVHLACIAR
270	D3ZE72	Methionine aminopeptidase 1 OS=Rattus norvegicus GN=Metap1 PE=3 SV=1 - [D3ZE72_RAT]	catalytic activity; metal ion binding	nucleus; cytoplasm; ribosome	NCYPSPLNYYNFPK
271	F7EY92	Methyl-CpG binding domain protein 3 (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Mbd3 PE=4 SV=1 - [F7EY92_RAT]	DNA binding; nucleotide binding; protein binding	chromosome; nucleus; cytoplasm	ACAEEEEEEEEEEEEPEPERV
271	F7EY92	Methyl-CpG binding domain protein 3 (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Mbd3 PE=4 SV=1 - [F7EY92_RAT]	DNA binding; nucleotide binding; protein binding	chromosome; nucleus; cytoplasm	NPGVWLNTAQPLCK
271	F7EY92	Methyl-CpG binding domain protein 3 (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Mbd3 PE=4 SV=1 - [F7EY92_RAT]	DNA binding; nucleotide binding; protein binding	chromosome; nucleus; cytoplasm	WECPALPQGWER
272	F1LWH6	Methyl-CpG-binding protein 2 (Fragment) OS=Rattus norvegicus GN=Mecp2 PE=4 SV=1 - [F1LWH6_RAT]	DNA binding; RNA binding; protein binding; nucleotide binding	nucleus; cytoplasm; cytosol	AGSLESDGCPKEPAK
274	P34926	Microtubule-associated protein 1A OS=Rattus norvegicus GN=Map1a PE=1 SV=1 - [MAP1A_RAT]	protein binding; catalytic activity	cytoplasm; cytosol; cytoskeleton	SAPCGSLAFSGDR
275	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=1 - [F1LRL9_RAT]	protein binding; catalytic activity	cytosol; membrane	ASAEGEATAVVSPGVTQAVVEEHCASPEEK
275	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=1 - [F1LRL9_RAT]	protein binding; catalytic activity	cytosol; membrane	ASLTLFCPEEGDWK
275	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=1 - [F1LRL9_RAT]	protein binding; catalytic activity	cytosol; membrane	GSAESPDEGITTTEGEGECEQTPEELEPVEK
275	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=1 - [F1LRL9_RAT]	protein binding; catalytic activity	cytosol; membrane	LLDDISNGYDDTEDGGHTLGDCSYSYETTEK
275	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=1 - [F1LRL9_RAT]	protein binding; catalytic activity	cytosol; membrane	RSTEEACFTLQYLNK
275	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=1 - [F1LRL9_RAT]	protein binding; catalytic activity	cytosol; membrane	SPCDSGYSYETIEK
275	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=1 - [F1LRL9_RAT]	protein binding; catalytic activity	cytosol; membrane	SPDTSAYCYETMEK
275	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=1 - [F1LRL9_RAT]	protein binding; catalytic activity	cytosol; membrane	STEEACFTLQYLNK
275	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=1 - [F1LRL9_RAT]	protein binding; catalytic activity	cytosol; membrane	SWDTNLIECNLDQELK

275	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=1 - [F1LRL9_RAT]	protein binding; catalytic activity	cytosol; membrane	TIKSPCDSGYSYETIEK
275	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=1 - [F1LRL9_RAT]	protein binding; catalytic activity	cytosol; membrane	TPEDGGYSCEITEKTTR
275	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=1 - [F1LRL9_RAT]	protein binding; catalytic activity	cytosol; membrane	TPQASTYSYETSDRCYTPERK
275	F1LRL9	Microtubule-associated protein 1B OS=Rattus norvegicus GN=Map1b PE=1 SV=1 - [F1LRL9_RAT]	protein binding; catalytic activity	cytosol; membrane	TTKTPEDGGYSCEITEK
277	P0C5W1	Microtubule-associated protein 1S OS=Rattus norvegicus GN=Map1s PE=1 SV=1 - [MAP1S_RAT]	DNA binding; catalytic activity; protein binding	nucleus; cytoplasm; cytosol; cytoskeleton	ALCYVISGQGQR
277	P0C5W1	Microtubule-associated protein 1S OS=Rattus norvegicus GN=Map1s PE=1 SV=1 - [MAP1S_RAT]	DNA binding; catalytic activity; protein binding	nucleus; cytoplasm; cytosol; cytoskeleton	GGEDEAVCAR
277	P0C5W1	Microtubule-associated protein 1S OS=Rattus norvegicus GN=Map1s PE=1 SV=1 - [MAP1S_RAT]	DNA binding; catalytic activity; protein binding	nucleus; cytoplasm; cytosol; cytoskeleton	GPQPSCPTVLFEK
277	P0C5W1	Microtubule-associated protein 1S OS=Rattus norvegicus GN=Map1s PE=1 SV=1 - [MAP1S_RAT]	DNA binding; catalytic activity; protein binding	nucleus; cytoplasm; cytosol; cytoskeleton	SWEDVDPDVCSLDEQLK
277	P0C5W1	Microtubule-associated protein 1S OS=Rattus norvegicus GN=Map1s PE=1 SV=1 - [MAP1S_RAT]	DNA binding; catalytic activity; protein binding	nucleus; cytoplasm; cytosol; cytoskeleton	VLGSGSLVSMQDEAFPACK
278	Q5M7W5	Microtubule-associated protein 4 OS=Rattus norvegicus GN=Map4 PE=1 SV=1 - [MAP4_RAT]	protein binding; RNA binding	cytoplasm; cytoskeleton; membrane	ETSGSQPPELCSGVSR
278	Q5M7W5	Microtubule-associated protein 4 OS=Rattus norvegicus GN=Map4 PE=1 SV=1 - [MAP4_RAT]	protein binding; RNA binding	cytoplasm; cytoskeleton; membrane	VKPMSAPCR
280	F1MAQ5	Microtubule-associated protein OS=Rattus norvegicus GN=Map2 PE=4 SV=2 - [F1MAQ5_RAT]	protein binding	cytoplasm; endoplasmic reticulum; cytoskeleton	EEFVETCPGEHK
280	F1MAQ5	Microtubule-associated protein OS=Rattus norvegicus GN=Map2 PE=4 SV=2 - [F1MAQ5_RAT]	protein binding	cytoplasm; endoplasmic reticulum; cytoskeleton	IPCFPIESKEEEDKTEQAK
280	F1MAQ5	Microtubule-associated protein OS=Rattus norvegicus GN=Map2 PE=4 SV=2 - [F1MAQ5_RAT]	protein binding	cytoplasm; endoplasmic reticulum; cytoskeleton	LSVEIPCPPPVSEADSSIDEK
283	Q66HR2	Microtubule-associated protein RP/EB family member 1 OS=Rattus norvegicus GN=Mapre1 PE=1 SV=3 - [MARE1_RAT]	protein binding; RNA binding	cytoplasm; Golgi; cytoskeleton	NIELICQENEGENDPVLQR
285	R9PXR4	Mitochondrial import receptor subunit TOM70 OS=Rattus norvegicus GN=Tomm70a PE=1 SV=1 - [R9PXR4_RAT]	protein binding	mitochondrion; membrane	ADEMYDKCIDLEPDNATTYVHK
285	R9PXR4	Mitochondrial import receptor subunit TOM70 OS=Rattus norvegicus GN=Tomm70a PE=1 SV=1 - [R9PXR4_RAT]	protein binding	mitochondrion; membrane	CFALYR
285	R9PXR4	Mitochondrial import receptor subunit TOM70 OS=Rattus norvegicus GN=Tomm70a PE=1 SV=1 - [R9PXR4_RAT]	protein binding	mitochondrion; membrane	WKEVAQDCTK
287	F1M754	Mitogen-activated protein kinase kinase kinase kinase 4 (Predicted) OS=Rattus norvegicus GN=Map4k4 PE=4 SV=2 - [F1M754_RAT]	catalytic activity; signal transducer activity; nucleotide binding	cytoplasm	QGWTTVGDLEGCVHYK
287	F1M754	Mitogen-activated protein kinase kinase kinase kinase 4 (Predicted) OS=Rattus norvegicus GN=Map4k4 PE=4 SV=2 - [F1M754_RAT]	catalytic activity; signal transducer activity; nucleotide binding	cytoplasm	SQDPCPPSR
290	O35821	Myb-binding protein 1A OS=Rattus norvegicus GN=Mybbp1a PE=2 SV=2 - [MBB1A_RAT]	DNA binding; catalytic activity; RNA binding	nucleus; cytoplasm; membrane	HQAQACLLLQK
290	O35821	Myb-binding protein 1A OS=Rattus norvegicus GN=Mybbp1a PE=2 SV=2 - [MBB1A_RAT]	DNA binding; catalytic activity; RNA binding	nucleus; cytoplasm; membrane	HYCHEVEPGAEALHAQVER
293	Q64119	Myosin light polypeptide 6 OS=Rattus norvegicus GN=Myl6 PE=1 SV=3 - [MYL6_RAT]	catalytic activity; motor activity; metal ion binding; structural molecule activity		ILYSQCGDVMR
296	Q66HF1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Rattus norvegicus GN=Ndufs1 PE=1 SV=1 - [NDUS1_RAT]	catalytic activity; metal ion binding	mitochondrion; membrane	LSVAGNCR
296	Q66HF1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Rattus norvegicus GN=Ndufs1 PE=1 SV=1 - [NDUS1_RAT]	catalytic activity; metal ion binding	mitochondrion; membrane	MCLVEIEK

296	Q66HF1	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Rattus norvegicus GN=Ndufs1 PE=1 SV=1 - [NDUS1_RAT]	catalytic activity; metal ion binding	mitochondrion; membrane	VVAACAMPVMK
297	P55161	Nck-associated protein 1 OS=Rattus norvegicus GN=Nckap1 PE=2 SV=1 - [NCKP1_RAT]	protein binding	membrane	MFQQCLELPSQSR
297	P55161	Nck-associated protein 1 OS=Rattus norvegicus GN=Nckap1 PE=2 SV=1 - [NCKP1_RAT]	protein binding	membrane	SLSLCNMFLDEMAK
298	Q63689	Neurogenic differentiation factor 2 OS=Rattus norvegicus GN=Neurod2 PE=1 SV=2 - [NDF2_RAT]	DNA binding; protein binding	nucleus	GLSQPTTNLVAGCLQLNSR
298	Q63689	Neurogenic differentiation factor 2 OS=Rattus norvegicus GN=Neurod2 PE=1 SV=2 - [NDF2_RAT]	DNA binding; protein binding	nucleus	KVVPCYSK
299	P42676	Neurolysin, mitochondrial OS=Rattus norvegicus GN=Nln PE=1 SV=1 - [NEUL_RAT]	catalytic activity; metal ion binding	cytoplasm; mitochondrion; membrane	IVHLQETCDLEK
299	P42676	Neurolysin, mitochondrial OS=Rattus norvegicus GN=Nln PE=1 SV=1 - [NEUL_RAT]	catalytic activity; metal ion binding	cytoplasm; mitochondrion; membrane	MSELCIDFNK
301	G3V997	Neuronal migration protein doublecortin OS=Rattus norvegicus GN=Dcx PE=4 SV=1 - [G3V997_RAT]	protein binding	cytoplasm	YAQDDFSLDENECRVMKGNPSATAGPK
303	P55770	NHP2-like protein 1 OS=Rattus norvegicus GN=Nhp2l1 PE=2 SV=4 - [NH2L1_RAT]	RNA binding	nucleus; spliceosomal complex	LLDLVQQSCNYK
304	Q56A27	Nuclear cap-binding protein subunit 1 OS=Rattus norvegicus GN=Ncbp1 PE=2 SV=1 - [NCBP1_RAT]	RNA binding; DNA binding; protein binding	nucleus; cytoplasm; mitochondrion; membrane	FVIEENLHCIIK
304	Q56A27	Nuclear cap-binding protein subunit 1 OS=Rattus norvegicus GN=Ncbp1 PE=2 SV=1 - [NCBP1_RAT]	RNA binding; DNA binding; protein binding	nucleus; cytoplasm; mitochondrion; membrane	KTCAAQLVSYPGK
304	Q56A27	Nuclear cap-binding protein subunit 1 OS=Rattus norvegicus GN=Ncbp1 PE=2 SV=1 - [NCBP1_RAT]	RNA binding; DNA binding; protein binding	nucleus; cytoplasm; mitochondrion; membrane	KTSDANETEDHLESLICK
304	Q56A27	Nuclear cap-binding protein subunit 1 OS=Rattus norvegicus GN=Ncbp1 PE=2 SV=1 - [NCBP1_RAT]	RNA binding; DNA binding; protein binding	nucleus; cytoplasm; mitochondrion; membrane	LDTMSTTCVDR
304	Q56A27	Nuclear cap-binding protein subunit 1 OS=Rattus norvegicus GN=Ncbp1 PE=2 SV=1 - [NCBP1_RAT]	RNA binding; DNA binding; protein binding	nucleus; cytoplasm; mitochondrion; membrane	TCAAQLVSYPGK
307	F2Z3R4	Nuclear factor 1 OS=Rattus norvegicus GN=Nfix PE=3 SV=1 - [F2Z3R4_RAT]	DNA binding	nucleus	EFVQFVCSDGSGQATGQHSQR
307	F2Z3R4	Nuclear factor 1 OS=Rattus norvegicus GN=Nfix PE=3 SV=1 - [F2Z3R4_RAT]	DNA binding	nucleus	LDFCSALSSQGSSPR

308	F1LSL2	Nuclear pore complex protein Nup107 OS=Rattus norvegicus GN=Nup107 PE=4 SV=2 - [F1LSL2_RAT]	transporter activity; structural molecule activity	chromosome; nucleus; membrane	CGQAWR
308	F1LSL2	Nuclear pore complex protein Nup107 OS=Rattus norvegicus GN=Nup107 PE=4 SV=2 - [F1LSL2_RAT]	transporter activity; structural molecule activity	chromosome; nucleus; membrane	HQCLELAK
310	P49793	Nuclear pore complex protein Nup98-Nup96 OS=Rattus norvegicus GN=Nup98 PE=1 SV=2 - [NUP98_RAT]	protein binding; structural molecule activity	chromosome; nucleus; membrane	FASGTFLSPSASVQECR
310	P49793	Nuclear pore complex protein Nup98-Nup96 OS=Rattus norvegicus GN=Nup98 PE=1 SV=2 - [NUP98_RAT]	protein binding; structural molecule activity	chromosome; nucleus; membrane	GDTAQEICSPR
310	P49793	Nuclear pore complex protein Nup98-Nup96 OS=Rattus norvegicus GN=Nup98 PE=1 SV=2 - [NUP98_RAT]	protein binding; structural molecule activity	chromosome; nucleus; membrane	GECIVSDFTIGR
310	P49793	Nuclear pore complex protein Nup98-Nup96 OS=Rattus norvegicus GN=Nup98 PE=1 SV=2 - [NUP98_RAT]	protein binding; structural molecule activity	chromosome; nucleus; membrane	HCQLSETPESWAK
310	P49793	Nuclear pore complex protein Nup98-Nup96 OS=Rattus norvegicus GN=Nup98 PE=1 SV=2 - [NUP98_RAT]	protein binding; structural molecule activity	chromosome; nucleus; membrane	IEQIPCYNAK
310	P49793	Nuclear pore complex protein Nup98-Nup96 OS=Rattus norvegicus GN=Nup98 PE=1 SV=2 - [NUP98_RAT]	protein binding; structural molecule activity	chromosome; nucleus; membrane	IQQVDCSGYELEHLHTK
310	P49793	Nuclear pore complex protein Nup98-Nup96 OS=Rattus norvegicus GN=Nup98 PE=1 SV=2 - [NUP98_RAT]	protein binding; structural molecule activity	chromosome; nucleus; membrane	LCVPAEWIHEAK
311	G3V7F5	Nuclear receptor subfamily 2 group C member 2 OS=Rattus norvegicus GN=Nr2c2 PE=3 SV=1 - [G3V7F5_RAT]	DNA binding; receptor activity; signal transducer activity; metal ion binding; protein binding	nucleus	LQEFCNSMAK
311	G3V7F5	Nuclear receptor subfamily 2 group C member 2 OS=Rattus norvegicus GN=Nr2c2 PE=3 SV=1 - [G3V7F5_RAT]	DNA binding; receptor activity; signal transducer activity; metal ion binding; protein binding	nucleus	SIPAFQALGQDCNTSLVR
311	G3V7F5	Nuclear receptor subfamily 2 group C member 2 OS=Rattus norvegicus GN=Nr2c2 PE=3 SV=1 - [G3V7F5_RAT]	DNA binding; receptor activity; signal transducer activity; metal ion binding; protein binding	nucleus	SSQDCIINK
312	F1MA52	Nuclear RNA export factor 1 OS=Rattus norvegicus GN=Nxf1 PE=4 SV=1 - [F1MA52_RAT]	nucleotide binding; RNA binding; transporter activity; protein binding	nucleus; cytoplasm	CLQDNNWDYTR
312	F1MA52	Nuclear RNA export factor 1 OS=Rattus norvegicus GN=Nxf1 PE=4 SV=1 - [F1MA52_RAT]	nucleotide binding; RNA binding; transporter activity; protein binding	nucleus; cytoplasm	CSVPFNPIEFHYENTR
312	F1MA52	Nuclear RNA export factor 1 OS=Rattus norvegicus GN=Nxf1 PE=4 SV=1 - [F1MA52_RAT]	nucleotide binding; RNA binding; transporter activity; protein binding	nucleus; cytoplasm	GCMAAALR
312	F1MA52	Nuclear RNA export factor 1 OS=Rattus norvegicus GN=Nxf1 PE=4 SV=1 - [F1MA52_RAT]	nucleotide binding; RNA binding; transporter activity; protein binding	nucleus; cytoplasm	LDGHELPPPIAFDVEAPTMLPPCK
313	Q9QZ86	Nucleolar protein 58 OS=Rattus norvegicus GN=Nop58 PE=1 SV=1 - [NOP58_RAT]	catalytic activity; RNA binding; protein binding	nucleus; cytoplasm; membrane	EMAAMCLGLAHSLSR
313	Q9QZ86	Nucleolar protein 58 OS=Rattus norvegicus GN=Nop58 PE=1 SV=1 - [NOP58_RAT]	catalytic activity; RNA binding; protein binding	nucleus; cytoplasm; membrane	IISDNLTYCK
313	Q9QZ86	Nucleolar protein 58 OS=Rattus norvegicus GN=Nop58 PE=1 SV=1 - [NOP58_RAT]	catalytic activity; RNA binding; protein binding	nucleus; cytoplasm; membrane	TYDPSGDSTLPTCSK
314	Q4KLK7	Nucleolar protein 5A OS=Rattus norvegicus GN=Nop56 PE=2 SV=1 - [Q4KLK7_RAT]	RNA binding	membrane	FSEEPEAAASCTK
314	Q4KLK7	Nucleolar protein 5A OS=Rattus norvegicus GN=Nop56 PE=2 SV=1 - [Q4KLK7_RAT]	RNA binding	membrane	GLTDLSACK
314	Q4KLK7	Nucleolar protein 5A OS=Rattus norvegicus GN=Nop56 PE=2 SV=1 - [Q4KLK7_RAT]	RNA binding	membrane	IDCFSEVPTSVFGEK
314	Q4KLK7	Nucleolar protein 5A OS=Rattus norvegicus GN=Nop56 PE=2 SV=1 - [Q4KLK7_RAT]	RNA binding	membrane	IINDNATYCR
314	Q4KLK7	Nucleolar protein 5A OS=Rattus norvegicus GN=Nop56 PE=2 SV=1 - [Q4KLK7_RAT]	RNA binding	membrane	KFSEEPEAAASCTK
315	Q3B8Q1	Nucleolar RNA helicase 2 OS=Rattus norvegicus GN=Ddx21 PE=2 SV=1 - [DDX21_RAT]	nucleotide binding; RNA binding; catalytic activity	nucleus; membrane	KDAQELSQNTCIK
315	Q3B8Q1	Nucleolar RNA helicase 2 OS=Rattus norvegicus GN=Ddx21 PE=2 SV=1 - [DDX21_RAT]	nucleotide binding; RNA binding; catalytic activity	nucleus; membrane	LGVCFDVR
315	Q3B8Q1	Nucleolar RNA helicase 2 OS=Rattus norvegicus GN=Ddx21 PE=2 SV=1 - [DDX21_RAT]	nucleotide binding; RNA binding; catalytic activity	nucleus; membrane	LSVACFYGGTPYGGQIER

315	Q3B8Q1	Nucleolar RNA helicase 2 OS=Rattus norvegicus GN=Ddx21 PE=2 SV=1 - [DDX21_RAT]	nucleotide binding; RNA binding; catalytic activity	nucleus; membrane	TIIFCETK
316	P25977	Nucleolar transcription factor 1 OS=Rattus norvegicus GN=Ubtf PE=1 SV=1 - [UBF1_RAT]	DNA binding; protein binding; RNA binding	nucleus	MVLCSQQWK
318	P13084	Nucleophosmin OS=Rattus norvegicus GN=Npm1 PE=1 SV=1 - [NPM_RAT]	DNA binding; RNA binding; enzyme regulator activity; protein binding	nucleus; cytoplasm; cytosol; cytoskeleton; membrane	CGSGPVHISGQHLVAVEEDAESEDEDEEDVK
319	D4A7R3	Nucleoporin 205kDa (Predicted) OS=Rattus norvegicus GN=Nup205 PE=4 SV=1 - [D4A7R3_RAT]	transporter activity; structural molecule activity	cytoplasm; membrane	AQIEQVIANCEHK
319	D4A7R3	Nucleoporin 205kDa (Predicted) OS=Rattus norvegicus GN=Nup205 PE=4 SV=1 - [D4A7R3_RAT]	transporter activity; structural molecule activity	cytoplasm; membrane	DACDGHEIGR
319	D4A7R3	Nucleoporin 205kDa (Predicted) OS=Rattus norvegicus GN=Nup205 PE=4 SV=1 - [D4A7R3_RAT]	transporter activity; structural molecule activity	cytoplasm; membrane	KPISTTNLQDPGVLGCPR
319	D4A7R3	Nucleoporin 205kDa (Predicted) OS=Rattus norvegicus GN=Nup205 PE=4 SV=1 - [D4A7R3_RAT]	transporter activity; structural molecule activity	cytoplasm; membrane	LAQCQVYDMRPEVDSHSMFGMR
319	D4A7R3	Nucleoporin 205kDa (Predicted) OS=Rattus norvegicus GN=Nup205 PE=4 SV=1 - [D4A7R3_RAT]	transporter activity; structural molecule activity	cytoplasm; membrane	NLQGQTVCNVK
319	D4A7R3	Nucleoporin 205kDa (Predicted) OS=Rattus norvegicus GN=Nup205 PE=4 SV=1 - [D4A7R3_RAT]	transporter activity; structural molecule activity	cytoplasm; membrane	QCLGLLSR
321	F1MA98	Nucleoprotein TPR OS=Rattus norvegicus GN=Tpr PE=1 SV=1 - [TPR_RAT]	RNA binding; catalytic activity; motor activity; transporter activity; nucleotide binding; protein binding	chromosome; nucleus; cytoplasm; cytoskeleton; membrane	AESQLLECK
321	F1MA98	Nucleoprotein TPR OS=Rattus norvegicus GN=Tpr PE=1 SV=1 - [TPR_RAT]	RNA binding; catalytic activity; motor activity; transporter activity; nucleotide binding; protein binding	chromosome; nucleus; cytoplasm; cytoskeleton; membrane	FLAEQQSEIDCLK
322	P19804	Nucleoside diphosphate kinase B OS=Rattus norvegicus GN=Nme2 PE=1 SV=1 - [NDKB_RAT]	nucleotide binding; catalytic activity; protein binding; metal ion binding	nucleus; cytoplasm; mitochondrion; cytosol; membrane	GDFCIQVGR
323	A1L1I3	Numb-like protein OS=Rattus norvegicus GN=Numbl PE=1 SV=1 - [NUMBL_RAT]	protein binding	cytoplasm	ECGVTAAFDASR
323	A1L1I3	Numb-like protein OS=Rattus norvegicus GN=Numbl PE=1 SV=1 - [NUMBL_RAT]	protein binding	cytoplasm	KGTCSFPVR
323	A1L1I3	Numb-like protein OS=Rattus norvegicus GN=Numbl PE=1 SV=1 - [NUMBL_RAT]	protein binding	cytoplasm	VSFCAPDR
324	G3V6F4	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase), isoform CRA_b OS=Rattus norvegicus GN=Ogt PE=4 SV=2 - [G3V6F4_RAT]	protein binding; enzyme regulator activity; catalytic activity	nucleus; cytoplasm; mitochondrion; cytosol; membrane	EKGSVAEAEDCYNTALR
324	G3V6F4	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase), isoform CRA_b OS=Rattus norvegicus GN=Ogt PE=4 SV=2 - [G3V6F4_RAT]	protein binding; enzyme regulator activity; catalytic activity	nucleus; cytoplasm; mitochondrion; cytosol; membrane	EMQDVQGALQCYTR
324	G3V6F4	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase), isoform CRA_b OS=Rattus norvegicus GN=Ogt PE=4 SV=2 - [G3V6F4_RAT]	protein binding; enzyme regulator activity; catalytic activity	nucleus; cytoplasm; mitochondrion; cytosol; membrane	HGNLCLDK
324	G3V6F4	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase), isoform CRA_b OS=Rattus norvegicus GN=Ogt PE=4 SV=2 - [G3V6F4_RAT]	protein binding; enzyme regulator activity; catalytic activity	nucleus; cytoplasm; mitochondrion; cytosol; membrane	LCPTHADSLNNLANIK
324	G3V6F4	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase), isoform CRA_b OS=Rattus norvegicus GN=Ogt PE=4 SV=2 - [G3V6F4_RAT]	protein binding; enzyme regulator activity; catalytic activity	nucleus; cytoplasm; mitochondrion; cytosol; membrane	VMAEANHFIDLSQIPCNGK
325	D3ZJ19	One cut domain family member OS=Rattus norvegicus GN=Satb2 PE=3 SV=1 - [D3ZJ19_RAT]	DNA binding	nucleus; cytoplasm	ECPLSQSMISSIVNSTYYANVSATK
325	D3ZJ19	One cut domain family member OS=Rattus norvegicus GN=Satb2 PE=3 SV=1 - [D3ZJ19_RAT]	DNA binding	nucleus; cytoplasm	ESSPPREEAPPPPPPTEDSCAK

325	D3ZJ19	One cut domain family member OS=Rattus norvegicus GN=Satb2 PE=3 SV=1 - [D3ZJ19_RAT]	DNA binding	nucleus; cytoplasm	IQLQSCSKLEDLPAEQWNHATVR
326	F2Z3T0	Parafibromin OS=Rattus norvegicus GN=Cdc73 PE=4 SV=1 - [F2Z3T0_RAT]	protein binding	nucleus	IEDEECVRLDK
327	F1SW39	PC4 and SFRS1 interacting protein 1 OS=Rattus norvegicus GN=Psip1 PE=2 SV=1 - [F1SW39_RAT]	protein binding; RNA binding; DNA binding	nucleus	QPCPSESDMVIDEDKSK
329	P10111	Peptidyl-prolyl cis-trans isomerase A OS=Rattus norvegicus GN=Ppia PE=1 SV=2 - [PPIA_RAT]	catalytic activity; RNA binding	extracellular; nucleus; cytoplasm; cytosol; membrane	IIPGFMCQGGDFTR
329	P10111	Peptidyl-prolyl cis-trans isomerase A OS=Rattus norvegicus GN=Ppia PE=1 SV=2 - [PPIA_RAT]	catalytic activity; RNA binding	extracellular; nucleus; cytoplasm; cytosol; membrane	KITISDCGQL
329	P10111	Peptidyl-prolyl cis-trans isomerase A OS=Rattus norvegicus GN=Ppia PE=1 SV=2 - [PPIA_RAT]	catalytic activity; RNA binding	extracellular; nucleus; cytoplasm; cytosol; membrane	VCFELFADKVPK
331	P97852	Peroxisomal multifunctional enzyme type 2 OS=Rattus norvegicus GN=Hsd17b4 PE=1 SV=3 - [DHB4_RAT]	nucleotide binding; catalytic activity; protein binding	mitochondrion; membrane	ICDFSNASKPK
331	P97852	Peroxisomal multifunctional enzyme type 2 OS=Rattus norvegicus GN=Hsd17b4 PE=1 SV=3 - [DHB4_RAT]	nucleotide binding; catalytic activity; protein binding	mitochondrion; membrane	KNNIHCNTIAPNAGSR
332	F1LWX5	PHD finger protein 2 (Predicted) OS=Rattus norvegicus GN=Phf2 PE=4 SV=2 - [F1LWX5_RAT]	metal ion binding; protein binding; catalytic activity	nucleus; cytoplasm	TVRPEVNAVASSDEVCDGDR
334	D3ZKI5	PHD finger protein 3 (Predicted) OS=Rattus norvegicus GN=Phf3 PE=4 SV=1 - [D3ZKI5_RAT]	protein binding; metal ion binding	nucleus	CQGKEEVYASLK
334	D3ZKI5	PHD finger protein 3 (Predicted) OS=Rattus norvegicus GN=Phf3 PE=4 SV=1 - [D3ZKI5_RAT]	protein binding; metal ion binding	nucleus	DSAALTCAGEK
334	D3ZKI5	PHD finger protein 3 (Predicted) OS=Rattus norvegicus GN=Phf3 PE=4 SV=1 - [D3ZKI5_RAT]	protein binding; metal ion binding	nucleus	GSATSSSHFEGGNTCQSEFPSK
334	D3ZKI5	PHD finger protein 3 (Predicted) OS=Rattus norvegicus GN=Phf3 PE=4 SV=1 - [D3ZKI5_RAT]	protein binding; metal ion binding	nucleus	GSVDGNVSCSENLVANTR
334	D3ZKI5	PHD finger protein 3 (Predicted) OS=Rattus norvegicus GN=Phf3 PE=4 SV=1 - [D3ZKI5_RAT]	protein binding; metal ion binding	nucleus	HSVCAPSYNREPVEPVSGEGKPSSLEK
334	D3ZKI5	PHD finger protein 3 (Predicted) OS=Rattus norvegicus GN=Phf3 PE=4 SV=1 - [D3ZKI5_RAT]	protein binding; metal ion binding	nucleus	LEQESEEIKFSCEGDR
334	D3ZKI5	PHD finger protein 3 (Predicted) OS=Rattus norvegicus GN=Phf3 PE=4 SV=1 - [D3ZKI5_RAT]	protein binding; metal ion binding	nucleus	NEGAQCHLELK
334	D3ZKI5	PHD finger protein 3 (Predicted) OS=Rattus norvegicus GN=Phf3 PE=4 SV=1 - [D3ZKI5_RAT]	protein binding; metal ion binding	nucleus	QHLFDLNCK
334	D3ZKI5	PHD finger protein 3 (Predicted) OS=Rattus norvegicus GN=Phf3 PE=4 SV=1 - [D3ZKI5_RAT]	protein binding; metal ion binding	nucleus	RTEALMECK
334	D3ZKI5	PHD finger protein 3 (Predicted) OS=Rattus norvegicus GN=Phf3 PE=4 SV=1 - [D3ZKI5_RAT]	protein binding; metal ion binding	nucleus	SQQTVSDSKDGESCR
334	D3ZKI5	PHD finger protein 3 (Predicted) OS=Rattus norvegicus GN=Phf3 PE=4 SV=1 - [D3ZKI5_RAT]	protein binding; metal ion binding	nucleus	TEALMECK
335	P83871	PHD finger-like domain-containing protein 5A OS=Rattus norvegicus GN=Phf5a PE=2 SV=1 - [PHF5A_RAT]	DNA binding; RNA binding	nucleus; spliceosomal complex	HHPDLIFCR
336	G3V741	Phosphate carrier protein, mitochondrial OS=Rattus norvegicus GN=Slc25a3 PE=3 SV=1 - [G3V741_RAT]	transporter activity; protein binding	mitochondrion; membrane	FACFERTVEALYK
338	F1LPG3	Phosphofurin acidic cluster sorting protein 1 OS=Rattus norvegicus GN=Pacs1 PE=4 SV=1 - [F1LPG3_RAT]	protein binding	Golgi	SSSSCVPR
341	P63004	Platelet-activating factor acetylhydrolase IB subunit alpha OS=Rattus norvegicus GN=Pafah1b1 PE=1 SV=2 - [LIS1_RAT]	protein binding; catalytic activity	chromosome; nucleus; cytoplasm; cytosol; cytoskeleton; membrane	LLASCSADMTIK
341	P63004	Platelet-activating factor acetylhydrolase IB subunit alpha OS=Rattus norvegicus GN=Pafah1b1 PE=1 SV=2 - [LIS1_RAT]	protein binding; catalytic activity	chromosome; nucleus; cytoplasm; cytosol; cytoskeleton; membrane	MVRPNQDGTLIASCSNDQTVR
341	P63004	Platelet-activating factor acetylhydrolase IB subunit alpha OS=Rattus norvegicus GN=Pafah1b1 PE=1 SV=2 - [LIS1_RAT]	protein binding; catalytic activity	chromosome; nucleus; cytoplasm; cytosol; cytoskeleton; membrane	MWEVQTGYCVK
342	P27008	Poly [ADP-ribose] polymerase 1 OS=Rattus norvegicus GN=Parp1 PE=1 SV=4 - [PARP1_RAT]	DNA binding; catalytic activity; protein binding; metal ion binding; RNA binding; nucleotide binding	nucleus; cytoplasm; membrane	ASLCISTK

342	P27008	Poly [ADP-ribose] polymerase 1 OS=Rattus norvegicus GN=Parp1 PE=1 SV=4 - [PARP1_RAT]	DNA binding; catalytic activity; protein binding; metal ion binding; RNA binding; nucleotide binding	nucleus; cytoplasm; membrane	ECSGQLVFK
342	P27008	Poly [ADP-ribose] polymerase 1 OS=Rattus norvegicus GN=Parp1 PE=1 SV=4 - [PARP1_RAT]	DNA binding; catalytic activity; protein binding; metal ion binding; RNA binding; nucleotide binding	nucleus; cytoplasm; membrane	RKCDEVDGIDEVAK
342	P27008	Poly [ADP-ribose] polymerase 1 OS=Rattus norvegicus GN=Parp1 PE=1 SV=4 - [PARP1_RAT]	DNA binding; catalytic activity; protein binding; metal ion binding; RNA binding; nucleotide binding	nucleus; cytoplasm; membrane	SDAYYCTGDVTAWTK
342	P27008	Poly [ADP-ribose] polymerase 1 OS=Rattus norvegicus GN=Parp1 PE=1 SV=4 - [PARP1_RAT]	DNA binding; catalytic activity; protein binding; metal ion binding; RNA binding; nucleotide binding	nucleus; cytoplasm; membrane	VADGMAFGALLPCK
342	P27008	Poly [ADP-ribose] polymerase 1 OS=Rattus norvegicus GN=Parp1 PE=1 SV=4 - [PARP1_RAT]	DNA binding; catalytic activity; protein binding; metal ion binding; RNA binding; nucleotide binding	nucleus; cytoplasm; membrane	VVCEDFLQDVSASAK
344	Q6AYU5	Poly(RC) binding protein 2 OS=Rattus norvegicus GN=Pcbp2 PE=2 SV=1 - [Q6AYU5_RAT]	RNA binding; protein binding	nucleus; cytoplasm; membrane	AITIAGIPQSIIECVK
345	Q6AY48	Poly(RC) binding protein 3 OS=Rattus norvegicus GN=Pcbp3 PE=2 SV=1 - [Q6AY48_RAT]	RNA binding	nucleus; mitochondrion; cytosol	AVTISGTPDAIIQCVK
345	Q6AY48	Poly(RC) binding protein 3 OS=Rattus norvegicus GN=Pcbp3 PE=2 SV=1 - [Q6AY48_RAT]	RNA binding	nucleus; mitochondrion; cytosol	QICVVMLESPPK
346	Q9EPH8	Polyadenylate-binding protein 1 OS=Rattus norvegicus GN=Pabpc1 PE=1 SV=1 - [PABP1_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex; cytoplasm; membrane	GFGFVCFSSPEEATK
348	D4A2B0	Polymerase (DNA-directed), delta interacting protein 3 (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Poldip3 PE=4 SV=1 - [D4A2B0_RAT]	nucleotide binding; RNA binding	nucleus	CLDGQPMK
351	F1M7A3	POU domain protein (Fragment) OS=Rattus norvegicus GN=Pou3f3 PE=3 SV=2 - [F1M7A3_RAT]	DNA binding; protein binding	nucleus	CPKPSAQEITNLADSLQLEK
355	Q9JMJ4	Pre-mRNA-processing factor 19 OS=Rattus norvegicus GN=Prpf19 PE=1 SV=2 - [PRP19_RAT]	DNA binding; catalytic activity; protein binding	nucleus; spliceosomal complex; cytoplasm; cytoskeleton; membrane	IWSVPNTSCVQVVR
355	Q9JMJ4	Pre-mRNA-processing factor 19 OS=Rattus norvegicus GN=Prpf19 PE=1 SV=2 - [PRP19_RAT]	DNA binding; catalytic activity; protein binding	nucleus; spliceosomal complex; cytoplasm; cytoskeleton; membrane	QELSHALYQHDAACR
356	A1A5S1	Pre-mRNA-processing factor 6 OS=Rattus norvegicus GN=Prpf6 PE=2 SV=1 - [PRP6_RAT]	RNA binding; protein binding	nucleus; spliceosomal complex; membrane	AGSVATCQAVMR
356	A1A5S1	Pre-mRNA-processing factor 6 OS=Rattus norvegicus GN=Prpf6 PE=2 SV=1 - [PRP6_RAT]	RNA binding; protein binding	nucleus; spliceosomal complex; membrane	CEHDPHVLLAVAK
356	A1A5S1	Pre-mRNA-processing factor 6 OS=Rattus norvegicus GN=Prpf6 PE=2 SV=1 - [PRP6_RAT]	RNA binding; protein binding	nucleus; spliceosomal complex; membrane	EQWIQDAEECDR
356	A1A5S1	Pre-mRNA-processing factor 6 OS=Rattus norvegicus GN=Prpf6 PE=2 SV=1 - [PRP6_RAT]	RNA binding; protein binding	nucleus; spliceosomal complex; membrane	HGELWCAVSK
358	Q56B11	Proline-, glutamic acid- and leucine-rich protein 1 OS=Rattus norvegicus GN=Pelp1 PE=2 SV=2 - [PELP1_RAT]	protein binding; RNA binding	nucleus; cytoplasm; membrane	ACVTYFPR
358	Q56B11	Proline-, glutamic acid- and leucine-rich protein 1 OS=Rattus norvegicus GN=Pelp1 PE=2 SV=2 - [PELP1_RAT]	protein binding; RNA binding	nucleus; cytoplasm; membrane	NADSDVCAAALR
358	Q56B11	Proline-, glutamic acid- and leucine-rich protein 1 OS=Rattus norvegicus GN=Pelp1 PE=2 SV=2 - [PELP1_RAT]	protein binding; RNA binding	nucleus; cytoplasm; membrane	TILMCGPLVK
358	Q56B11	Proline-, glutamic acid- and leucine-rich protein 1 OS=Rattus norvegicus GN=Pelp1 PE=2 SV=2 - [PELP1_RAT]	protein binding; RNA binding	nucleus; cytoplasm; membrane	VPPLQSSGPACPTPAPVPPPEAPSSFR
359	E9PST5	Protein Acin1 OS=Rattus norvegicus GN=Acin1 PE=1 SV=1 - [E9PST5_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm; membrane	AAPCIYWLPLTESQIVQK
359	E9PST5	Protein Acin1 OS=Rattus norvegicus GN=Acin1 PE=1 SV=1 - [E9PST5_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm; membrane	KCEAEEAEPPAATQPQTSEPQLSQLPEAER
359	E9PST5	Protein Acin1 OS=Rattus norvegicus GN=Acin1 PE=1 SV=1 - [E9PST5_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm; membrane	SHCFVTYSTVEEAVATR
361	D3ZIE9	Protein Aldh18a1 OS=Rattus norvegicus GN=Aldh18a1 PE=4 SV=1 - [D3ZIE9_RAT]	catalytic activity; RNA binding	cytoplasm; mitochondrion	EEVEDLCRLDK
361	D3ZIE9	Protein Aldh18a1 OS=Rattus norvegicus GN=Aldh18a1 PE=4 SV=1 - [D3ZIE9_RAT]	catalytic activity; RNA binding	cytoplasm; mitochondrion	GDECGLALGR

361	D3ZIE9	Protein Aldh18a1 OS=Rattus norvegicus GN=Aldh18a1 PE=4 SV=1 - [D3ZIE9_RAT]	catalytic activity; RNA binding	cytoplasm; mitochondrion	GIPVMGHSEGICHMYVDSEASVDK
362	F1M9N9	Protein Ank2 (Fragment) OS=Rattus norvegicus GN=Ank2 PE=4 SV=2 - [F1M9N9_RAT]	structural molecule activity; protein binding	cytoskeleton; membrane	ATVIPDSLCK
362	F1M9N9	Protein Ank2 (Fragment) OS=Rattus norvegicus GN=Ank2 PE=4 SV=2 - [F1M9N9_RAT]	structural molecule activity; protein binding	cytoskeleton; membrane	DGLTPLHCAAR
362	F1M9N9	Protein Ank2 (Fragment) OS=Rattus norvegicus GN=Ank2 PE=4 SV=2 - [F1M9N9_RAT]	structural molecule activity; protein binding	cytoskeleton; membrane	DSQLPLVSSACK
362	F1M9N9	Protein Ank2 (Fragment) OS=Rattus norvegicus GN=Ank2 PE=4 SV=2 - [F1M9N9_RAT]	structural molecule activity; protein binding	cytoskeleton; membrane	DTTQEPCGR
362	F1M9N9	Protein Ank2 (Fragment) OS=Rattus norvegicus GN=Ank2 PE=4 SV=2 - [F1M9N9_RAT]	structural molecule activity; protein binding	cytoskeleton; membrane	GGIDINTCNQNGLNALHLAAK
362	F1M9N9	Protein Ank2 (Fragment) OS=Rattus norvegicus GN=Ank2 PE=4 SV=2 - [F1M9N9_RAT]	structural molecule activity; protein binding	cytoskeleton; membrane	HATDTVLIECLTK
362	F1M9N9	Protein Ank2 (Fragment) OS=Rattus norvegicus GN=Ank2 PE=4 SV=2 - [F1M9N9_RAT]	structural molecule activity; protein binding	cytoskeleton; membrane	MNEEVKEDPGNPEEDKDCK
362	F1M9N9	Protein Ank2 (Fragment) OS=Rattus norvegicus GN=Ank2 PE=4 SV=2 - [F1M9N9_RAT]	structural molecule activity; protein binding	cytoskeleton; membrane	QHAPVEIAEHPCVEVR
362	F1M9N9	Protein Ank2 (Fragment) OS=Rattus norvegicus GN=Ank2 PE=4 SV=2 - [F1M9N9_RAT]	structural molecule activity; protein binding	cytoskeleton; membrane	QTSCPTFPEPVGQLDFSTVTR
362	F1M9N9	Protein Ank2 (Fragment) OS=Rattus norvegicus GN=Ank2 PE=4 SV=2 - [F1M9N9_RAT]	structural molecule activity; protein binding	cytoskeleton; membrane	VESTQASLPSEHSSLSSSSHCAVPEENESAK
362	F1M9N9	Protein Ank2 (Fragment) OS=Rattus norvegicus GN=Ank2 PE=4 SV=2 - [F1M9N9_RAT]	structural molecule activity; protein binding	cytoskeleton; membrane	VRDTTQEPCGR
364	F1LXQ7	Protein Arhgap21 (Fragment) OS=Rattus norvegicus GN=Arhgap21 PE=1 SV=2 - [F1LXQ7_RAT]	protein binding	Golgi	EGGPAFEAGLCTGDR
364	F1LXQ7	Protein Arhgap21 (Fragment) OS=Rattus norvegicus GN=Arhgap21 PE=1 SV=2 - [F1LXQ7_RAT]	protein binding	Golgi	LDDCPPAHTNR
364	F1LXQ7	Protein Arhgap21 (Fragment) OS=Rattus norvegicus GN=Arhgap21 PE=1 SV=2 - [F1LXQ7_RAT]	protein binding	Golgi	LIECDTLSR
364	F1LXQ7	Protein Arhgap21 (Fragment) OS=Rattus norvegicus GN=Arhgap21 PE=1 SV=2 - [F1LXQ7_RAT]	protein binding	Golgi	SLLTQKPHCEETGSDSGTLSSQASLAR
365	D3ZJU0	Protein Arid2 OS=Rattus norvegicus GN=Arid2 PE=4 SV=2 - [D3ZJU0_RAT]	DNA binding; metal ion binding	nucleus; membrane	AEMYSEYLSTCSK
365	D3ZJU0	Protein Arid2 OS=Rattus norvegicus GN=Arid2 PE=4 SV=2 - [D3ZJU0_RAT]	DNA binding; metal ion binding	nucleus; membrane	GMEILGNLCK
365	D3ZJU0	Protein Arid2 OS=Rattus norvegicus GN=Arid2 PE=4 SV=2 - [D3ZJU0_RAT]	DNA binding; metal ion binding	nucleus; membrane	IEVMENPSCR
365	D3ZJU0	Protein Arid2 OS=Rattus norvegicus GN=Arid2 PE=4 SV=2 - [D3ZJU0_RAT]	DNA binding; metal ion binding	nucleus; membrane	IICQKEEEAK
365	D3ZJU0	Protein Arid2 OS=Rattus norvegicus GN=Arid2 PE=4 SV=2 - [D3ZJU0_RAT]	DNA binding; metal ion binding	nucleus; membrane	IVTISDPNNAGCSATMVAVPAGADPSTVAK
365	D3ZJU0	Protein Arid2 OS=Rattus norvegicus GN=Arid2 PE=4 SV=2 - [D3ZJU0_RAT]	DNA binding; metal ion binding	nucleus; membrane	KIEVMENPSCR
365	D3ZJU0	Protein Arid2 OS=Rattus norvegicus GN=Arid2 PE=4 SV=2 - [D3ZJU0_RAT]	DNA binding; metal ion binding	nucleus; membrane	SCSNAAFALK
365	D3ZJU0	Protein Arid2 OS=Rattus norvegicus GN=Arid2 PE=4 SV=2 - [D3ZJU0_RAT]	DNA binding; metal ion binding	nucleus; membrane	TCNHVGNGEVSPVEPQGTLGATQQETAK
366	D3ZSY3	Protein Bcl11a OS=Rattus norvegicus GN=Bcl11a PE=4 SV=1 - [D3ZSY3_RAT]	DNA binding; metal ion binding; protein binding	nucleus	ASNPVEVGIQVTPEDDDCLSTSSR
366	D3ZSY3	Protein Bcl11a OS=Rattus norvegicus GN=Bcl11a PE=4 SV=1 - [D3ZSY3_RAT]	DNA binding; metal ion binding; protein binding	nucleus	DTCDEDSVAGESDR
366	D3ZSY3	Protein Bcl11a OS=Rattus norvegicus GN=Bcl11a PE=4 SV=1 - [D3ZSY3_RAT]	DNA binding; metal ion binding; protein binding	nucleus	GCSPGESASGGLSK
366	D3ZSY3	Protein Bcl11a OS=Rattus norvegicus GN=Bcl11a PE=4 SV=1 - [D3ZSY3_RAT]	DNA binding; metal ion binding; protein binding	nucleus	KASNPVEVGIQVTPEDDDCLSTSSR

366	D3ZSY3	Protein Bcl11a OS=Rattus norvegicus GN=Bcl11a PE=4 SV=1 - [D3ZSY3_RAT]	DNA binding; metal ion binding; protein binding	nucleus	SAHGALIPTPGMSAEYAPQGICK
366	D3ZSY3	Protein Bcl11a OS=Rattus norvegicus GN=Bcl11a PE=4 SV=1 - [D3ZSY3_RAT]	DNA binding; metal ion binding; protein binding	nucleus	SHLAEAEGHRDTCDEDSVAGESDRIDDGTVNGR
368	F7FMD6	Protein Camlg OS=Rattus norvegicus GN=Camlg PE=4 SV=1 - [F7FMD6_RAT]	protein binding	endoplasmic reticulum	APECSSKDGVELR
369	D4A2P1	Protein Ccar1 OS=Rattus norvegicus GN=Ccar1 PE=4 SV=2 - [D4A2P1_RAT]	metal ion binding; RNA binding		SCALAEDPQDLR
370	D4AC23	Protein Cct7 OS=Rattus norvegicus GN=Cct7 PE=3 SV=1 - [D4AC23_RAT]	nucleotide binding; protein binding	cytoplasm; mitochondrion	CAMTALSSK
370	D4AC23	Protein Cct7 OS=Rattus norvegicus GN=Cct7 PE=3 SV=1 - [D4AC23_RAT]	nucleotide binding; protein binding	cytoplasm; mitochondrion	CQVFEETQIGGER
370	D4AC23	Protein Cct7 OS=Rattus norvegicus GN=Cct7 PE=3 SV=1 - [D4AC23_RAT]	nucleotide binding; protein binding	cytoplasm; mitochondrion	QLCDNAGFDATNILNK
370	D4AC23	Protein Cct7 OS=Rattus norvegicus GN=Cct7 PE=3 SV=1 - [D4AC23_RAT]	nucleotide binding; protein binding	cytoplasm; mitochondrion	TCTIILR
370	D4AC23	Protein Cct7 OS=Rattus norvegicus GN=Cct7 PE=3 SV=1 - [D4AC23_RAT]	nucleotide binding; protein binding	cytoplasm; mitochondrion	YNFFTGCPK
371	B5DEG7	Protein Champ1 OS=Rattus norvegicus GN=Champ1 PE=2 SV=1 - [B5DEG7_RAT]	metal ion binding	chromosome; nucleus	CESLVQEGLLATPK
371	B5DEG7	Protein Champ1 OS=Rattus norvegicus GN=Champ1 PE=2 SV=1 - [B5DEG7_RAT]	metal ion binding	chromosome; nucleus	CNFESNFPR
371	B5DEG7	Protein Champ1 OS=Rattus norvegicus GN=Champ1 PE=2 SV=1 - [B5DEG7_RAT]	metal ion binding	chromosome; nucleus	SALVSCKPQR
372	F1LPP8	Protein Chd3 (Fragment) OS=Rattus norvegicus GN=Chd3 PE=4 SV=2 - [F1LPP8_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding; metal ion binding	nucleus; cytoplasm; cytoskeleton	AGSCVFQGDEGPEPEAEESDLDSGSVHSASGRPDGPVR
372	F1LPP8	Protein Chd3 (Fragment) OS=Rattus norvegicus GN=Chd3 PE=4 SV=2 - [F1LPP8_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding; metal ion binding	nucleus; cytoplasm; cytoskeleton	AYHLVCLDPELDRAPEGK
372	F1LPP8	Protein Chd3 (Fragment) OS=Rattus norvegicus GN=Chd3 PE=4 SV=2 - [F1LPP8_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding; metal ion binding	nucleus; cytoplasm; cytoskeleton	FAEAECLAESHQHLSK
372	F1LPP8	Protein Chd3 (Fragment) OS=Rattus norvegicus GN=Chd3 PE=4 SV=2 - [F1LPP8_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding; metal ion binding	nucleus; cytoplasm; cytoskeleton	HLCEPGADGSETFADGVPR
372	F1LPP8	Protein Chd3 (Fragment) OS=Rattus norvegicus GN=Chd3 PE=4 SV=2 - [F1LPP8_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding; metal ion binding	nucleus; cytoplasm; cytoskeleton	WACLVVDEAHR
373	E9PU01	Protein Chd4 OS=Rattus norvegicus GN=Chd4 PE=4 SV=2 - [E9PU01_RAT]	protein binding; DNA binding; catalytic activity; nucleotide binding; metal ion binding	nucleus; cytoplasm	AYHMVCLDPDMEKAPEGK
373	E9PU01	Protein Chd4 OS=Rattus norvegicus GN=Chd4 PE=4 SV=2 - [E9PU01_RAT]	protein binding; DNA binding; catalytic activity; nucleotide binding; metal ion binding	nucleus; cytoplasm	FAEVECLAESHQHLSK
375	F1LNR0	Protein Clasp1 OS=Rattus norvegicus GN=Clasp1 PE=4 SV=2 - [F1LNR0_RAT]	protein binding		DCDIVSR
375	F1LNR0	Protein Clasp1 OS=Rattus norvegicus GN=Clasp1 PE=4 SV=2 - [F1LNR0_RAT]	protein binding		QTEDVAEVLNHCASSNWSER
376	D4A6H8	Protein Ctnna2 (Fragment) OS=Rattus norvegicus GN=Ctnna2 PE=4 SV=2 - [D4A6H8_RAT]	structural molecule activity; protein binding	cytoplasm; cytoskeleton; membrane	CVIALQEGDVDTLDR
376	D4A6H8	Protein Ctnna2 (Fragment) OS=Rattus norvegicus GN=Ctnna2 PE=4 SV=2 - [D4A6H8_RAT]	structural molecule activity; protein binding	cytoplasm; cytoskeleton; membrane	IASSEFADDPCSSVKR
376	D4A6H8	Protein Ctnna2 (Fragment) OS=Rattus norvegicus GN=Ctnna2 PE=4 SV=2 - [D4A6H8_RAT]	structural molecule activity; protein binding	cytoplasm; cytoskeleton; membrane	LVEVANLACSISNNEEGVK
376	D4A6H8	Protein Ctnna2 (Fragment) OS=Rattus norvegicus GN=Ctnna2 PE=4 SV=2 - [D4A6H8_RAT]	structural molecule activity; protein binding	cytoplasm; cytoskeleton; membrane	QQELKDPHCRDEMAAAR
378	D3ZN21	Protein Ddx3y OS=Rattus norvegicus GN=Ddx3y PE=3 SV=1 - [D3ZN21_RAT]	nucleotide binding; DNA binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; membrane	DLMACAQTGSGK
378	D3ZN21	Protein Ddx3y OS=Rattus norvegicus GN=Ddx3y PE=3 SV=1 - [D3ZN21_RAT]	nucleotide binding; DNA binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; membrane	GCHLLVATPGR
378	D3ZN21	Protein Ddx3y OS=Rattus norvegicus GN=Ddx3y PE=3 SV=1 - [D3ZN21_RAT]	nucleotide binding; DNA binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; membrane	RDLMACAQTGSGK

379	Q6AXS3	Protein DEK OS=Rattus norvegicus GN=Dek PE=2 SV=1 - [DEK_RAT]	DNA binding; protein binding; RNA binding	nucleus	SICEVLDLER
380	D3ZWL9	Protein Dido1 OS=Rattus norvegicus GN=Dido1 PE=4 SV=1 - [D3ZWL9_RAT]	protein binding; metal ion binding	nucleus	AHLFDLNCK
380	D3ZWL9	Protein Dido1 OS=Rattus norvegicus GN=Dido1 PE=4 SV=1 - [D3ZWL9_RAT]	protein binding; metal ion binding	nucleus	HDSSPPDAVPSTADEGIAETPENTCDPDLETV SSLNQER
380	D3ZWL9	Protein Dido1 OS=Rattus norvegicus GN=Dido1 PE=4 SV=1 - [D3ZWL9_RAT]	protein binding; metal ion binding	nucleus	ICTGQVPSSEDEPAPK
380	D3ZWL9	Protein Dido1 OS=Rattus norvegicus GN=Dido1 PE=4 SV=1 - [D3ZWL9_RAT]	protein binding; metal ion binding	nucleus	TALSGSCTVTASMAAHMDNSQTSETK
383	F1LM66	Protein Eftud2 OS=Rattus norvegicus GN=Eftud2 PE=4 SV=1 - [F1LM66_RAT]	nucleotide binding; catalytic activity; RNA binding	nucleus; cytoplasm; membrane; spliceosomal complex	EGPLCDELIR
383	F1LM66	Protein Eftud2 OS=Rattus norvegicus GN=Eftud2 PE=4 SV=1 - [F1LM66_RAT]	nucleotide binding; catalytic activity; RNA binding	nucleus; cytoplasm; membrane; spliceosomal complex	VLGENYTLEDEEDSQICTVGR
383	F1LM66	Protein Eftud2 OS=Rattus norvegicus GN=Eftud2 PE=4 SV=1 - [F1LM66_RAT]	nucleotide binding; catalytic activity; RNA binding	nucleus; cytoplasm; membrane; spliceosomal complex	YDQDLCYTDILFTEQER
384	D4A005	Protein Ehmt1 OS=Rattus norvegicus GN=Ehmt1 PE=4 SV=2 - [D4A005_RAT]	protein binding; catalytic activity; metal ion binding	nucleus; chromosome	APLLVLCEDHR
384	D4A005	Protein Ehmt1 OS=Rattus norvegicus GN=Ehmt1 PE=4 SV=2 - [D4A005_RAT]	protein binding; catalytic activity; metal ion binding	nucleus; chromosome	DAEGSTCLHLAAK
384	D4A005	Protein Ehmt1 OS=Rattus norvegicus GN=Ehmt1 PE=4 SV=2 - [D4A005_RAT]	protein binding; catalytic activity; metal ion binding	nucleus; chromosome	EISTLANNQCMATESVDHELGR
384	D4A005	Protein Ehmt1 OS=Rattus norvegicus GN=Ehmt1 PE=4 SV=2 - [D4A005_RAT]	protein binding; catalytic activity; metal ion binding	nucleus; chromosome	KKPSSMLGSEACK
384	D4A005	Protein Ehmt1 OS=Rattus norvegicus GN=Ehmt1 PE=4 SV=2 - [D4A005_RAT]	protein binding; catalytic activity; metal ion binding	nucleus; chromosome	YVSQNCVTSPMNIDR
385	D4AE02	Protein Fam98b OS=Rattus norvegicus GN=Fam98b PE=4 SV=2 - [D4AE02_RAT]			SLCNLEESITSAGR
386	F1LQ48	Protein Fblim1 OS=Rattus norvegicus GN=Hnrnpl PE=4 SV=2 - [F1LQ48_RAT]	nucleotide binding; RNA binding; DNA binding	nucleus; membrane	LCFSTAQHAS
386	F1LQ48	Protein Fblim1 OS=Rattus norvegicus GN=Hnrnpl PE=4 SV=2 - [F1LQ48_RAT]	nucleotide binding; RNA binding; DNA binding	nucleus; membrane	MNVCVSK
386	F1LQ48	Protein Fblim1 OS=Rattus norvegicus GN=Hnrnpl PE=4 SV=2 - [F1LQ48_RAT]	nucleotide binding; RNA binding; DNA binding	nucleus; membrane	QPAIMPGQSYGLEDGSCSYKDFSESR
388	M0R7H8	Protein Fsd1 OS=Rattus norvegicus GN=Fsd1 PE=4 SV=1 - [M0R7H8_RAT]		cytoplasm	TYELQNQLTACTR
389	D3ZC90	Protein Fsd1l (Fragment) OS=Rattus norvegicus GN=Fsd1l PE=4 SV=2 - [D3ZC90_RAT]	protein binding		CWEVIDNIK
391	G3V829	Protein Fubp3 OS=Rattus norvegicus GN=Fubp3 PE=4 SV=1 - [G3V829_RAT]	RNA binding	nucleus; cytoplasm	CGLVIGK
392	D3ZVD8	Protein Hdac6 OS=Rattus norvegicus GN=Hdac6 PE=4 SV=2 - [D3ZVD8_RAT]	metal ion binding; catalytic activity		IMCHLEEVGLAAR
394	F1M3H8	Protein Hnrnpa0 OS=Rattus norvegicus GN=Hnrnpa0 PE=4 SV=2 - [F1M3H8_RAT]	nucleotide binding; RNA binding; protein binding	nucleus	CFGFVTYSNVEEADAAMAASPHAVDGNTVEL K
394	F1M3H8	Protein Hnrnpa0 OS=Rattus norvegicus GN=Hnrnpa0 PE=4 SV=2 - [F1M3H8_RAT]	nucleotide binding; RNA binding; protein binding	nucleus	GHFEAFGTLTDCVVVVNPQTK
395	D4A3E1	Protein Hnrnpll OS=Rattus norvegicus GN=Hnrnpll PE=4 SV=1 - [D4A3E1_RAT]	nucleotide binding; RNA binding	nucleus; membrane	CKTDAVEALTALNHYQIR
395	D4A3E1	Protein Hnrnpll OS=Rattus norvegicus GN=Hnrnpll PE=4 SV=1 - [D4A3E1_RAT]	nucleotide binding; RNA binding	nucleus; membrane	GLCESVVEADLVEALEK
395	D4A3E1	Protein Hnrnpll OS=Rattus norvegicus GN=Hnrnpll PE=4 SV=1 - [D4A3E1_RAT]	nucleotide binding; RNA binding	nucleus; membrane	LCFSTSSHL
395	D4A3E1	Protein Hnrnpll OS=Rattus norvegicus GN=Hnrnpll PE=4 SV=1 - [D4A3E1_RAT]	nucleotide binding; RNA binding	nucleus; membrane	LCNDHEVLPFIK
395	D4A3E1	Protein Hnrnpll OS=Rattus norvegicus GN=Hnrnpll PE=4 SV=1 - [D4A3E1_RAT]	nucleotide binding; RNA binding	nucleus; membrane	LNVCVSK

396	D4ABT8	Protein Hnrnpul2 OS=Rattus norvegicus GN=Hnrnpul2 PE=1 SV=1 - [D4ABT8_RAT]	protein binding; nucleotide binding; catalytic activity; RNA binding	nucleus; membrane	ANFSLPEKCDYMDEVTYGELEKEEAQPIVTK
396	D4ABT8	Protein Hnrnpul2 OS=Rattus norvegicus GN=Hnrnpul2 PE=1 SV=1 - [D4ABT8_RAT]	protein binding; nucleotide binding; catalytic activity; RNA binding	nucleus; membrane	DLLVQQASQCLSK
396	D4ABT8	Protein Hnrnpul2 OS=Rattus norvegicus GN=Hnrnpul2 PE=1 SV=1 - [D4ABT8_RAT]	protein binding; nucleotide binding; catalytic activity; RNA binding	nucleus; membrane	EGCTEVSLLR
396	D4ABT8	Protein Hnrnpul2 OS=Rattus norvegicus GN=Hnrnpul2 PE=1 SV=1 - [D4ABT8_RAT]	protein binding; nucleotide binding; catalytic activity; RNA binding	nucleus; membrane	LQEALDAEMLEDEAGVGGAGPGGACK
396	D4ABT8	Protein Hnrnpul2 OS=Rattus norvegicus GN=Hnrnpul2 PE=1 SV=1 - [D4ABT8_RAT]	protein binding; nucleotide binding; catalytic activity; RNA binding	nucleus; membrane	NCVIELNFGQK
396	D4ABT8	Protein Hnrnpul2 OS=Rattus norvegicus GN=Hnrnpul2 PE=1 SV=1 - [D4ABT8_RAT]	protein binding; nucleotide binding; catalytic activity; RNA binding	nucleus; membrane	NFILDQCNVYNSGQR
396	D4ABT8	Protein Hnrnpul2 OS=Rattus norvegicus GN=Hnrnpul2 PE=1 SV=1 - [D4ABT8_RAT]	protein binding; nucleotide binding; catalytic activity; RNA binding	nucleus; membrane	SRDLLVQQASQCLSK
396	D4ABT8	Protein Hnrnpul2 OS=Rattus norvegicus GN=Hnrnpul2 PE=1 SV=1 - [D4ABT8_RAT]	protein binding; nucleotide binding; catalytic activity; RNA binding	nucleus; membrane	VTQNLPMKEGCTEVSLLR
397	D3ZZQ6	Protein Ints4 OS=Rattus norvegicus GN=Ints4 PE=4 SV=1 - [D3ZZQ6_RAT]			GVDPLFGMCEK
397	D3ZZQ6	Protein Ints4 OS=Rattus norvegicus GN=Ints4 PE=4 SV=1 - [D3ZZQ6_RAT]			ICHMVSDGSWVVR
397	D3ZZQ6	Protein Ints4 OS=Rattus norvegicus GN=Ints4 PE=4 SV=1 - [D3ZZQ6_RAT]			SAALHIDLCK
397	D3ZZQ6	Protein Ints4 OS=Rattus norvegicus GN=Ints4 PE=4 SV=1 - [D3ZZQ6_RAT]			TCPTMPALFSDHTLR
398	D4AD67	Protein Ktn1 OS=Rattus norvegicus GN=Ktn1 PE=4 SV=2 - [D4AD67_RAT]	protein binding		ACMAGPSDTEAVK
398	D4AD67	Protein Ktn1 OS=Rattus norvegicus GN=Ktn1 PE=4 SV=2 - [D4AD67_RAT]	protein binding		EKEITDLCNELESLK
399	D3ZJT9	Protein L3mbtl3 OS=Rattus norvegicus GN=L3mbtl3 PE=4 SV=1 - [D3ZJT9_RAT]	protein binding	nucleus	DGGEDNDEEDPKCSR
399	D3ZJT9	Protein L3mbtl3 OS=Rattus norvegicus GN=L3mbtl3 PE=4 SV=1 - [D3ZJT9_RAT]	protein binding	nucleus	YLGTQSGANCPYSEINLSK
400	F1LWZ8	Protein Lemd3 OS=Rattus norvegicus GN=Lemd3 PE=4 SV=2 - [F1LWZ8_RAT]	nucleotide binding	membrane	LAQIAGDHECGR
400	F1LWZ8	Protein Lemd3 OS=Rattus norvegicus GN=Lemd3 PE=4 SV=2 - [F1LWZ8_RAT]	nucleotide binding	membrane	NLEEAAAEPGGGGGGGGCDQVDSIPR
400	F1LWZ8	Protein Lemd3 OS=Rattus norvegicus GN=Lemd3 PE=4 SV=2 - [F1LWZ8_RAT]	nucleotide binding	membrane	WVQPSASCDK
401	D3ZZK1	Protein LOC100359563 OS=Rattus norvegicus GN=LOC100359563 PE=3 SV=1 - [D3ZZK1_RAT]	RNA binding; structural molecule activity	cytoplasm; ribosome; membrane	SLEKVCADLIR
406	D3ZLL8	Protein LOC100909878 OS=Rattus norvegicus GN=LOC691716 PE=3 SV=1 - [D3ZLL8_RAT]	structural molecule activity	ribosome	CGVISPR
406	D3ZLL8	Protein LOC100909878 OS=Rattus norvegicus GN=LOC691716 PE=3 SV=1 - [D3ZLL8_RAT]	structural molecule activity	ribosome	QVLIRPCSK
407	D4A0F5	Protein LOC100910754 OS=Rattus norvegicus GN=Sept7 PE=3 SV=2 - [D4A0F5_RAT]	nucleotide binding		ADTLTPEECQQFK
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	CGFEGLFTR
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	DAVAHCHEADR
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	DCLITPHVSHLSTPR
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	ECVIVWEK
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	EPATQDNKDICK

409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	EQLLDCKGEDGWNK
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	EYLESLQCLDSDK
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	ICANHYISPDMK
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	KAEDIENDALSPEEQEECKNYLR
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	KIEECQQNIMK
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	LKDAVAHCHEADR
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	LKEQLLDCK
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	MICQQVEAIKK
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	SSLEWNSCVVQTLK
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	TAQEKDCLITPHVSHLSTPR
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	TGEEDEEEFFCNR
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	TKEITECFK
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	VCANHVITK
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	VVPDFICQGGDITK
409	M0R3M4	Protein LOC100911178 OS=Rattus norvegicus GN=LOC100911178 PE=4 SV=1 - [M0R3M4_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; mitochondrion; membrane	VWVWTACDFADGER
410	Q5FVG4	Protein LOC100911440 OS=Rattus norvegicus GN=LOC100911440 PE=2 SV=1 - [Q5FVG4_RAT]	transporter activity	nucleus; mitochondrion; membrane	GVNEDTYSGFLDCARK
410	Q5FVG4	Protein LOC100911440 OS=Rattus norvegicus GN=LOC100911440 PE=2 SV=1 - [Q5FVG4_RAT]	transporter activity	nucleus; mitochondrion; membrane	MYASMSDCLIK
411	D4A510	Protein LOC685179 OS=Rattus norvegicus GN=Smarcc2 PE=4 SV=2 - [D4A510_RAT]	DNA binding; protein binding	nucleus	NLAGDVCAIMR
412	D3Z8C1	Protein Lsm14b OS=Rattus norvegicus GN=Lsm14b PE=4 SV=1 - [D3Z8C1_RAT]			GDEKDPAVMAQSEETPPEEDLLGPNCYYDK
415	D3ZAG3	Protein Map9 OS=Rattus norvegicus GN=Map9 PE=4 SV=1 - [D3ZAG3_RAT]		nucleus; cytoplasm; Golgi; cytoskeleton	ESPGGCISPGSQEK
415	D3ZAG3	Protein Map9 OS=Rattus norvegicus GN=Map9 PE=4 SV=1 - [D3ZAG3_RAT]		nucleus; cytoplasm; Golgi; cytoskeleton	VCSENLDLEDSLLQSLTSSSLK
416	D3ZBD0	Protein Msl1 OS=Rattus norvegicus GN=Msl1 PE=4 SV=1 - [D3ZBD0_RAT]		nucleus	GLLLPAGAAPGQQEESWGGSVPLPCPPPATK
416	D3ZBD0	Protein Msl1 OS=Rattus norvegicus GN=Msl1 PE=4 SV=1 - [D3ZBD0_RAT]		nucleus	KSPLGGGGGSGASSQAACLK
416	D3ZBD0	Protein Msl1 OS=Rattus norvegicus GN=Msl1 PE=4 SV=1 - [D3ZBD0_RAT]		nucleus	LKEPGPPLASTQGGSPAPSPAGCGGGK
416	D3ZBD0	Protein Msl1 OS=Rattus norvegicus GN=Msl1 PE=4 SV=1 - [D3ZBD0_RAT]		nucleus	QAGIGGEPVAAGAGCSPRPK
417	D4AEI5	Protein Myef2 OS=Rattus norvegicus GN=Myef2 PE=4 SV=1 - [D4AEI5_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm; Golgi	EKFSQCGHVMFAEIK
417	D4AEI5	Protein Myef2 OS=Rattus norvegicus GN=Myef2 PE=4 SV=1 - [D4AEI5_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm; Golgi	FESPESAEKACR
417	D4AEI5	Protein Myef2 OS=Rattus norvegicus GN=Myef2 PE=4 SV=1 - [D4AEI5_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm; Golgi	FSQCGHVMFAEIK

417	D4AEI5	Protein Myef2 OS=Rattus norvegicus GN=Myef2 PE=4 SV=1 - [D4AEI5_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm; Golgi	GCGTVRFESPESAEK
417	D4AEI5	Protein Myef2 OS=Rattus norvegicus GN=Myef2 PE=4 SV=1 - [D4AEI5_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm; Golgi	GCGVVEFKDEEFVKK
417	D4AEI5	Protein Myef2 OS=Rattus norvegicus GN=Myef2 PE=4 SV=1 - [D4AEI5_RAT]	nucleotide binding; RNA binding	nucleus; cytoplasm; Golgi	SRGCGVVEFKDEEFVK
418	F1M6E5	Protein Nacad OS=Rattus norvegicus GN=Nacad PE=4 SV=2 - [F1M6E5_RAT]			ATCTLSR
418	F1M6E5	Protein Nacad OS=Rattus norvegicus GN=Nacad PE=4 SV=2 - [F1M6E5_RAT]			CAPPFQHPEPVLGLGSGEQPK
418	F1M6E5	Protein Nacad OS=Rattus norvegicus GN=Nacad PE=4 SV=2 - [F1M6E5_RAT]			GTSMILGCKPLTAK
418	F1M6E5	Protein Nacad OS=Rattus norvegicus GN=Nacad PE=4 SV=2 - [F1M6E5_RAT]			IVMGEETCQVLPSPR
418	F1M6E5	Protein Nacad OS=Rattus norvegicus GN=Nacad PE=4 SV=2 - [F1M6E5_RAT]			LGSCPGSPAR
418	F1M6E5	Protein Nacad OS=Rattus norvegicus GN=Nacad PE=4 SV=2 - [F1M6E5_RAT]			TDLPCDAAIATILK
418	F1M6E5	Protein Nacad OS=Rattus norvegicus GN=Nacad PE=4 SV=2 - [F1M6E5_RAT]			TSEPLSCMGEK
418	F1M6E5	Protein Nacad OS=Rattus norvegicus GN=Nacad PE=4 SV=2 - [F1M6E5_RAT]			VRPECEEQEEEEEEVEEAGLEPR
419	F1LPV0	Protein Nars OS=Rattus norvegicus GN=Nars PE=3 SV=2 - [F1LPV0_RAT]	nucleotide binding; catalytic activity	cytoplasm; mitochondrion	LEDLVCDVVDR
419	F1LPV0	Protein Nars OS=Rattus norvegicus GN=Nars PE=3 SV=2 - [F1LPV0_RAT]	nucleotide binding; catalytic activity	cytoplasm; mitochondrion	LMTDTINEPILLCR
419	F1LPV0	Protein Nars OS=Rattus norvegicus GN=Nars PE=3 SV=2 - [F1LPV0_RAT]	nucleotide binding; catalytic activity	cytoplasm; mitochondrion	NDPSLPEPACVK
419	F1LPV0	Protein Nars OS=Rattus norvegicus GN=Nars PE=3 SV=2 - [F1LPV0_RAT]	nucleotide binding; catalytic activity	cytoplasm; mitochondrion	YGTCPHGGYGLGLER
420	F1M4H5	Protein Nova2 (Fragment) OS=Rattus norvegicus GN=Nova2 PE=4 SV=2 - [F1M4H5_RAT]	RNA binding	nucleus	VCLVQGTAEALNAAHSFIAEK
422	F1LW91	Protein Numa1 (Fragment) OS=Rattus norvegicus GN=Numa1 PE=4 SV=1 - [F1LW91_RAT]	catalytic activity; receptor activity; signal transducer activity; protein binding	membrane; nucleus; cytoplasm	EAGEIHGEGQTGQQQSQLAQLHACLAK
422	F1LW91	Protein Numa1 (Fragment) OS=Rattus norvegicus GN=Numa1 PE=4 SV=1 - [F1LW91_RAT]	catalytic activity; receptor activity; signal transducer activity; protein binding	membrane; nucleus; cytoplasm	GSLEEEKCR
422	F1LW91	Protein Numa1 (Fragment) OS=Rattus norvegicus GN=Numa1 PE=4 SV=1 - [F1LW91_RAT]	catalytic activity; receptor activity; signal transducer activity; protein binding	membrane; nucleus; cytoplasm	HLCQQLQAEQAAAEKR
422	F1LW91	Protein Numa1 (Fragment) OS=Rattus norvegicus GN=Numa1 PE=4 SV=1 - [F1LW91_RAT]	catalytic activity; receptor activity; signal transducer activity; protein binding	membrane; nucleus; cytoplasm	HPSSTQCLVSVQK
422	F1LW91	Protein Numa1 (Fragment) OS=Rattus norvegicus GN=Numa1 PE=4 SV=1 - [F1LW91_RAT]	catalytic activity; receptor activity; signal transducer activity; protein binding	membrane; nucleus; cytoplasm	IGELHACIEAAHQEQR
422	F1LW91	Protein Numa1 (Fragment) OS=Rattus norvegicus GN=Numa1 PE=4 SV=1 - [F1LW91_RAT]	catalytic activity; receptor activity; signal transducer activity; protein binding	membrane; nucleus; cytoplasm	KHPSSTQCLVSVQK
422	F1LW91	Protein Numa1 (Fragment) OS=Rattus norvegicus GN=Numa1 PE=4 SV=1 - [F1LW91_RAT]	catalytic activity; receptor activity; signal transducer activity; protein binding	membrane; nucleus; cytoplasm	NSFYMGTCQDEPEQVDDWNR
422	F1LW91	Protein Numa1 (Fragment) OS=Rattus norvegicus GN=Numa1 PE=4 SV=1 - [F1LW91_RAT]	catalytic activity; receptor activity; signal transducer activity; protein binding	membrane; nucleus; cytoplasm	VETLECER
423	D3Z8B2	Protein Nup133 (Fragment) OS=Rattus norvegicus GN=Nup133 PE=4 SV=2 - [D3Z8B2_RAT]	transporter activity		ECEVPPSLTPADVFFR
423	D3Z8B2	Protein Nup133 (Fragment) OS=Rattus norvegicus GN=Nup133 PE=4 SV=2 - [D3Z8B2_RAT]	transporter activity		LEILCR
424	D3ZBL6	Protein Nup160 OS=Rattus norvegicus GN=Nup160 PE=4 SV=2 - [D3ZBL6_RAT]	transporter activity	chromosome	CYLVTGEVQK
424	D3ZBL6	Protein Nup160 OS=Rattus norvegicus GN=Nup160 PE=4 SV=2 - [D3ZBL6_RAT]	transporter activity	chromosome	EFTVCDLGTANAAFGAVK

424	D3ZBL6	Protein Nup160 OS=Rattus norvegicus GN=Nup160 PE=4 SV=2 - [D3ZBL6_RAT]	transporter activity	chromosome	NHDGECTAAPTNR
424	D3ZBL6	Protein Nup160 OS=Rattus norvegicus GN=Nup160 PE=4 SV=2 - [D3ZBL6_RAT]	transporter activity	chromosome	QIEILELEDLEKECSLAR
424	D3ZBL6	Protein Nup160 OS=Rattus norvegicus GN=Nup160 PE=4 SV=2 - [D3ZBL6_RAT]	transporter activity	chromosome	QLVVVLCER
424	D3ZBL6	Protein Nup160 OS=Rattus norvegicus GN=Nup160 PE=4 SV=2 - [D3ZBL6_RAT]	transporter activity	chromosome	RNHDGECTAAPTNR
424	D3ZBL6	Protein Nup160 OS=Rattus norvegicus GN=Nup160 PE=4 SV=2 - [D3ZBL6_RAT]	transporter activity	chromosome	TLQQEFWCK
424	D3ZBL6	Protein Nup160 OS=Rattus norvegicus GN=Nup160 PE=4 SV=2 - [D3ZBL6_RAT]	transporter activity	chromosome	VQNNLYHHCVINK
425	D4ACK1	Protein Nup214 (Fragment) OS=Rattus norvegicus GN=Nup214 PE=4 SV=2 - [D4ACK1_RAT]	transporter activity; protein binding		ACFQVGTPEEMK
425	D4ACK1	Protein Nup214 (Fragment) OS=Rattus norvegicus GN=Nup214 PE=4 SV=2 - [D4ACK1_RAT]	transporter activity; protein binding		QGSLINSFKPSGPTPVSCQLSSGDK
425	D4ACK1	Protein Nup214 (Fragment) OS=Rattus norvegicus GN=Nup214 PE=4 SV=2 - [D4ACK1_RAT]	transporter activity; protein binding		YYEDLDEGSSASSVAHPLEGEDARPTPTCREEEAVVPVPR
426	D4A8C8	Protein Paxbp1 OS=Rattus norvegicus GN=Paxbp1 PE=4 SV=1 - [D4A8C8_RAT]	DNA binding; protein binding	nucleus; cytosol	NSIGCSDVEK
426	D4A8C8	Protein Paxbp1 OS=Rattus norvegicus GN=Paxbp1 PE=4 SV=1 - [D4A8C8_RAT]	DNA binding; protein binding	nucleus; cytosol	TISQLENFCR
427	D3ZT52	Protein Pbrm1 OS=Rattus norvegicus GN=Pbrm1 PE=4 SV=1 - [D3ZT52_RAT]	DNA binding; protein binding	chromosome	CAVLSFK
427	D3ZT52	Protein Pbrm1 OS=Rattus norvegicus GN=Pbrm1 PE=4 SV=1 - [D3ZT52_RAT]	DNA binding; protein binding	chromosome	DEDVFVCESR
427	D3ZT52	Protein Pbrm1 OS=Rattus norvegicus GN=Pbrm1 PE=4 SV=1 - [D3ZT52_RAT]	DNA binding; protein binding	chromosome	EKEDVPVEMSNGEPGCHYFEQLR
427	D3ZT52	Protein Pbrm1 OS=Rattus norvegicus GN=Pbrm1 PE=4 SV=1 - [D3ZT52_RAT]	DNA binding; protein binding	chromosome	IRDELCK
427	D3ZT52	Protein Pbrm1 OS=Rattus norvegicus GN=Pbrm1 PE=4 SV=1 - [D3ZT52_RAT]	DNA binding; protein binding	chromosome	LCDLFMVKPSK
427	D3ZT52	Protein Pbrm1 OS=Rattus norvegicus GN=Pbrm1 PE=4 SV=1 - [D3ZT52_RAT]	DNA binding; protein binding	chromosome	TYSQDCSFK
427	D3ZT52	Protein Pbrm1 OS=Rattus norvegicus GN=Pbrm1 PE=4 SV=1 - [D3ZT52_RAT]	DNA binding; protein binding	chromosome	VGDCVFIK
428	D3ZNI3	Protein Pdcd11 OS=Rattus norvegicus GN=Pdcd11 PE=4 SV=1 - [D3ZNI3_RAT]	RNA binding; protein binding	nucleus; cytosol	HSHVSQCVSR
428	D3ZNI3	Protein Pdcd11 OS=Rattus norvegicus GN=Pdcd11 PE=4 SV=1 - [D3ZNI3_RAT]	RNA binding; protein binding	nucleus; cytosol	QYQAGQTVTCFLK
428	D3ZNI3	Protein Pdcd11 OS=Rattus norvegicus GN=Pdcd11 PE=4 SV=1 - [D3ZNI3_RAT]	RNA binding; protein binding	nucleus; cytosol	VAVLNCEPSKER
428	D3ZNI3	Protein Pdcd11 OS=Rattus norvegicus GN=Pdcd11 PE=4 SV=1 - [D3ZNI3_RAT]	RNA binding; protein binding	nucleus; cytosol	VLCLSQSEK
428	D3ZNI3	Protein Pdcd11 OS=Rattus norvegicus GN=Pdcd11 PE=4 SV=1 - [D3ZNI3_RAT]	RNA binding; protein binding	nucleus; cytosol	VSVFHLSDSYSEEPLTDFCPQK
430	G3V629	Protein Ppp1r18 OS=Rattus norvegicus GN=Ppp1r18 PE=2 SV=2 - [G3V629_RAT]	protein binding		ALIVDESCRR
430	G3V629	Protein Ppp1r18 OS=Rattus norvegicus GN=Ppp1r18 PE=2 SV=2 - [G3V629_RAT]	protein binding		CSGPSPLPPEHSGTEGSR
430	G3V629	Protein Ppp1r18 OS=Rattus norvegicus GN=Ppp1r18 PE=2 SV=2 - [G3V629_RAT]	protein binding		KDYLEECGSEEEK
430	G3V629	Protein Ppp1r18 OS=Rattus norvegicus GN=Ppp1r18 PE=2 SV=2 - [G3V629_RAT]	protein binding		RCVPPASPAPPVNPATADAAGSGSGK
431	Q5XI34	Protein Ppp2r1a OS=Rattus norvegicus GN=Ppp2r1a PE=2 SV=1 - [Q5XI34_RAT]	catalytic activity; protein binding	cytosol	ENVIMTQILPCIK

431	Q5XI34	Protein Ppp2r1a OS=Rattus norvegicus GN=Ppp2r1a PE=2 SV=1 - [Q5XI34_RAT]	catalytic activity; protein binding	cytosol	NLCSDDTPMVR
432	D3ZHI9	Protein Ppp2r5e OS=Rattus norvegicus GN=Ppp2r5e PE=4 SV=1 - [D3ZHI9_RAT]	enzyme regulator activity	cytoplasm	GCLTEQTYPEVVR
432	D3ZHI9	Protein Ppp2r5e OS=Rattus norvegicus GN=Ppp2r5e PE=4 SV=1 - [D3ZHI9_RAT]	enzyme regulator activity	cytoplasm	MVSCNIFR
433	D4A6M5	Protein Prr12 OS=Rattus norvegicus GN=Prr12 PE=4 SV=2 - [D4A6M5_RAT]	DNA binding		ASLACSPLGGGEPSPGAGEPSK
433	D4A6M5	Protein Prr12 OS=Rattus norvegicus GN=Prr12 PE=4 SV=2 - [D4A6M5_RAT]	DNA binding		CQSLGGPAAAYATGK
433	D4A6M5	Protein Prr12 OS=Rattus norvegicus GN=Prr12 PE=4 SV=2 - [D4A6M5_RAT]	DNA binding		FVPLTSICFPDSLLQDEER
433	D4A6M5	Protein Prr12 OS=Rattus norvegicus GN=Prr12 PE=4 SV=2 - [D4A6M5_RAT]	DNA binding		QFCATSNYLGYFGDAK
433	D4A6M5	Protein Prr12 OS=Rattus norvegicus GN=Prr12 PE=4 SV=2 - [D4A6M5_RAT]	DNA binding		TGAGPPPGPTAYDPYGPYCGGR
436	B5DFB2	Protein Rbbp4 OS=Rattus norvegicus GN=Rbbp4 PE=2 SV=1 - [B5DFB2_RAT]	DNA binding; protein binding; catalytic activity	nucleus	HPSKPDPSGECNPDLR
437	M0R3Z8	Protein Rbm15 OS=Rattus norvegicus GN=Rbm15 PE=1 SV=1 - [M0R3Z8_RAT]	nucleotide binding	nucleus	DKENTGVLHAFPPCEFSQQFLDSPAK
438	D3ZHD6	Protein Rbm15b OS=Rattus norvegicus GN=Rbm15b PE=4 SV=2 - [D3ZHD6_RAT]	nucleotide binding; RNA binding	nucleus	GRPYSYQAVCEEDLMPEDDQR
440	D3Z8R4	Protein Rbm25l1 OS=Rattus norvegicus GN=Rbm25l1 PE=4 SV=2 - [D3Z8R4_RAT]	nucleotide binding; RNA binding	spliceosomal complex	CGLVLSWK
440	D3Z8R4	Protein Rbm25l1 OS=Rattus norvegicus GN=Rbm25l1 PE=4 SV=2 - [D3Z8R4_RAT]	nucleotide binding; RNA binding	spliceosomal complex	ENDENCGPTTTVFVGNISEK
440	D3Z8R4	Protein Rbm25l1 OS=Rattus norvegicus GN=Rbm25l1 PE=4 SV=2 - [D3Z8R4_RAT]	nucleotide binding; RNA binding	spliceosomal complex	LKENDENCGPTTTVFVGNISEK
440	D3Z8R4	Protein Rbm25l1 OS=Rattus norvegicus GN=Rbm25l1 PE=4 SV=2 - [D3Z8R4_RAT]	nucleotide binding; RNA binding	spliceosomal complex	LQAFGFCEYKEPESTLR
443	D4ACW0	Protein Rbm6 OS=Rattus norvegicus GN=Rbm6 PE=4 SV=1 - [D4ACW0_RAT]	nucleotide binding; RNA binding; metal ion binding	nucleus	EVGPCMEFK
443	D4ACW0	Protein Rbm6 OS=Rattus norvegicus GN=Rbm6 PE=4 SV=1 - [D4ACW0_RAT]	nucleotide binding; RNA binding; metal ion binding	nucleus	GGCTQQATGWR
443	D4ACW0	Protein Rbm6 OS=Rattus norvegicus GN=Rbm6 PE=4 SV=1 - [D4ACW0_RAT]	nucleotide binding; RNA binding; metal ion binding	nucleus	SMEYCDVDHR
445	D3ZKC9	Protein RGD1559904 (Fragment) OS=Rattus norvegicus GN=RGD1559904 PE=4 SV=2 - [D3ZKC9_RAT]			CTLTLLK
445	D3ZKC9	Protein RGD1559904 (Fragment) OS=Rattus norvegicus GN=RGD1559904 PE=4 SV=2 - [D3ZKC9_RAT]			ELVPLLYFSCPYK
445	D3ZKC9	Protein RGD1559904 (Fragment) OS=Rattus norvegicus GN=RGD1559904 PE=4 SV=2 - [D3ZKC9_RAT]			FPCVVYINEVR
445	D3ZKC9	Protein RGD1559904 (Fragment) OS=Rattus norvegicus GN=RGD1559904 PE=4 SV=2 - [D3ZKC9_RAT]			SFSGTTCQPIQHMLR
447	D3ZPT0	Protein RGD1566084 OS=Rattus norvegicus GN=Prr36 PE=4 SV=2 - [D3ZPT0_RAT]			VTAAACAGASSR
448	F1M5X1	Protein Rrbp1 OS=Rattus norvegicus GN=Rrbp1 PE=4 SV=2 - [F1M5X1_RAT]			EAEETQNSLQAECDQYR
448	F1M5X1	Protein Rrbp1 OS=Rattus norvegicus GN=Rrbp1 PE=4 SV=2 - [F1M5X1_RAT]			ELESQVSCLEKETSELK
448	F1M5X1	Protein Rrbp1 OS=Rattus norvegicus GN=Rrbp1 PE=4 SV=2 - [F1M5X1_RAT]			KGEPGPPDCDSPLFLPYK
448	F1M5X1	Protein Rrbp1 OS=Rattus norvegicus GN=Rrbp1 PE=4 SV=2 - [F1M5X1_RAT]			LREAEETQNSLQAECDQYR
448	F1M5X1	Protein Rrbp1 OS=Rattus norvegicus GN=Rrbp1 PE=4 SV=2 - [F1M5X1_RAT]			LTAEFEEAQSTACR

448	F1M5X1	Protein Rrbp1 OS=Rattus norvegicus GN=Rrbp1 PE=4 SV=2 - [F1M5X1_RAT]			SKCEELSDLHGQLK
449	G3V8T5	Protein Ruvbl2 OS=Rattus norvegicus GN=Ruvbl2 PE=4 SV=1 - [G3V8T5_RAT]	nucleotide binding; DNA binding; catalytic activity; protein binding	nucleus; cytoplasm	FVQCPDGELQKR
454	Q4KLI7	Protein Sf3a3 OS=Rattus norvegicus GN=Sf3a3 PE=2 SV=1 - [Q4KLI7_RAT]	RNA binding; metal ion binding	nucleus; spliceosomal complex	CGGTLEER
454	Q4KLI7	Protein Sf3a3 OS=Rattus norvegicus GN=Sf3a3 PE=2 SV=1 - [Q4KLI7_RAT]	RNA binding; metal ion binding	nucleus; spliceosomal complex	YLDLHDCYLK
455	E9PT66	Protein Sf3b3 OS=Rattus norvegicus GN=Sf3b3 PE=4 SV=2 - [E9PT66_RAT]	RNA binding; protein binding	nucleus; spliceosomal complex	FGNICVVR
455	E9PT66	Protein Sf3b3 OS=Rattus norvegicus GN=Sf3b3 PE=4 SV=2 - [E9PT66_RAT]	RNA binding; protein binding	nucleus; spliceosomal complex	NVIDGDLCEQFNSMEPNK
455	E9PT66	Protein Sf3b3 OS=Rattus norvegicus GN=Sf3b3 PE=4 SV=2 - [E9PT66_RAT]	RNA binding; protein binding	nucleus; spliceosomal complex	SEHPPLCGR
455	E9PT66	Protein Sf3b3 OS=Rattus norvegicus GN=Sf3b3 PE=4 SV=2 - [E9PT66_RAT]	RNA binding; protein binding	nucleus; spliceosomal complex	YFDTVPVAAAMCVLK
457	D3ZBP2	Protein Sin3a OS=Rattus norvegicus GN=Sin3a PE=4 SV=1 - [D3ZBP2_RAT]	DNA binding; protein binding; RNA binding; catalytic activity	chromosome; nucleus; cytoplasm	KAEQLMSDENCFK
458	D4AE49	Protein Skiv2l2 (Fragment) OS=Rattus norvegicus GN=Skiv2l2 PE=4 SV=2 - [D4AE49_RAT]	nucleotide binding; catalytic activity	nucleus; spliceosomal complex	KDCEAYALQMTK
458	D4AE49	Protein Skiv2l2 (Fragment) OS=Rattus norvegicus GN=Skiv2l2 PE=4 SV=2 - [D4AE49_RAT]	nucleotide binding; catalytic activity	nucleus; spliceosomal complex	MYSHPLHNDPNLETVYTLCEK
459	D3ZIE5	Protein Smarca1 OS=Rattus norvegicus GN=Smarca1 PE=4 SV=2 - [D3ZIE5_RAT]	DNA binding; catalytic activity; nucleotide binding; protein binding	nucleus	VICFVGDKDVR
460	E9PTG1	Protein Smarca2 OS=Rattus norvegicus GN=Smarca2 PE=4 SV=1 - [E9PTG1_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding	nucleus; cytoskeleton	GIVEDVHCGSMK
460	E9PTG1	Protein Smarca2 OS=Rattus norvegicus GN=Smarca2 PE=4 SV=1 - [E9PTG1_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding	nucleus; cytoskeleton	LTCEEEEEKIFGR
460	E9PTG1	Protein Smarca2 OS=Rattus norvegicus GN=Smarca2 PE=4 SV=1 - [E9PTG1_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding	nucleus; cytoskeleton	QEVVACMR
461	F1LNL2	Protein Smarca5 OS=Rattus norvegicus GN=Smarca5 PE=4 SV=2 - [F1LNL2_RAT]	DNA binding; catalytic activity; nucleotide binding; protein binding	chromosome; nucleus	CNTLITLIER
461	F1LNL2	Protein Smarca5 OS=Rattus norvegicus GN=Smarca5 PE=4 SV=2 - [F1LNL2_RAT]	DNA binding; catalytic activity; nucleotide binding; protein binding	chromosome; nucleus	SVCLIGDKEQR
461	F1LNL2	Protein Smarca5 OS=Rattus norvegicus GN=Smarca5 PE=4 SV=2 - [F1LNL2_RAT]	DNA binding; catalytic activity; nucleotide binding; protein binding	chromosome; nucleus	VLDILEDYCMWR
462	Q4KLI0	Protein Smarcb1 OS=Rattus norvegicus GN=Smarcb1 PE=1 SV=1 - [Q4KLI0_RAT]	DNA binding; protein binding	chromosome; nucleus	NSQWVPTLPNSSHHLDAVPCSTTINR
462	Q4KLI0	Protein Smarcb1 OS=Rattus norvegicus GN=Smarcb1 PE=1 SV=1 - [Q4KLI0_RAT]	DNA binding; protein binding	chromosome; nucleus	NTGDADQWCPLLETLTDAEMEK
462	Q4KLI0	Protein Smarcb1 OS=Rattus norvegicus GN=Smarcb1 PE=1 SV=1 - [Q4KLI0_RAT]	DNA binding; protein binding	chromosome; nucleus	TFPLCFDDHDPAVIHENASQPEVLVPIR
463	D3ZJU5	Protein Smarcc1 OS=Rattus norvegicus GN=Smarcc1 PE=4 SV=1 - [D3ZJU5_RAT]	DNA binding; protein binding	chromosome; nucleus	CFMDFK
463	D3ZJU5	Protein Smarcc1 OS=Rattus norvegicus GN=Smarcc1 PE=4 SV=1 - [D3ZJU5_RAT]	DNA binding; protein binding	chromosome; nucleus	ENEENKELTDTCKER
463	D3ZJU5	Protein Smarcc1 OS=Rattus norvegicus GN=Smarcc1 PE=4 SV=1 - [D3ZJU5_RAT]	DNA binding; protein binding	chromosome; nucleus	NLTGDVCAVMR
463	D3ZJU5	Protein Smarcc1 OS=Rattus norvegicus GN=Smarcc1 PE=4 SV=1 - [D3ZJU5_RAT]	DNA binding; protein binding	chromosome; nucleus	VDPTYGLESSCIAGTGPDEPEKLEGSEEEK
464	D3ZBS9	Protein Smarcd1 OS=Rattus norvegicus GN=Smarcd1 PE=4 SV=1 - [D3ZBS9_RAT]	protein binding; structural molecule activity	nucleus	AEFYFQPWAQEAVCR
464	D3ZBS9	Protein Smarcd1 OS=Rattus norvegicus GN=Smarcd1 PE=4 SV=1 - [D3ZBS9_RAT]	protein binding; structural molecule activity	nucleus	DPQGFINDWLQSQCR
466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	ASVCQTIGISSEEK

466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	CIYDETQGR
466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	DGDIDGCR
466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	EITCDNFDDTVK
466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	ETYPDDPCFPSK
466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	GLAPIECFNR
466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	GPNCVIQGVIAK
466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	IEVTECPIPTKR
466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	IKDNDKEDGCFYFR
466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	ITHCPTLLTR
466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	LCTLPNYTK
466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	LRDEDDDDDCFIPEK
466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	LSSGMSRPPANAEIFSCNK
466	D4AAG8	Protein Smchd1 OS=Rattus norvegicus GN=Smchd1 PE=4 SV=1 - [D4AAG8_RAT]	protein binding; nucleotide binding	chromosome	QCVDLGK
467	B5DES0	Protein Snrpd2 OS=Rattus norvegicus GN=Snrpd2 PE=2 SV=1 - [B5DES0_RAT]	RNA binding	spliceosomal complex; cytosol	HCNMVLENVK
467	B5DES0	Protein Snrpd2 OS=Rattus norvegicus GN=Snrpd2 PE=2 SV=1 - [B5DES0_RAT]	RNA binding	spliceosomal complex; cytosol	NNTQVLINCR
468	G3V6S0	Protein Sptbn1 OS=Rattus norvegicus GN=Sptbn1 PE=4 SV=2 - [G3V6S0_RAT]	protein binding; structural molecule activity	nucleus; cytoplasm; membrane; cytoskeleton	AELFTQSCADLDK
468	G3V6S0	Protein Sptbn1 OS=Rattus norvegicus GN=Sptbn1 PE=4 SV=2 - [G3V6S0_RAT]	protein binding; structural molecule activity	nucleus; cytoplasm; membrane; cytoskeleton	DALLSALSIQNYHLECNETK
468	G3V6S0	Protein Sptbn1 OS=Rattus norvegicus GN=Sptbn1 PE=4 SV=2 - [G3V6S0_RAT]	protein binding; structural molecule activity	nucleus; cytoplasm; membrane; cytoskeleton	EAICEVALDYKK
468	G3V6S0	Protein Sptbn1 OS=Rattus norvegicus GN=Sptbn1 PE=4 SV=2 - [G3V6S0_RAT]	protein binding; structural molecule activity	nucleus; cytoplasm; membrane; cytoskeleton	FATDGEGYKPCDPQVIR
468	G3V6S0	Protein Sptbn1 OS=Rattus norvegicus GN=Sptbn1 PE=4 SV=2 - [G3V6S0_RAT]	protein binding; structural molecule activity	nucleus; cytoplasm; membrane; cytoskeleton	SLLDACEGRR
469	M0R7E6	Protein Srrt OS=Rattus norvegicus GN=Srrt PE=4 SV=1 - [M0R7E6_RAT]	DNA binding	cytoplasm	DKWLCPLSGK
469	M0R7E6	Protein Srrt OS=Rattus norvegicus GN=Srrt PE=4 SV=1 - [M0R7E6_RAT]	DNA binding	cytoplasm	DTAGLECKPRPLHK
469	M0R7E6	Protein Srrt OS=Rattus norvegicus GN=Srrt PE=4 SV=1 - [M0R7E6_RAT]	DNA binding	cytoplasm	IVHSLDYYNTCEYPNEDEMPNR
469	M0R7E6	Protein Srrt OS=Rattus norvegicus GN=Srrt PE=4 SV=1 - [M0R7E6_RAT]	DNA binding	cytoplasm	TCSLFMR
469	M0R7E6	Protein Srrt OS=Rattus norvegicus GN=Srrt PE=4 SV=1 - [M0R7E6_RAT]	DNA binding	cytoplasm	WLCPLSGK
470	D4A9L2	Protein Srsf1 OS=Rattus norvegicus GN=Srsf1 PE=4 SV=1 - [D4A9L2_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex	EAGDVCYADVYR
473	D4A720	Protein Srsf7 OS=Rattus norvegicus GN=Srsf7 PE=4 SV=1 - [D4A720_RAT]	nucleotide binding; metal ion binding; RNA binding	nucleus	GHYAYDCHR
475	M0R7D8	Protein Suz12 OS=Rattus norvegicus GN=Suz12 PE=4 SV=1 - [M0R7D8_RAT]			IDVSINECYDGSYAGNPQDIHR

475	M0R7D8	Protein Suz12 OS=Rattus norvegicus GN=Suz12 PE=4 SV=1 - [M0R7D8_RAT]			KDVSCPIR
476	F1LSH0	Protein Sympk OS=Rattus norvegicus GN=Sympk PE=4 SV=2 - [F1LSH0_RAT]		nucleus; cytoplasm; membrane	AVACSGAAQVR
476	F1LSH0	Protein Sympk OS=Rattus norvegicus GN=Sympk PE=4 SV=2 - [F1LSH0_RAT]		nucleus; cytoplasm; membrane	CLHSLTDKVPPSPELVK
476	F1LSH0	Protein Sympk OS=Rattus norvegicus GN=Sympk PE=4 SV=2 - [F1LSH0_RAT]		nucleus; cytoplasm; membrane	GMGMNSPELLLLVENCPK
477	I6L9G6	Protein Tardbp OS=Rattus norvegicus GN=Tardbp PE=2 SV=1 - [I6L9G6_RAT]	nucleotide binding; DNA binding; RNA binding; protein binding	nucleus; cytoplasm	NPVSQCMR
477	I6L9G6	Protein Tardbp OS=Rattus norvegicus GN=Tardbp PE=2 SV=1 - [I6L9G6_RAT]	nucleotide binding; DNA binding; RNA binding; protein binding	nucleus; cytoplasm	VAQSLCGEDLIIK
477	I6L9G6	Protein Tardbp OS=Rattus norvegicus GN=Tardbp PE=2 SV=1 - [I6L9G6_RAT]	nucleotide binding; DNA binding; RNA binding; protein binding	nucleus; cytoplasm	YRNPVSQCMR
478	A0A096MJZ2	Protein Tbl2 OS=Rattus norvegicus GN=Tbl2 PE=4 SV=1 - [A0A096MJZ2_RAT]	protein binding; RNA binding		AEEKPSQPICQKENESK
478	A0A096MJZ2	Protein Tbl2 OS=Rattus norvegicus GN=Tbl2 PE=4 SV=1 - [A0A096MJZ2_RAT]	protein binding; RNA binding		FEEASTMPCR
478	A0A096MJZ2	Protein Tbl2 OS=Rattus norvegicus GN=Tbl2 PE=4 SV=1 - [A0A096MJZ2_RAT]	protein binding; RNA binding		FVGSCGFTPDVK
478	A0A096MJZ2	Protein Tbl2 OS=Rattus norvegicus GN=Tbl2 PE=4 SV=1 - [A0A096MJZ2_RAT]	protein binding; RNA binding		GQVLSTINTNQMNNSHAVISPCSR
478	A0A096MJZ2	Protein Tbl2 OS=Rattus norvegicus GN=Tbl2 PE=4 SV=1 - [A0A096MJZ2_RAT]	protein binding; RNA binding		VWEVCFGK
479	D4A206	Protein Tcof1 OS=Rattus norvegicus GN=Tcof1 PE=1 SV=2 - [D4A206_RAT]	protein binding	nucleus; cytoplasm	KGANPPCLGK
481	Q52KJ9	Protein Tmx1 OS=Rattus norvegicus GN=Tmx1 PE=2 SV=1 - [Q52KJ9_RAT]	catalytic activity	endoplasmic reticulum; membrane	CVGPSSATDKS
481	Q52KJ9	Protein Tmx1 OS=Rattus norvegicus GN=Tmx1 PE=2 SV=1 - [Q52KJ9_RAT]	catalytic activity	endoplasmic reticulum; membrane	QRCVGPSSATDKS
482	D3ZZQ0	Protein Tnik OS=Rattus norvegicus GN=Tnik PE=4 SV=1 - [D3ZZQ0_RAT]	nucleotide binding; catalytic activity; signal transducer activity	nucleus; cytoplasm; cytoskeleton; membrane	EEWIAYICR
482	D3ZZQ0	Protein Tnik OS=Rattus norvegicus GN=Tnik PE=4 SV=1 - [D3ZZQ0_RAT]	nucleotide binding; catalytic activity; signal transducer activity	nucleus; cytoplasm; cytoskeleton; membrane	FQSFIESCLVK
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	ASQSFCESSSETPFHFTLPK
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	CEEQSTDAISIIEPSK
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	EAPKEECPEAMEVETSVISIDSPQK
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	GGGLHSSSLTVECSK
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	GISQTGAPVCEEDGDAGLGIR
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	HLGSEGSCQQLEK
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	ILMERPTQSNIGIQTMDHSLCAPETVSAATQTVK
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	KGISQTGAPVCEEDGDAGLGIR
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	KSATVKPGTVGAAELVSPCESGDNTGEPSVLEEPR
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	LLFDDGYECDVLGK
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	LMLSTSECSQSSK

483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	NFTDDLGLSMTGDSCK
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	NVCEQGTSTVEQNSGK
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	QYTECQLR
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	RVECDGDSKAETTEK
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	SATVKPGTVGAAELVSPCESGDNTGEPSVLEEPR
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	TASDGCSTPSR
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	VADDKHLGSEGSCQQLEK
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	VDISCEPVEGVGK
483	F1M842	Protein Tp53bp1 (Fragment) OS=Rattus norvegicus GN=Tp53bp1 PE=4 SV=2 - [F1M842_RAT]	protein binding; DNA binding	chromosome; nucleus; cytoplasm	VECDGDSKAETTEK
484	A0A096MKD9	Protein Trim46 (Fragment) OS=Rattus norvegicus GN=Trim46 PE=4 SV=1 - [A0A096MKD9_RAT]			DGPAASCTVPLPPR
484	A0A096MKD9	Protein Trim46 (Fragment) OS=Rattus norvegicus GN=Trim46 PE=4 SV=1 - [A0A096MKD9_RAT]			LGICLDYER
484	A0A096MKD9	Protein Trim46 (Fragment) OS=Rattus norvegicus GN=Trim46 PE=4 SV=1 - [A0A096MKD9_RAT]			SYWACAVDPASYLVK
486	F1M0Z1	Protein Trio OS=Rattus norvegicus GN=Trio PE=4 SV=2 - [F1M0Z1_RAT]	catalytic activity; protein binding; nucleotide binding		AVEVMCIVPK
486	F1M0Z1	Protein Trio OS=Rattus norvegicus GN=Trio PE=4 SV=2 - [F1M0Z1_RAT]	catalytic activity; protein binding; nucleotide binding		CNDMMNVGR
486	F1M0Z1	Protein Trio OS=Rattus norvegicus GN=Trio PE=4 SV=2 - [F1M0Z1_RAT]	catalytic activity; protein binding; nucleotide binding		CVTAVDKR
486	F1M0Z1	Protein Trio OS=Rattus norvegicus GN=Trio PE=4 SV=2 - [F1M0Z1_RAT]	catalytic activity; protein binding; nucleotide binding		DLGCVVEGYMALMK
486	F1M0Z1	Protein Trio OS=Rattus norvegicus GN=Trio PE=4 SV=2 - [F1M0Z1_RAT]	catalytic activity; protein binding; nucleotide binding		EEDWCGGADK
486	F1M0Z1	Protein Trio OS=Rattus norvegicus GN=Trio PE=4 SV=2 - [F1M0Z1_RAT]	catalytic activity; protein binding; nucleotide binding		KHLEQCVQLR
486	F1M0Z1	Protein Trio OS=Rattus norvegicus GN=Trio PE=4 SV=2 - [F1M0Z1_RAT]	catalytic activity; protein binding; nucleotide binding		LFTSELGVTEHVEGDPCK
486	F1M0Z1	Protein Trio OS=Rattus norvegicus GN=Trio PE=4 SV=2 - [F1M0Z1_RAT]	catalytic activity; protein binding; nucleotide binding		NHSGGGGSGSGGSSGGGGGSGGSGASSGGSSSHGSGPSSCSSGPSSSR
486	F1M0Z1	Protein Trio OS=Rattus norvegicus GN=Trio PE=4 SV=2 - [F1M0Z1_RAT]	catalytic activity; protein binding; nucleotide binding		REEDWCGGADK
486	F1M0Z1	Protein Trio OS=Rattus norvegicus GN=Trio PE=4 SV=2 - [F1M0Z1_RAT]	catalytic activity; protein binding; nucleotide binding		TSEQVCSVLESLEQEYKR
486	F1M0Z1	Protein Trio OS=Rattus norvegicus GN=Trio PE=4 SV=2 - [F1M0Z1_RAT]	catalytic activity; protein binding; nucleotide binding		YMSNVDSWCK
488	Q3KR55	Protein U2af1 OS=Rattus norvegicus GN=U2af1 PE=2 SV=1 - [Q3KR55_RAT]	nucleotide binding; RNA binding; metal ion binding; protein binding	nucleus; spliceosomal complex	DKVNCSFYFK
488	Q3KR55	Protein U2af1 OS=Rattus norvegicus GN=U2af1 PE=2 SV=1 - [Q3KR55_RAT]	nucleotide binding; RNA binding; metal ion binding; protein binding	nucleus; spliceosomal complex	QYEMGECTR
488	Q3KR55	Protein U2af1 OS=Rattus norvegicus GN=U2af1 PE=2 SV=1 - [Q3KR55_RAT]	nucleotide binding; RNA binding; metal ion binding; protein binding	nucleus; spliceosomal complex	VNCSFYFK
489	F2Z3T9	Protein U2af2 OS=Rattus norvegicus GN=U2af2 PE=4 SV=1 - [F2Z3T9_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex	SIEIPRPVDGVEVPGCGK
489	F2Z3T9	Protein U2af2 OS=Rattus norvegicus GN=U2af2 PE=4 SV=1 - [F2Z3T9_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex	VVVTKYCDPDSYHR

489	F2Z3T9	Protein U2af2 OS=Rattus norvegicus GN=U2af2 PE=4 SV=1 - [F2Z3T9_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; spliceosomal complex	YCDPDSYHR
490	D4A4B4	Protein U2surp OS=Rattus norvegicus GN=U2surp PE=4 SV=1 - [D4A4B4_RAT]	nucleotide binding; RNA binding	nucleus	LCQIFSDLNATYR
491	F7F1N8	Protein Usp39 OS=Rattus norvegicus GN=Usp39 PE=4 SV=1 - [F7F1N8_RAT]	catalytic activity; metal ion binding		HCPYLDTINR
492	D3ZPY0	Protein Wtap OS=Rattus norvegicus GN=Wtap PE=4 SV=1 - [D3ZPY0_RAT]		nucleus; membrane	EQEMQECTTQIQYLK
492	D3ZPY0	Protein Wtap OS=Rattus norvegicus GN=Wtap PE=4 SV=1 - [D3ZPY0_RAT]		nucleus; membrane	TTSSEPVDQAEATSKDCSR
494	F1M0V0	Protein Zfp280d OS=Rattus norvegicus GN=Zfp280d PE=4 SV=2 - [F1M0V0_RAT]	metal ion binding		CPNSASNPVAALPVNFHPESR
494	F1M0V0	Protein Zfp280d OS=Rattus norvegicus GN=Zfp280d PE=4 SV=2 - [F1M0V0_RAT]	metal ion binding		DASVCEAAAAANR
496	D4A169	Protein Zfp462 OS=Rattus norvegicus GN=Zfp462 PE=4 SV=2 - [D4A169_RAT]	metal ion binding		DCSFYTGFK
496	D4A169	Protein Zfp462 OS=Rattus norvegicus GN=Zfp462 PE=4 SV=2 - [D4A169_RAT]	metal ion binding		FCSYTSPNVR
496	D4A169	Protein Zfp462 OS=Rattus norvegicus GN=Zfp462 PE=4 SV=2 - [D4A169_RAT]	metal ion binding		FCVEVHPTLR
496	D4A169	Protein Zfp462 OS=Rattus norvegicus GN=Zfp462 PE=4 SV=2 - [D4A169_RAT]	metal ion binding		FQNSTFQCK
496	D4A169	Protein Zfp462 OS=Rattus norvegicus GN=Zfp462 PE=4 SV=2 - [D4A169_RAT]	metal ion binding		HDIDAYYTHCLAASR
496	D4A169	Protein Zfp462 OS=Rattus norvegicus GN=Zfp462 PE=4 SV=2 - [D4A169_RAT]	metal ion binding		HSFCDNLPK
496	D4A169	Protein Zfp462 OS=Rattus norvegicus GN=Zfp462 PE=4 SV=2 - [D4A169_RAT]	metal ion binding		LCPYTHGTLEK
496	D4A169	Protein Zfp462 OS=Rattus norvegicus GN=Zfp462 PE=4 SV=2 - [D4A169_RAT]	metal ion binding		NQKPASCVLLPASGMER
496	D4A169	Protein Zfp462 OS=Rattus norvegicus GN=Zfp462 PE=4 SV=2 - [D4A169_RAT]	metal ion binding		QCSYTSPYFYALR
496	D4A169	Protein Zfp462 OS=Rattus norvegicus GN=Zfp462 PE=4 SV=2 - [D4A169_RAT]	metal ion binding		RHDIDAYYTHCLAASR
496	D4A169	Protein Zfp462 OS=Rattus norvegicus GN=Zfp462 PE=4 SV=2 - [D4A169_RAT]	metal ion binding		TFTPECENQK
497	D3ZIF0	Protein Zfp512 OS=Rattus norvegicus GN=Zfp512 PE=4 SV=1 - [D3ZIF0_RAT]	metal ion binding	nucleus	AHLGSCTLGTFVAGK
497	D3ZIF0	Protein Zfp512 OS=Rattus norvegicus GN=Zfp512 PE=4 SV=1 - [D3ZIF0_RAT]	metal ion binding	nucleus	DNSFQYTIPHEDSLSGSSSASSCEPVGDFPATFR
497	D3ZIF0	Protein Zfp512 OS=Rattus norvegicus GN=Zfp512 PE=4 SV=1 - [D3ZIF0_RAT]	metal ion binding	nucleus	SEHGPVFFPESGQPDCLK
498	D4A0U3	Protein Zfp638 OS=Rattus norvegicus GN=Zfp638 PE=4 SV=1 - [D4A0U3_RAT]	nucleotide binding; metal ion binding; RNA binding	nucleus	DWIQHQNTSTHIESCR
498	D4A0U3	Protein Zfp638 OS=Rattus norvegicus GN=Zfp638 PE=4 SV=1 - [D4A0U3_RAT]	nucleotide binding; metal ion binding; RNA binding	nucleus	ISDVLLVPCR
498	D4A0U3	Protein Zfp638 OS=Rattus norvegicus GN=Zfp638 PE=4 SV=1 - [D4A0U3_RAT]	nucleotide binding; metal ion binding; RNA binding	nucleus	QNPQNIGDHVLSCTLSPK
500	D4A7J8	PRP4 pre-mRNA processing factor 4 homolog (Yeast) OS=Rattus norvegicus GN=Prpf4 PE=4 SV=1 - [D4A7J8_RAT]	protein binding; RNA binding	nucleus	CVYTIPAHQNLVTGVK
500	D4A7J8	PRP4 pre-mRNA processing factor 4 homolog (Yeast) OS=Rattus norvegicus GN=Prpf4 PE=4 SV=1 - [D4A7J8_RAT]	protein binding; RNA binding	nucleus	DVNLASCAADGSVK
500	D4A7J8	PRP4 pre-mRNA processing factor 4 homolog (Yeast) OS=Rattus norvegicus GN=Prpf4 PE=4 SV=1 - [D4A7J8_RAT]	protein binding; RNA binding	nucleus	FLGTTCYDR

501	Q5BJS0	Putative ATP-dependent RNA helicase DHX30 OS=Rattus norvegicus GN=Dhx30 PE=1 SV=1 - [DHX30_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; mitochondrion	CNVIITQPR
501	Q5BJS0	Putative ATP-dependent RNA helicase DHX30 OS=Rattus norvegicus GN=Dhx30 PE=1 SV=1 - [DHX30_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; mitochondrion	GEPGGILCFLPGWQEIK
501	Q5BJS0	Putative ATP-dependent RNA helicase DHX30 OS=Rattus norvegicus GN=Dhx30 PE=1 SV=1 - [DHX30_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; mitochondrion	GPCGSFDVR
501	Q5BJS0	Putative ATP-dependent RNA helicase DHX30 OS=Rattus norvegicus GN=Dhx30 PE=1 SV=1 - [DHX30_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; mitochondrion	LPPMCVNPAPGGTISR
501	Q5BJS0	Putative ATP-dependent RNA helicase DHX30 OS=Rattus norvegicus GN=Dhx30 PE=1 SV=1 - [DHX30_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; mitochondrion	QAAAAACQLFK
501	Q5BJS0	Putative ATP-dependent RNA helicase DHX30 OS=Rattus norvegicus GN=Dhx30 PE=1 SV=1 - [DHX30_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; mitochondrion	RPCTIQVPEPILR
501	Q5BJS0	Putative ATP-dependent RNA helicase DHX30 OS=Rattus norvegicus GN=Dhx30 PE=1 SV=1 - [DHX30_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; cytoplasm; mitochondrion	VSCLETVWVSR
502	Q5RKH0	Putative oxidoreductase GLYR1 OS=Rattus norvegicus GN=Glyr1 PE=2 SV=1 - [GLYR1_RAT]	nucleotide binding; DNA binding; catalytic activity; protein binding	nucleus; cytoplasm; Golgi	TAEKCDLFIQEGAR
504	D3ZXI0	Pyrroline-5-carboxylate reductase OS=Rattus norvegicus GN=Pycr1 PE=3 SV=1 - [D3ZXI0_RAT]	nucleotide binding; catalytic activity; protein binding	cytoplasm; mitochondrion	CMTNTPVVVR
504	D3ZXI0	Pyrroline-5-carboxylate reductase OS=Rattus norvegicus GN=Pycr1 PE=3 SV=1 - [D3ZXI0_RAT]	nucleotide binding; catalytic activity; protein binding	cytoplasm; mitochondrion	SLLINAVEASCIR
505	P11980	Pyruvate kinase PKM OS=Rattus norvegicus GN=Pkm PE=1 SV=3 - [KPYM_RAT]	nucleotide binding; metal ion binding; catalytic activity; protein binding; RNA binding	nucleus; cytoplasm; mitochondrion; membrane	AGKPVICATQMLESMIK
506	Q6RUV5	Ras-related C3 botulinum toxin substrate 1 OS=Rattus norvegicus GN=Rac1 PE=1 SV=1 - [RAC1_RAT]	nucleotide binding; catalytic activity; protein binding	membrane; cytoplasm; cytosol	EIGAVKYLECSALTQR
506	Q6RUV5	Ras-related C3 botulinum toxin substrate 1 OS=Rattus norvegicus GN=Rac1 PE=1 SV=1 - [RAC1_RAT]	nucleotide binding; catalytic activity; protein binding	membrane; cytoplasm; cytosol	HHCPNTPIILVGTK
507	Q6NYB7	Ras-related protein Rab-1A OS=Rattus norvegicus GN=Rab1A PE=1 SV=3 - [RAB1A_RAT]	nucleotide binding; catalytic activity	membrane; nucleus; cytoplasm; mitochondrion; endosome; endoplasmic reticulum; Golgi; cytosol	LLVGNKCDLTTK
507	Q6NYB7	Ras-related protein Rab-1A OS=Rattus norvegicus GN=Rab1A PE=1 SV=3 - [RAB1A_RAT]	nucleotide binding; catalytic activity	membrane; nucleus; cytoplasm; mitochondrion; endosome; endoplasmic reticulum; Golgi; cytosol	SCLLLR
511	D4AD82	Rho GTPase-activating protein 35 OS=Rattus norvegicus GN=Arhgap35 PE=4 SV=2 - [D4AD82_RAT]	nucleotide binding		ALCTNDDKYVIDGK
511	D4AD82	Rho GTPase-activating protein 35 OS=Rattus norvegicus GN=Arhgap35 PE=4 SV=2 - [D4AD82_RAT]	nucleotide binding		FTSIPCSQPQHK
511	D4AD82	Rho GTPase-activating protein 35 OS=Rattus norvegicus GN=Arhgap35 PE=4 SV=2 - [D4AD82_RAT]	nucleotide binding		LQCVFLDPASAGIGYGR
511	D4AD82	Rho GTPase-activating protein 35 OS=Rattus norvegicus GN=Arhgap35 PE=4 SV=2 - [D4AD82_RAT]	nucleotide binding		SSHCGSSNSVLLELPIGVHK
512	O55215	Ribosomal protein S2 OS=Rattus norvegicus GN=Rps2-ps6 PE=2 SV=1 - [O55215_RAT]	RNA binding; structural molecule activity; protein binding	nucleus; cytoplasm; ribosome; membrane	CGSVLVR
512	O55215	Ribosomal protein S2 OS=Rattus norvegicus GN=Rps2-ps6 PE=2 SV=1 - [O55215_RAT]	RNA binding; structural molecule activity; protein binding	nucleus; cytoplasm; ribosome; membrane	CSKEVATAIR
512	O55215	Ribosomal protein S2 OS=Rattus norvegicus GN=Rps2-ps6 PE=2 SV=1 - [O55215_RAT]	RNA binding; structural molecule activity; protein binding	nucleus; cytoplasm; ribosome; membrane	GCTATLGNFAK
512	O55215	Ribosomal protein S2 OS=Rattus norvegicus GN=Rps2-ps6 PE=2 SV=1 - [O55215_RAT]	RNA binding; structural molecule activity; protein binding	nucleus; cytoplasm; ribosome; membrane	LLMMAGIDDCYTSAR
513	Q4V886	RNA polymerase II-associated factor 1 homolog OS=Rattus norvegicus GN=Paf1 PE=2 SV=1 - [PAF1_RAT]	protein binding	nucleus; mitochondrion	YCNSLPDIPFDPK
514	B2GV05	RNA-binding protein 5 OS=Rattus norvegicus GN=Rbm5 PE=2 SV=1 - [RBM5_RAT]	nucleotide binding; RNA binding; metal ion binding	nucleus; spliceosomal complex	CQGITAPIEAQVR
514	B2GV05	RNA-binding protein 5 OS=Rattus norvegicus GN=Rbm5 PE=2 SV=1 - [RBM5_RAT]	nucleotide binding; RNA binding; metal ion binding	nucleus; spliceosomal complex	FEDWLCNK
514	B2GV05	RNA-binding protein 5 OS=Rattus norvegicus GN=Rbm5 PE=2 SV=1 - [RBM5_RAT]	nucleotide binding; RNA binding; metal ion binding	nucleus; spliceosomal complex	KCQGITAPIEAQVR

515	P60123	RuvB-like 1 OS=Rattus norvegicus GN=Ruvbl1 PE=1 SV=1 - [RUVB1_RAT]	nucleotide binding; catalytic activity	nucleus; cytoplasm; Golgi	EVYEGEVTELTPCETENPMGGYGK
515	P60123	RuvB-like 1 OS=Rattus norvegicus GN=Ruvbl1 PE=1 SV=1 - [RUVB1_RAT]	nucleotide binding; catalytic activity	nucleus; cytoplasm; Golgi	VPFCPMVGSEVYSTEIK
516	Q6PEC4	S-phase kinase-associated protein 1 OS=Rattus norvegicus GN=Skp1 PE=2 SV=3 - [SKP1_RAT]	catalytic activity	cytosol	KENQWCEEK
517	Q6AY30	Saccharopine dehydrogenase-like oxidoreductase OS=Rattus norvegicus GN=Sccpdh PE=2 SV=1 - [SCPDL_RAT]	nucleotide binding; catalytic activity	nucleus; mitochondrion; membrane	ATLVLNCVGPYR
519	O88453	Scaffold attachment factor B1 OS=Rattus norvegicus GN=Safb PE=1 SV=2 - [SAFB1_RAT]	nucleotide binding; DNA binding; RNA binding; protein binding	nucleus	CYGFVTMSTAEEATK
519	O88453	Scaffold attachment factor B1 OS=Rattus norvegicus GN=Safb PE=1 SV=2 - [SAFB1_RAT]	nucleotide binding; DNA binding; RNA binding; protein binding	nucleus	FAFDACNDVPAAPK
519	O88453	Scaffold attachment factor B1 OS=Rattus norvegicus GN=Safb PE=1 SV=2 - [SAFB1_RAT]	nucleotide binding; DNA binding; RNA binding; protein binding	nucleus	ILDILGETCK
519	O88453	Scaffold attachment factor B1 OS=Rattus norvegicus GN=Safb PE=1 SV=2 - [SAFB1_RAT]	nucleotide binding; DNA binding; RNA binding; protein binding	nucleus	KFAFDACNDVPAAPK
522	Q5U3Z7	Serine hydroxymethyltransferase OS=Rattus norvegicus GN=Shmt2 PE=2 SV=1 - [Q5U3Z7_RAT]	catalytic activity; protein binding	mitochondrion; membrane; organelle lumen; cytoskeleton	AALEALGSCLNNK
522	Q5U3Z7	Serine hydroxymethyltransferase OS=Rattus norvegicus GN=Shmt2 PE=2 SV=1 - [Q5U3Z7_RAT]	catalytic activity; protein binding	mitochondrion; membrane; organelle lumen; cytoskeleton	QACTPMFR
523	Q6P799	Serine--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Sars PE=1 SV=3 - [SYSC_RAT]	nucleotide binding; catalytic activity	cytoplasm; mitochondrion	TICAILENYQTEK
524	B2DD29	Serine/threonine-protein kinase BRSK1 OS=Rattus norvegicus GN=Brsk1 PE=1 SV=1 - [BRSK1_RAT]	nucleotide binding; metal ion binding; catalytic activity; protein binding	nucleus; cytoplasm; cytoskeleton; membrane	HEPDPCLEPAPGR
525	O08875	Serine/threonine-protein kinase DCLK1 OS=Rattus norvegicus GN=Dclk1 PE=2 SV=1 - [DCLK1_RAT]	nucleotide binding; catalytic activity		TIGDGNFAVVKECIER
525	O08875	Serine/threonine-protein kinase DCLK1 OS=Rattus norvegicus GN=Dclk1 PE=2 SV=1 - [DCLK1_RAT]	nucleotide binding; catalytic activity		VCSSMDENDGPGEEESDEGFQIPATITER
526	E9PSS1	Serine/threonine-protein kinase DCLK2 OS=Rattus norvegicus GN=Dclk2 PE=1 SV=2 - [E9PSS1_RAT]	nucleotide binding; catalytic activity		CSESFTLLEK
526	E9PSS1	Serine/threonine-protein kinase DCLK2 OS=Rattus norvegicus GN=Dclk2 PE=1 SV=2 - [E9PSS1_RAT]	nucleotide binding; catalytic activity		DIKPENLLVCEYPDGTK
526	E9PSS1	Serine/threonine-protein kinase DCLK2 OS=Rattus norvegicus GN=Dclk2 PE=1 SV=2 - [E9PSS1_RAT]	nucleotide binding; catalytic activity		YAQDDFVLDHSECR
528	O88664	Serine/threonine-protein kinase TAO1 OS=Rattus norvegicus GN=Taok1 PE=1 SV=1 - [TAOK1_RAT]	nucleotide binding; catalytic activity; signal transducer activity; protein binding; enzyme regulator activity	cytoplasm	LDEAQEAECQVLK
528	O88664	Serine/threonine-protein kinase TAO1 OS=Rattus norvegicus GN=Taok1 PE=1 SV=1 - [TAOK1_RAT]	nucleotide binding; catalytic activity; signal transducer activity; protein binding; enzyme regulator activity	cytoplasm	QYLELECR
534	P62142	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Rattus norvegicus GN=Ppp1cb PE=1 SV=3 - [PP1B_RAT]	catalytic activity; protein binding; metal ion binding	nucleus; cytoplasm; cytosol	ICGDIHGQYTDLLR
537	A4L9P7	Sister chromatid cohesion protein PDS5 homolog A OS=Rattus norvegicus GN=Pds5a PE=2 SV=1 - [PDS5A_RAT]		chromosome; nucleus; membrane	QPTSEANCSAMFGK
537	A4L9P7	Sister chromatid cohesion protein PDS5 homolog A OS=Rattus norvegicus GN=Pds5a PE=2 SV=1 - [PDS5A_RAT]		chromosome; nucleus; membrane	SALCNADSPKDPVLPMK
539	D4A208	SLIT-ROBO Rho GTPase-activating protein 2 OS=Rattus norvegicus GN=Srgap2 PE=1 SV=1 - [SRGP2_RAT]	enzyme regulator activity; protein binding	nucleus; cytoplasm; membrane; cytosol	CSISGHGSLNSISR
539	D4A208	SLIT-ROBO Rho GTPase-activating protein 2 OS=Rattus norvegicus GN=Srgap2 PE=1 SV=1 - [SRGP2_RAT]	enzyme regulator activity; protein binding	nucleus; cytoplasm; membrane; cytosol	FEFQPHMGDMASQLCAQQPVQSELVQR
539	D4A208	SLIT-ROBO Rho GTPase-activating protein 2 OS=Rattus norvegicus GN=Srgap2 PE=1 SV=1 - [SRGP2_RAT]	enzyme regulator activity; protein binding	nucleus; cytoplasm; membrane; cytosol	KQDSSQAIPLVVESCIR

539	D4A208	SLIT-ROBO Rho GTPase-activating protein 2 OS=Rattus norvegicus GN=Srgap2 PE=1 SV=1 - [SRGP2_RAT]	enzyme regulator activity; protein binding	nucleus; cytoplasm; membrane; cytosol	SASTAGDIACAFRPVK
539	D4A208	SLIT-ROBO Rho GTPase-activating protein 2 OS=Rattus norvegicus GN=Srgap2 PE=1 SV=1 - [SRGP2_RAT]	enzyme regulator activity; protein binding	nucleus; cytoplasm; membrane; cytosol	SDSHGLGSSLTDSSSPGVGASCRPSSQPIMSQNLPK
539	D4A208	SLIT-ROBO Rho GTPase-activating protein 2 OS=Rattus norvegicus GN=Srgap2 PE=1 SV=1 - [SRGP2_RAT]	enzyme regulator activity; protein binding	nucleus; cytoplasm; membrane; cytosol	TDCSLAR
539	D4A208	SLIT-ROBO Rho GTPase-activating protein 2 OS=Rattus norvegicus GN=Srgap2 PE=1 SV=1 - [SRGP2_RAT]	enzyme regulator activity; protein binding	nucleus; cytoplasm; membrane; cytosol	TGASCPSGGHVADIYLANINK
542	P16086	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 - [SPTN1_RAT]	protein binding; metal ion binding	cytoplasm; cytosol; cytoskeleton; membrane	ALCAEADR
542	P16086	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 - [SPTN1_RAT]	protein binding; metal ion binding	cytoplasm; cytosol; cytoskeleton; membrane	CNSLEEIK
542	P16086	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 - [SPTN1_RAT]	protein binding; metal ion binding	cytoplasm; cytosol; cytoskeleton; membrane	CTELNQAWTSLGK
542	P16086	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 - [SPTN1_RAT]	protein binding; metal ion binding	cytoplasm; cytosol; cytoskeleton; membrane	DCEQAENWMAAR
542	P16086	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 - [SPTN1_RAT]	protein binding; metal ion binding	cytoplasm; cytosol; cytoskeleton; membrane	ECEDVMDWINDK
542	P16086	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 - [SPTN1_RAT]	protein binding; metal ion binding	cytoplasm; cytosol; cytoskeleton; membrane	EQADYCVSHMKPYVDGK
542	P16086	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 - [SPTN1_RAT]	protein binding; metal ion binding	cytoplasm; cytosol; cytoskeleton; membrane	GACAGSEDAVK
542	P16086	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 - [SPTN1_RAT]	protein binding; metal ion binding	cytoplasm; cytosol; cytoskeleton; membrane	TYLLDGSCMVEESGTLESQLEATKR
542	P16086	Spectrin alpha chain, non-erythrocytic 1 OS=Rattus norvegicus GN=Sptan1 PE=1 SV=2 - [SPTN1_RAT]	protein binding; metal ion binding	cytoplasm; cytosol; cytoskeleton; membrane	VNDVCTNGQDLIKK
543	D3ZDD7	Spermatid perinuclear RNA binding protein, isoform CRA_a OS=Rattus norvegicus GN=Strbp PE=4 SV=1 - [D3ZDD7_RAT]	DNA binding; RNA binding	nucleus; cytoplasm; cytoskeleton	CLNALASLR
543	D3ZDD7	Spermatid perinuclear RNA binding protein, isoform CRA_a OS=Rattus norvegicus GN=Strbp PE=4 SV=1 - [D3ZDD7_RAT]	DNA binding; RNA binding	nucleus; cytoplasm; cytoskeleton	NDTVSSNSSNNTGNCTTETSSTLEVR
543	D3ZDD7	Spermatid perinuclear RNA binding protein, isoform CRA_a OS=Rattus norvegicus GN=Strbp PE=4 SV=1 - [D3ZDD7_RAT]	DNA binding; RNA binding	nucleus; cytoplasm; cytoskeleton	SIGTCNRPLGAGEALR
543	D3ZDD7	Spermatid perinuclear RNA binding protein, isoform CRA_a OS=Rattus norvegicus GN=Strbp PE=4 SV=1 - [D3ZDD7_RAT]	DNA binding; RNA binding	nucleus; cytoplasm; cytoskeleton	YQVEQCINEASIIIR
544	Q63413	Spliceosome RNA helicase Ddx39b OS=Rattus norvegicus GN=Ddx39b PE=1 SV=3 - [DX39B_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; spliceosomal complex; cytoplasm	HFILDECDK
544	Q63413	Spliceosome RNA helicase Ddx39b OS=Rattus norvegicus GN=Ddx39b PE=1 SV=3 - [DX39B_RAT]	nucleotide binding; RNA binding; catalytic activity; protein binding	nucleus; spliceosomal complex; cytoplasm	NCPHIVVGTPGR
546	F1LSM7	Splicing factor, arginine/serine-rich 15 OS=Rattus norvegicus GN=Scaf4 PE=4 SV=2 - [F1LSM7_RAT]	nucleotide binding	nucleus	GCAYIVMVHR
546	F1LSM7	Splicing factor, arginine/serine-rich 15 OS=Rattus norvegicus GN=Scaf4 PE=4 SV=2 - [F1LSM7_RAT]	nucleotide binding	nucleus	SETASVCSTTLWVGQLDK
548	Q02769	Squalene synthase OS=Rattus norvegicus GN=Fdft1 PE=2 SV=1 - [FDFT_RAT]	catalytic activity	endoplasmic reticulum; membrane	CLGHPEEFYNLLR
548	Q02769	Squalene synthase OS=Rattus norvegicus GN=Fdft1 PE=2 SV=1 - [FDFT_RAT]	catalytic activity	endoplasmic reticulum; membrane	MGCGMAEFLNK
548	Q02769	Squalene synthase OS=Rattus norvegicus GN=Fdft1 PE=2 SV=1 - [FDFT_RAT]	catalytic activity	endoplasmic reticulum; membrane	NSLSNSLKTCYK
548	Q02769	Squalene synthase OS=Rattus norvegicus GN=Fdft1 PE=2 SV=1 - [FDFT_RAT]	catalytic activity	endoplasmic reticulum; membrane	TCYKYLDQTSR
548	Q02769	Squalene synthase OS=Rattus norvegicus GN=Fdft1 PE=2 SV=1 - [FDFT_RAT]	catalytic activity	endoplasmic reticulum; membrane	TQSLPNCQLISR

548	Q02769	Squalene synthase OS=Rattus norvegicus GN=Fdft1 PE=2 SV=1 - [FDFT_RAT]	catalytic activity	endoplasmic reticulum; membrane	YQTVIADICHR
549	Q66X93	Staphylococcal nuclease domain-containing protein 1 OS=Rattus norvegicus GN=Snd1 PE=2 SV=1 - [SND1_RAT]	catalytic activity; RNA binding	nucleus; cytoplasm; mitochondrion; membrane	EVCFTIENK
549	Q66X93	Staphylococcal nuclease domain-containing protein 1 OS=Rattus norvegicus GN=Snd1 PE=2 SV=1 - [SND1_RAT]	catalytic activity; RNA binding	nucleus; cytoplasm; mitochondrion; membrane	LSECEEQAK
549	Q66X93	Staphylococcal nuclease domain-containing protein 1 OS=Rattus norvegicus GN=Snd1 PE=2 SV=1 - [SND1_RAT]	catalytic activity; RNA binding	nucleus; cytoplasm; mitochondrion; membrane	MVLSGCAIIVR
550	F1M953	Stress-70 protein, mitochondrial OS=Rattus norvegicus GN=Hspa9 PE=3 SV=1 - [F1M953_RAT]	nucleotide binding; protein binding; RNA binding	mitochondrion; cell surface	DQLPADECNK
550	F1M953	Stress-70 protein, mitochondrial OS=Rattus norvegicus GN=Hspa9 PE=3 SV=1 - [F1M953_RAT]	nucleotide binding; protein binding; RNA binding	mitochondrion; cell surface	MEEFKDQLPADECNK
551	O35814	Stress-induced-phosphoprotein 1 OS=Rattus norvegicus GN=Stip1 PE=1 SV=1 - [STIP1_RAT]	protein binding; RNA binding	nucleus; cytoplasm	ALDLDSSCKEAADGYQR
551	O35814	Stress-induced-phosphoprotein 1 OS=Rattus norvegicus GN=Stip1 PE=1 SV=1 - [STIP1_RAT]	protein binding; RNA binding	nucleus; cytoplasm	ALSAGNIDDALQCYSEAIK
551	O35814	Stress-induced-phosphoprotein 1 OS=Rattus norvegicus GN=Stip1 PE=1 SV=1 - [STIP1_RAT]	protein binding; RNA binding	nucleus; cytoplasm	AYEDGCKTVDLKPDWGK
551	O35814	Stress-induced-phosphoprotein 1 OS=Rattus norvegicus GN=Stip1 PE=1 SV=1 - [STIP1_RAT]	protein binding; RNA binding	nucleus; cytoplasm	CMMAQYNR
552	F1LM47	Succinyl-CoA ligase subunit beta OS=Rattus norvegicus GN=Sucla2 PE=3 SV=1 - [F1LM47_RAT]	catalytic activity; nucleotide binding; metal ion binding	mitochondrion	ILACDDLDEAAK
553	Q68FU8	SURP and G-patch domain-containing protein 1 OS=Rattus norvegicus GN=Sugp1 PE=2 SV=1 - [SUGP1_RAT]	RNA binding	nucleus; spliceosomal complex	SAPEALSGAVPPITACPTPVAPAPAVNPTPSIP GKPTATATVK
554	Q4QQU6	Survival of motor neuron-related-splicing factor 30 OS=Rattus norvegicus GN=Smndc1 PE=2 SV=1 - [SPF30_RAT]	RNA binding	nucleus; spliceosomal complex; cytoplasm; cytoskeleton	VGVGTCGIADKPMTQYQDTSK
557	P28480	T-complex protein 1 subunit alpha OS=Rattus norvegicus GN=Tcp1 PE=1 SV=1 - [TCPA_RAT]	nucleotide binding; protein binding; RNA binding	nucleus; cytoplasm; Golgi; cytoskeleton; membrane	GANDFMCDEMER
557	P28480	T-complex protein 1 subunit alpha OS=Rattus norvegicus GN=Tcp1 PE=1 SV=1 - [TCPA_RAT]	nucleotide binding; protein binding; RNA binding	nucleus; cytoplasm; Golgi; cytoskeleton; membrane	IACLDFSLQK
557	P28480	T-complex protein 1 subunit alpha OS=Rattus norvegicus GN=Tcp1 PE=1 SV=1 - [TCPA_RAT]	nucleotide binding; protein binding; RNA binding	nucleus; cytoplasm; Golgi; cytoskeleton; membrane	ICDDELILIK
557	P28480	T-complex protein 1 subunit alpha OS=Rattus norvegicus GN=Tcp1 PE=1 SV=1 - [TCPA_RAT]	nucleotide binding; protein binding; RNA binding	nucleus; cytoplasm; Golgi; cytoskeleton; membrane	SLHDALCVVK
557	P28480	T-complex protein 1 subunit alpha OS=Rattus norvegicus GN=Tcp1 PE=1 SV=1 - [TCPA_RAT]	nucleotide binding; protein binding; RNA binding	nucleus; cytoplasm; Golgi; cytoskeleton; membrane	VLCELADLQDK
559	Q7TPB1	T-complex protein 1 subunit delta OS=Rattus norvegicus GN=Cct4 PE=1 SV=3 - [TCPD_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; cytoskeleton	DIEREDIEFICK
559	Q7TPB1	T-complex protein 1 subunit delta OS=Rattus norvegicus GN=Cct4 PE=1 SV=3 - [TCPD_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; cytoskeleton	ITGCTSPGK
559	Q7TPB1	T-complex protein 1 subunit delta OS=Rattus norvegicus GN=Cct4 PE=1 SV=3 - [TCPD_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; cytoskeleton	KTGCNVLLIQK
559	Q7TPB1	T-complex protein 1 subunit delta OS=Rattus norvegicus GN=Cct4 PE=1 SV=3 - [TCPD_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; cytoskeleton	LGGTIDDCELVEGLVLTQK
559	Q7TPB1	T-complex protein 1 subunit delta OS=Rattus norvegicus GN=Cct4 PE=1 SV=3 - [TCPD_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; cytoskeleton	TGCNVLLIQK
559	Q7TPB1	T-complex protein 1 subunit delta OS=Rattus norvegicus GN=Cct4 PE=1 SV=3 - [TCPD_RAT]	nucleotide binding; RNA binding; protein binding	nucleus; cytoplasm; cytoskeleton	TLSGMESYCVR
560	Q6P502	T-complex protein 1 subunit gamma OS=Rattus norvegicus GN=Cct3 PE=1 SV=1 - [TCPG_RAT]	nucleotide binding; RNA binding; protein binding	cytoplasm; membrane	ACTILLR
560	Q6P502	T-complex protein 1 subunit gamma OS=Rattus norvegicus GN=Cct3 PE=1 SV=1 - [TCPG_RAT]	nucleotide binding; RNA binding; protein binding	cytoplasm; membrane	HTQENCETWGVNGETGTLVDMK

560	Q6P502	T-complex protein 1 subunit gamma OS=Rattus norvegicus GN=Cct3 PE=1 SV=1 - [TCPG_RAT]	nucleotide binding; RNA binding; protein binding	cytoplasm; membrane	IPGGIIEDSCVLR
560	Q6P502	T-complex protein 1 subunit gamma OS=Rattus norvegicus GN=Cct3 PE=1 SV=1 - [TCPG_RAT]	nucleotide binding; RNA binding; protein binding	cytoplasm; membrane	KIGDEYFTFITDCKDPK
560	Q6P502	T-complex protein 1 subunit gamma OS=Rattus norvegicus GN=Cct3 PE=1 SV=1 - [TCPG_RAT]	nucleotide binding; RNA binding; protein binding	cytoplasm; membrane	NLQDAMQVCR
560	Q6P502	T-complex protein 1 subunit gamma OS=Rattus norvegicus GN=Cct3 PE=1 SV=1 - [TCPG_RAT]	nucleotide binding; RNA binding; protein binding	cytoplasm; membrane	TLIQNCGASTIR
560	Q6P502	T-complex protein 1 subunit gamma OS=Rattus norvegicus GN=Cct3 PE=1 SV=1 - [TCPG_RAT]	nucleotide binding; RNA binding; protein binding	cytoplasm; membrane	WSSLACNIALDAVK
561	Q5EAN7	Telomeric repeat-binding factor 2-interacting protein 1 OS=Rattus norvegicus GN=Terf2ip PE=2 SV=1 - [TE2IP_RAT]	DNA binding	nucleus; chromosome; cytoplasm	TPDLPEEECVKGETK
563	Q6AY87	THO complex subunit 6 homolog OS=Rattus norvegicus GN=Thoc6 PE=2 SV=1 - [THOC6_RAT]	RNA binding; protein binding	nucleus	AQVPGSSPGLLSLSLNQQPAAPECK
563	Q6AY87	THO complex subunit 6 homolog OS=Rattus norvegicus GN=Thoc6 PE=2 SV=1 - [THOC6_RAT]	RNA binding; protein binding	nucleus	GHTDYIHCLALR
563	Q6AY87	THO complex subunit 6 homolog OS=Rattus norvegicus GN=Thoc6 PE=2 SV=1 - [THOC6_RAT]	RNA binding; protein binding	nucleus	VLTASGNSCR
564	Q5XHY5	Threonine--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Tars PE=2 SV=1 - [SYTC_RAT]	nucleotide binding; catalytic activity; metal ion binding	cytoplasm; cytoskeleton	QVMVVPVGPTCDEYAQK
564	Q5XHY5	Threonine--tRNA ligase, cytoplasmic OS=Rattus norvegicus GN=Tars PE=2 SV=1 - [SYTC_RAT]	nucleotide binding; catalytic activity; metal ion binding	cytoplasm; cytoskeleton	TTPYQIACGISQGLADNTVVAK
566	G3V790	Transcription activator BRG1 OS=Rattus norvegicus GN=Smarca4 PE=4 SV=2 - [G3V790_RAT]	DNA binding; protein binding; catalytic activity; nucleotide binding	nucleus; membrane	CDMSALQR
566	G3V790	Transcription activator BRG1 OS=Rattus norvegicus GN=Smarca4 PE=4 SV=2 - [G3V790_RAT]	DNA binding; protein binding; catalytic activity; nucleotide binding	nucleus; membrane	LTCEEEEEKMFGR
566	G3V790	Transcription activator BRG1 OS=Rattus norvegicus GN=Smarca4 PE=4 SV=2 - [G3V790_RAT]	DNA binding; protein binding; catalytic activity; nucleotide binding	nucleus; membrane	QEVVVCMR
566	G3V790	Transcription activator BRG1 OS=Rattus norvegicus GN=Smarca4 PE=4 SV=2 - [G3V790_RAT]	DNA binding; protein binding; catalytic activity; nucleotide binding	nucleus; membrane	SCSTFEQWFNAPFAMTGEK
567	F1LQ90	Transcription factor 4 OS=Rattus norvegicus GN=Tcf4 PE=4 SV=2 - [F1LQ90_RAT]	DNA binding; protein binding	nucleus	SGTNHYSTSSCTPPANGTDSIMANR
568	O08629	Transcription intermediary factor 1-beta OS=Rattus norvegicus GN=Trim28 PE=1 SV=2 - [TIF1B_RAT]	DNA binding; catalytic activity; protein binding; metal ion binding; RNA binding	chromosome; nucleus	DCQLNAHKDHQYQFLEDAVR
568	O08629	Transcription intermediary factor 1-beta OS=Rattus norvegicus GN=Trim28 PE=1 SV=2 - [TIF1B_RAT]	DNA binding; catalytic activity; protein binding; metal ion binding; RNA binding	chromosome; nucleus	QQCYSKDIVENYFMR
569	Q9R1D1	Transcriptional repressor CTCF OS=Rattus norvegicus GN=Ctcf PE=2 SV=1 - [CTCF_RAT]	DNA binding; metal ion binding	chromosome; nucleus	EGLAESEPMICHTLPLPEGFQVVK
569	Q9R1D1	Transcriptional repressor CTCF OS=Rattus norvegicus GN=Ctcf PE=2 SV=1 - [CTCF_RAT]	DNA binding; metal ion binding	chromosome; nucleus	HADNCAGPDGVEGENGGETKK
569	Q9R1D1	Transcriptional repressor CTCF OS=Rattus norvegicus GN=Ctcf PE=2 SV=1 - [CTCF_RAT]	DNA binding; metal ion binding	chromosome; nucleus	YCDAVFHER
569	Q9R1D1	Transcriptional repressor CTCF OS=Rattus norvegicus GN=Ctcf PE=2 SV=1 - [CTCF_RAT]	DNA binding; metal ion binding	chromosome; nucleus	YHDPNFVPAAFVCSK
571	P61589	Transforming protein RhoA OS=Rattus norvegicus GN=Rhoa PE=1 SV=1 - [RHOA_RAT]	nucleotide binding; catalytic activity; signal transducer activity; protein binding	nucleus; cytoplasm; mitochondrion; cytosol; cytoskeleton; membrane	IGAFGYMECSAK
573	P46462	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus GN=Vcp PE=1 SV=3 - [TERA_RAT]	nucleotide binding; catalytic activity; RNA binding; protein binding; enzyme regulator activity	proteasome; nucleus; cytoplasm; endoplasmic reticulum; membrane; cytosol	AIANECQANFISIK
573	P46462	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus GN=Vcp PE=1 SV=3 - [TERA_RAT]	nucleotide binding; catalytic activity; RNA binding; protein binding; enzyme regulator activity	proteasome; nucleus; cytoplasm; endoplasmic reticulum; membrane; cytosol	EDEEESLNEVGYDDIGGCRK
573	P46462	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus GN=Vcp PE=1 SV=3 - [TERA_RAT]	nucleotide binding; catalytic activity; RNA binding; protein binding; enzyme regulator activity	proteasome; nucleus; cytoplasm; endoplasmic reticulum; membrane; cytosol	GVLFYGPPGCGK
573	P46462	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus GN=Vcp PE=1 SV=3 - [TERA_RAT]	nucleotide binding; catalytic activity; RNA binding; protein binding; enzyme regulator activity	proteasome; nucleus; cytoplasm; endoplasmic reticulum; membrane; cytosol	LGDVISIQPCPDVK
573	P46462	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus GN=Vcp PE=1 SV=3 - [TERA_RAT]	nucleotide binding; catalytic activity; RNA binding; protein binding; enzyme regulator activity	proteasome; nucleus; cytoplasm; endoplasmic reticulum; membrane; cytosol	MTNGFSGADLTEICQR

573	P46462	Transitional endoplasmic reticulum ATPase OS=Rattus norvegicus GN=Vcp PE=1 SV=3 - [TERA_RAT]	nucleotide binding; catalytic activity; RNA binding; protein binding; enzyme regulator activity	proteasome; nucleus; cytoplasm; endoplasmic reticulum; membrane; cytosol	QAAPCVLFFDELDSIAK
576	P32089	Tricarboxylate transport protein, mitochondrial OS=Rattus norvegicus GN=Slc25a1 PE=1 SV=1 - [TXTP_RAT]	transporter activity	nucleus; mitochondrion; membrane	NTLDCGVQILKNEGPK
576	P32089	Tricarboxylate transport protein, mitochondrial OS=Rattus norvegicus GN=Slc25a1 PE=1 SV=1 - [TXTP_RAT]	transporter activity	nucleus; mitochondrion; membrane	YRGIGDCVR
577	Q64428	Trifunctional enzyme subunit alpha, mitochondrial OS=Rattus norvegicus GN=Hadha PE=1 SV=2 - [ECHA_RAT]	catalytic activity; protein binding; nucleotide binding	cytoplasm; mitochondrion; membrane; organelle lumen	ALMGLYNGQVLCK
577	Q64428	Trifunctional enzyme subunit alpha, mitochondrial OS=Rattus norvegicus GN=Hadha PE=1 SV=2 - [ECHA_RAT]	catalytic activity; protein binding; nucleotide binding	cytoplasm; mitochondrion; membrane; organelle lumen	CLAPMMSEVIR
577	Q64428	Trifunctional enzyme subunit alpha, mitochondrial OS=Rattus norvegicus GN=Hadha PE=1 SV=2 - [ECHA_RAT]	catalytic activity; protein binding; nucleotide binding	cytoplasm; mitochondrion; membrane; organelle lumen	EVESVTPEHCIFASNTSALPINQIAAVSQRPEK
577	Q64428	Trifunctional enzyme subunit alpha, mitochondrial OS=Rattus norvegicus GN=Hadha PE=1 SV=2 - [ECHA_RAT]	catalytic activity; protein binding; nucleotide binding	cytoplasm; mitochondrion; membrane; organelle lumen	KYESAYGTQFTPCQLLR
578	G3V8D6	Tripartite motif protein 3, isoform CRA_a OS=Rattus norvegicus GN=Trim3 PE=4 SV=1 - [G3V8D6_RAT]	catalytic activity; protein binding; metal ion binding	cytoplasm; endosome	QALVSDLESICGAK
578	G3V8D6	Tripartite motif protein 3, isoform CRA_a OS=Rattus norvegicus GN=Trim3 PE=4 SV=1 - [G3V8D6_RAT]	catalytic activity; protein binding; metal ion binding	cytoplasm; endosome	QGQEHIGSSCSFAEQALR
578	G3V8D6	Tripartite motif protein 3, isoform CRA_a OS=Rattus norvegicus GN=Trim3 PE=4 SV=1 - [G3V8D6_RAT]	catalytic activity; protein binding; metal ion binding	cytoplasm; endosome	TGSAELCAEITGPDGVR
579	Q64560	Tripeptidyl-peptidase 2 OS=Rattus norvegicus GN=Tpp2 PE=2 SV=3 - [TPP2_RAT]	catalytic activity	nucleus; cytoplasm	ACVDSNENGDLGK
579	Q64560	Tripeptidyl-peptidase 2 OS=Rattus norvegicus GN=Tpp2 PE=2 SV=3 - [TPP2_RAT]	catalytic activity	nucleus; cytoplasm	AIEFCIAR
579	Q64560	Tripeptidyl-peptidase 2 OS=Rattus norvegicus GN=Tpp2 PE=2 SV=3 - [TPP2_RAT]	catalytic activity	nucleus; cytoplasm	ETGASSFLCR
579	Q64560	Tripeptidyl-peptidase 2 OS=Rattus norvegicus GN=Tpp2 PE=2 SV=3 - [TPP2_RAT]	catalytic activity	nucleus; cytoplasm	FCSLPEK
579	Q64560	Tripeptidyl-peptidase 2 OS=Rattus norvegicus GN=Tpp2 PE=2 SV=3 - [TPP2_RAT]	catalytic activity	nucleus; cytoplasm	GAGPGCYLAGSLTLSK
579	Q64560	Tripeptidyl-peptidase 2 OS=Rattus norvegicus GN=Tpp2 PE=2 SV=3 - [TPP2_RAT]	catalytic activity	nucleus; cytoplasm	GCALADHLLHAQPHDGAAAGDAEAK
579	Q64560	Tripeptidyl-peptidase 2 OS=Rattus norvegicus GN=Tpp2 PE=2 SV=3 - [TPP2_RAT]	catalytic activity	nucleus; cytoplasm	ICEVINEAVWK
579	Q64560	Tripeptidyl-peptidase 2 OS=Rattus norvegicus GN=Tpp2 PE=2 SV=3 - [TPP2_RAT]	catalytic activity	nucleus; cytoplasm	KETGASSFLCR
579	Q64560	Tripeptidyl-peptidase 2 OS=Rattus norvegicus GN=Tpp2 PE=2 SV=3 - [TPP2_RAT]	catalytic activity	nucleus; cytoplasm	NCIQLMK
579	Q64560	Tripeptidyl-peptidase 2 OS=Rattus norvegicus GN=Tpp2 PE=2 SV=3 - [TPP2_RAT]	catalytic activity	nucleus; cytoplasm	STLVDALCR
579	Q64560	Tripeptidyl-peptidase 2 OS=Rattus norvegicus GN=Tpp2 PE=2 SV=3 - [TPP2_RAT]	catalytic activity	nucleus; cytoplasm	YEDLAPCITLK
582	Q63610	Tropomyosin alpha-3 chain OS=Rattus norvegicus GN=Tpm3 PE=1 SV=2 - [TPM3_RAT]	protein binding	cytoplasm; cytoskeleton	CLSAAEEK
582	Q63610	Tropomyosin alpha-3 chain OS=Rattus norvegicus GN=Tpm3 PE=1 SV=2 - [TPM3_RAT]	protein binding	cytoplasm; cytoskeleton	EEHLCTQR
582	Q63610	Tropomyosin alpha-3 chain OS=Rattus norvegicus GN=Tpm3 PE=1 SV=2 - [TPM3_RAT]	protein binding	cytoplasm; cytoskeleton	LMDQNLKCLSAAEEK
587	Q4QRB4	Tubulin beta-3 chain OS=Rattus norvegicus GN=Tubb3 PE=1 SV=1 - [TBB3_RAT]	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	VAVCDIPPRGLK
591	M0RD75	Uncharacterized protein (Fragment) OS=Rattus norvegicus GN=Rps6 PE=4 SV=1 - [M0RD75_RAT]	structural molecule activity; protein binding	nucleus; cytoplasm; ribosome	LNISFPATGCQK

597	D4A7G0	Uncharacterized protein OS=Rattus norvegicus GN=Zc3h14 PE=4 SV=2 - [D4A7G0_RAT]	metal ion binding		ADCPFTHMSR
598	M0R5J4	Uncharacterized protein OS=Rattus norvegicus PE=3 SV=1 - [M0R5J4_RAT]	metal ion binding; catalytic activity		VNQIGSVTESIQACK
599	M0RCH8	Uncharacterized protein OS=Rattus norvegicus PE=4 SV=1 - [M0RCH8_RAT]	RNA binding		DECDSPEQTEGFYK
601	D4A567	Uncharacterized protein OS=Rattus norvegicus PE=4 SV=2 - [D4A567_RAT]	protein binding	chromosome; nucleus	TPCNAGTFSQPEK
602	Q9QYF3	Unconventional myosin-Va OS=Rattus norvegicus GN=Myo5a PE=1 SV=1 - [MYO5A_RAT]	catalytic activity; motor activity; protein binding; nucleotide binding; metal ion binding; RNA binding	extracellular; cytoplasm; vacuole; endosome; endoplasmic reticulum; Golgi; cytosol; membrane	ACGVLETIR
602	Q9QYF3	Unconventional myosin-Va OS=Rattus norvegicus GN=Myo5a PE=1 SV=1 - [MYO5A_RAT]	catalytic activity; motor activity; protein binding; nucleotide binding; metal ion binding; RNA binding	extracellular; cytoplasm; vacuole; endosome; endoplasmic reticulum; Golgi; cytosol; membrane	CALFEKPR
602	Q9QYF3	Unconventional myosin-Va OS=Rattus norvegicus GN=Myo5a PE=1 SV=1 - [MYO5A_RAT]	catalytic activity; motor activity; protein binding; nucleotide binding; metal ion binding; RNA binding	extracellular; cytoplasm; vacuole; endosome; endoplasmic reticulum; Golgi; cytosol; membrane	KQTCQNVLEK
602	Q9QYF3	Unconventional myosin-Va OS=Rattus norvegicus GN=Myo5a PE=1 SV=1 - [MYO5A_RAT]	catalytic activity; motor activity; protein binding; nucleotide binding; metal ion binding; RNA binding	extracellular; cytoplasm; vacuole; endosome; endoplasmic reticulum; Golgi; cytosol; membrane	LGILDLLDEECK
602	Q9QYF3	Unconventional myosin-Va OS=Rattus norvegicus GN=Myo5a PE=1 SV=1 - [MYO5A_RAT]	catalytic activity; motor activity; protein binding; nucleotide binding; metal ion binding; RNA binding	extracellular; cytoplasm; vacuole; endosome; endoplasmic reticulum; Golgi; cytosol; membrane	QNEHCLTNFDLAEYR
602	Q9QYF3	Unconventional myosin-Va OS=Rattus norvegicus GN=Myo5a PE=1 SV=1 - [MYO5A_RAT]	catalytic activity; motor activity; protein binding; nucleotide binding; metal ion binding; RNA binding	extracellular; cytoplasm; vacuole; endosome; endoplasmic reticulum; Golgi; cytosol; membrane	QTCQNVLEK
602	Q9QYF3	Unconventional myosin-Va OS=Rattus norvegicus GN=Myo5a PE=1 SV=1 - [MYO5A_RAT]	catalytic activity; motor activity; protein binding; nucleotide binding; metal ion binding; RNA binding	extracellular; cytoplasm; vacuole; endosome; endoplasmic reticulum; Golgi; cytosol; membrane	VEYQCEGFLEK
603	Q04462	Valine--tRNA ligase OS=Rattus norvegicus GN=Vars PE=2 SV=2 - [SYVC_RAT]	nucleotide binding; catalytic activity; protein binding	cytoplasm; mitochondrion; cytosol	ADFPAGIPECGTDALR
603	Q04462	Valine--tRNA ligase OS=Rattus norvegicus GN=Vars PE=2 SV=2 - [SYVC_RAT]	nucleotide binding; catalytic activity; protein binding	cytoplasm; mitochondrion; cytosol	CGEMAQAASAAVTR
603	Q04462	Valine--tRNA ligase OS=Rattus norvegicus GN=Vars PE=2 SV=2 - [SYVC_RAT]	nucleotide binding; catalytic activity; protein binding	cytoplasm; mitochondrion; cytosol	DNPMVVPLCNR
603	Q04462	Valine--tRNA ligase OS=Rattus norvegicus GN=Vars PE=2 SV=2 - [SYVC_RAT]	nucleotide binding; catalytic activity; protein binding	cytoplasm; mitochondrion; cytosol	FGLCAYTSQGR
603	Q04462	Valine--tRNA ligase OS=Rattus norvegicus GN=Vars PE=2 SV=2 - [SYVC_RAT]	nucleotide binding; catalytic activity; protein binding	cytoplasm; mitochondrion; cytosol	GETTLWNPGCDHAGIATQVVVEK
603	Q04462	Valine--tRNA ligase OS=Rattus norvegicus GN=Vars PE=2 SV=2 - [SYVC_RAT]	nucleotide binding; catalytic activity; protein binding	cytoplasm; mitochondrion; cytosol	ICLQPPPSSR
604	Q9Z270	Vesicle-associated membrane protein-associated protein A OS=Rattus norvegicus GN=Vapa PE=1 SV=3 - [VAPA_RAT]	signal transducer activity; structural molecule activity; protein binding	membrane; endoplasmic reticulum; cytoskeleton	CVFEMPNENDKLNDMEPSK
604	Q9Z270	Vesicle-associated membrane protein-associated protein A OS=Rattus norvegicus GN=Vapa PE=1 SV=3 - [VAPA_RAT]	signal transducer activity; structural molecule activity; protein binding	membrane; endoplasmic reticulum; cytoskeleton	KLMEECKR
607	P31000	Vimentin OS=Rattus norvegicus GN=Vim PE=1 SV=2 - [VIME_RAT]	protein binding; RNA binding; structural molecule activity	nucleus; cytoplasm; cytosol; cytoskeleton; membrane	QVQSLTCEVDALKGTNESLER
607	P31000	Vimentin OS=Rattus norvegicus GN=Vim PE=1 SV=2 - [VIME_RAT]	protein binding; RNA binding; structural molecule activity	nucleus; cytoplasm; cytosol; cytoskeleton; membrane	RQVQSLTCEVDALK
608	Q9Z2L0	Voltage-dependent anion-selective channel protein 1 OS=Rattus norvegicus GN=Vdac1 PE=1 SV=4 - [VDAC1_RAT]	nucleotide binding; transporter activity; protein binding	nucleus; mitochondrion; membrane	YQVDPDACFSAK
610	G3V6J7	Zinc finger and BTB domain-containing protein 18 OS=Rattus norvegicus GN=Zfp238 PE=4 SV=2 - [G3V6J7_RAT]	protein binding; DNA binding; metal ion binding	nucleus; cytoskeleton	EASCDESDVGTNDYDMEHSTVK

610	G3V6J7	Zinc finger and BTB domain-containing protein 18 OS=Rattus norvegicus GN=Zfp238 PE=4 SV=2 - [G3V6J7_RAT]	protein binding; DNA binding; metal ion binding	nucleus; cytoskeleton	HLLQCLSEQR
610	G3V6J7	Zinc finger and BTB domain-containing protein 18 OS=Rattus norvegicus GN=Zfp238 PE=4 SV=2 - [G3V6J7_RAT]	protein binding; DNA binding; metal ion binding	nucleus; cytoskeleton	TFSCMYTLK
610	G3V6J7	Zinc finger and BTB domain-containing protein 18 OS=Rattus norvegicus GN=Zfp238 PE=4 SV=2 - [G3V6J7_RAT]	protein binding; DNA binding; metal ion binding	nucleus; cytoskeleton	TVASPCSSTESLSQR
612	Q62806	Zinc finger protein 148 OS=Rattus norvegicus GN=Znf148 PE=2 SV=1 - [ZN148_RAT]	DNA binding; metal ion binding	nucleus; Golgi	CGGIDEMQSSR
613	O88553	Zinc finger protein 37 OS=Rattus norvegicus GN=Zfp37 PE=2 SV=1 - [ZFP37_RAT]	DNA binding; metal ion binding	nucleus	LETCSNPASMGNQDPK
614	Q562A2	Zinc finger RNA-binding protein OS=Rattus norvegicus GN=Zfr PE=1 SV=2 - [ZFR_RAT]	DNA binding; RNA binding; metal ion binding	nucleus; chromosome; cytoplasm	AEDLKGTDCIK
614	Q562A2	Zinc finger RNA-binding protein OS=Rattus norvegicus GN=Zfr PE=1 SV=2 - [ZFR_RAT]	DNA binding; RNA binding; metal ion binding	nucleus; chromosome; cytoplasm	ANGLQSCVIIIR
614	Q562A2	Zinc finger RNA-binding protein OS=Rattus norvegicus GN=Zfr PE=1 SV=2 - [ZFR_RAT]	DNA binding; RNA binding; metal ion binding	nucleus; chromosome; cytoplasm	CLDALAALR
614	Q562A2	Zinc finger RNA-binding protein OS=Rattus norvegicus GN=Zfr PE=1 SV=2 - [ZFR_RAT]	DNA binding; RNA binding; metal ion binding	nucleus; chromosome; cytoplasm	NVNLVLLCSEKPSK

Table S8

Direct detection of proteins S-nitrosylated upon CysNO-treatment of neurons

★transcription factor

• also present in BDNF-treated neurons

42 SNO-sites on 32 proteins

Hit No.	Accession	Description	Sequence	Modifications	Molecular Function	Cellular Componen	Biological Process
1	P04762	Catalase OS=Rattus norvegicus GN=Cat PE=1 SV=3 - [CATA_RAT]	DGPMCMHDNQGGAPNYYPNSFSAPEQQGS ALEHHSQCSADVK	M4(Oxidation); C5(Nitrosyl); M6(Oxidation); C37(Carbamidomethyl)	etal ion binding; nucleotide binding	mitochondrion; vacuole; membrane; endoplasmic reticulum; Golgi; cytosol	response to stimulus; cell differentiation; metabolic process; regulation of biological process; cell organization and biogenesis
2	•P45592	Cofilin-1 OS=Rattus norvegicus GN=Cfl1 PE=1 SV=3 - [COF1_RAT]	HELQANCYEEVKDR	C7(Nitrosyl)	protein binding	nucleus; cytoplasm; cytoskeleton; membrane	cellular component movement; metabolic process; transport; cell organization and biogenesis; response to stimulus; regulation of biological process
3	Q91XQ4	DNA-directed RNA polymerase II subunit GRINL1A OS=Rattus norvegicus GN=Polr2m PE=2 SV=2 - [GRL1A_RAT]	AQNSDLMLDTSSLVPECSSVDIESSKTTSET QGPTHLTHKGNEETLATGCTVNTCPSAR	C17(Carbamidomethyl); C50(Carbamidomethyl); C55(Nitrosyl)	catalytic activity	nucleus	metabolic process
4	•F1LTP6	Enolase (Fragment) OS=Rattus norvegicus PE=3 SV=1 - [F1LTP6_RAT]	VNQIGSVTESLQVCK	C14(Nitrosyl)	metal ion binding; catalytic activity		metabolic process
5	B5DEN5	Eukaryotic translation elongation factor 1 beta 2 OS=Rattus norvegicus GN=Eef1b2 PE=2 SV=1 - [B5DEN5_RAT]	KLQIQCVVEDDKVGTDMLEEQITAFEDYVQS MDVAAFNK	C6(Nitrosyl); M17(Oxidation); M32(Oxidation)	RNA binding		metabolic process
6	•F1LP06	Fructose-bisphosphate aldolase (Fragment) OS=Rattus norvegicus GN=Aldoal1 PE=3 SV=1 - [F1LP06_RAT]	ALSDHHVYLEGTLLKPNMVTPGHTCTQK	C25(Nitrosyl)	catalytic activity		metabolic process
7	•F1LU03	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Rattus norvegicus PE=3 SV=1 - [F1LU03_RAT]	GILGYTEDQVVSCNFNSNSHSSTFDAGASIAL NDNFVK	C13(Nitrosyl)	catalytic activity		metabolic process
7	•D3ZQ40	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus PE=3 SV=1 - [D3ZQ40_RAT]	IVSNVSCTTDCLAPLAK	C7(Nitrosyl); C11(Carbamidomethyl)	catalytic activity		metabolic process
7	•D4A3W5	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus PE=3 SV=1 - [D4A3W5_RAT]	GILGYTKDQVVSCYFNSNHSSTFDAEAGIALN DNFVK	C13(Nitrosyl)	catalytic activity		metabolic process
8	G3V7U4	Lamin-B1 OS=Rattus norvegicus GN=Lmnb1 PE=3 SV=1 - [G3V7U4_RAT]	VDLENRCQSLTEDLEFR	C7(Nitrosyl)	al molecule activity; protein binding	nucleus; membrane	regulation of biological process

9	D4A1G3	Molybdenum cofactor sulfurase (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Mocos PE=4 SV=1 - [D4A1G3_RAT]	WLSKFCGRPCHLIK	C10(Nitrosyl)	catalytic activity; metal ion binding		metabolic process
10	•G3V918	Phosphoribosylglycinamide formyltransferase, isoform CRA_a OS=Rattus norvegicus GN=Gart PE=3 SV=1 - [G3V918_RAT]	THTGEKPYECDVCGK	C10(Nitrosyl); C13(Carbamidomethyl)	ucleotide binding; metal ion binding	cytoplasm	metabolic process; response to stimulus
10	•G3V918	Phosphoribosylglycinamide formyltransferase, isoform CRA_a OS=Rattus norvegicus GN=Gart PE=3 SV=1 - [G3V918_RAT]	ISNAAVSINDHTALARFCKDEK	C18(Nitrosyl)	ucleotide binding; metal ion binding	cytoplasm	metabolic process; response to stimulus
10	•G3V918	Phosphoribosylglycinamide formyltransferase, isoform CRA_a OS=Rattus norvegicus GN=Gart PE=3 SV=1 - [G3V918_RAT]	ISNAAVSINDHTALARFCK	C18(Nitrosyl)	ucleotide binding; metal ion binding	cytoplasm	metabolic process; response to stimulus
11	★D4ACD0	Protein Hoxd13 OS=Rattus norvegicus GN=Hoxd13 PE=3 SV=1 - [D4ACD0_RAT]	ADGGAAGAAPASSSSSVAAPGQCRGFLSAP VFAGTHSGR	C23(Nitrosyl)	DNA binding	nucleus	regulation of biological process
12	F1LQZ3	Protein Kif3a (Fragment) OS=Rattus norvegicus GN=Kif3a PE=3 SV=1 - [F1LQZ3_RAT]	LLQDSLGGNSKTMMCANIGPADYNYDETIST LR	M13(Oxidation); M14(Oxidation); C15(Nitrosyl)	tivity; motor activity; protein binding		cellular component movement; regulation of biological process; response to stimulus; metabolic process; cell organization and biogenesis
13	D3Z860	Protein LOC100361234 OS=Rattus norvegicus GN=LOC100361234 PE=4 SV=1 - [D3Z860_RAT]	LCVDEAELIQAAR	C2(Nitrosyl)	protein binding		
14	F1LX30	Protein RGD1308093 (Fragment) OS=Rattus norvegicus GN=RGD1308093 PE=4 SV=1 - [F1LX30_RAT]	LSTCLLSAPSGIQR	C4(Nitrosyl)			regulation of biological process
15	F1LTM4	Protein RGD1561777 (Fragment) OS=Rattus norvegicus GN=RGD1561777 PE=4 SV=1 - [F1LTM4_RAT]	SPLCLWIATSVYGASLATTFPSGVSWIEQYTT LTGK	C4(Nitrosyl)			transport
16	D3ZN31	Protein RGD1565350 OS=Rattus norvegicus GN=RGD1565350 PE=4 SV=1 - [D3ZN31_RAT]	REQPPQAVPQACSASSASCGSAAACFSASS GSLPDDSGSTSDLIR	C12(Nitrosyl); C19(Carbamidomethyl)	protein binding		regulation of biological process; cell proliferation
17	F1LTI2	Protein Rufy2 (Fragment) OS=Rattus norvegicus GN=Rufy2 PE=4 SV=1 - [F1LTI2_RAT]	TLDSDYPPLQQFFVVMEHCLK	M16(Oxidation); C19(Nitrosyl)	catalytic activity; motor activity		transport
18	E9PTD6	Protein Samd9l OS=Rattus norvegicus GN=Samd9l PE=4 SV=1 - [E9PTD6_RAT]	FLPSCGSSSVILEK	C5(Nitrosyl)	protein binding		

19	G3V7T6	Protein Sf3b1 OS=Rattus norvegicus GN=Sf3b1 PE=4 SV=1 - [G3V7T6_RAT]	IVQQIAILMGCAILPHLR	M9(Oxidation); C11(Nitrosyl)	al transducer activity; RNA binding	nucleus; spliceosomal complex	regulation of biological process; response to stimulus
20	•G3V7C6	Protein Tubb2c OS=Rattus norvegicus GN=Tubb4b PE=3 SV=1 - [G3V7C6_RAT]	EAESCDCLQGFQLTHSLGGGTGSGMGTLLIS K	C5(Nitrosyl); C7(Carbamidomethyl)	activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cell organization and biogenesis
21	•Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	ECEHCDCLQGFQLTHSLGGGTGSGMGTLLIS K	C2(Nitrosyl); C5(Nitrosyl)	activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
21	•Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	ECEHCDCLQGFQLTHSLGGGTGSGMGTLLIS K	C3(Nitrosyl); C6(Nitrosyl); C8(Nitrosyl)	activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
21	•Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	ECEHCDCLQGFQLTHSLGGGTGSGMGTLLIS K	C2(Nitrosyl); C7(Carbamidomethyl)	activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
21	•Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	ECEHCDCLQGFQLTHSLGGGTGSGMGTLLIS K	C2(Nitrosyl); C5(Nitrosyl); C7(Nitrosyl)	activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
21	•Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	ECEHCDCLQGFQLTHSLGGGTGSGMGTLLIS K	C6(Carbamidomethyl); C8(Nitrosyl)	activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
21	•Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	MREIVHIQAGQCGNQIGTK	C12(Nitrosyl)	activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
22	Q496Z9	TRMT1-like protein OS=Rattus norvegicus GN=Trmt1l PE=2 SV=1 - [TRM1L_RAT]	LAFGTEGDVDSASSLNSDNLENIQTCPLCPK	C26(Nitrosyl)	catalytic activity; metal ion binding		response to stimulus; metabolic process
23	Q6AYZ1	Tubulin alpha-1C chain OS=Rattus norvegicus GN=Tuba1c PE=1 SV=1 - [TBA1C_RAT]	AYHEQLTVAEITNACFEPANQMVK	C15(Nitrosyl)	activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton	metabolic process; cellular component movement; cell organization and biogenesis
24	•P85108	Tubulin beta-2A chain OS=Rattus norvegicus GN=Tubb2a PE=1 SV=1 - [TBB2A_RAT]	ESESCDCLQGFQLTHSLGGGTGSGMGTLLIS K	C5(Nitrosyl); C7(Carbamidomethyl)	activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
25	•Q3KRE8	Tubulin beta-2B chain OS=Rattus norvegicus GN=Tubb2b PE=1 SV=1 - [TBB2B_RAT]	ESESCDCLQGFQLTHSLGGGTGSGMGTLLIS K	C5(Nitrosyl); C7(Carbamidomethyl)	activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	cellular component movement; metabolic process; cell organization and biogenesis
26	•P69897	Tubulin beta-5 chain OS=Rattus norvegicus GN=Tubb5 PE=1 SV=1 - [TBB5_RAT]	EAESCDCLQGFQLTHSLGGGTGSGMGTLLIS K	C5(Nitrosyl); C7(Carbamidomethyl)	al molecule activity; protein binding	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis

27	F1LU47	Uncharacterized protein (Fragment) OS=Rattus norvegicus PE=3 SV=1 - [F1LU47_RAT]	YNTHQPEACIAVEEGK	C9(Nitrosyl)			
28	F1LQ39	Uncharacterized protein (Fragment) OS=Rattus norvegicus PE=4 SV=1 - [F1LQ39_RAT]	IHTGEKPYRCNECGK	C10(Nitrosyl); C13(Carbamidomethyl)	metal ion binding		regulation of biological process
29	•F1LYR7	Uncharacterized protein (Fragment) OS=Rattus norvegicus PE=4 SV=1 - [F1LYR7_RAT]	SEGAIDDSLIGGNACTEGPEGKGTESTVVTG VGIVMNHHLQETSFTK	C15(Nitrosyl)			
30	•F1M842	Uncharacterized protein (Fragment) OS=Rattus norvegicus PE=4 SV=1 - [F1M842_RAT]	ILMERPTQSNIGIQTMDHSLCAPETVSAATQT VK	C21(Nitrosyl)	protein binding; DNA binding	chromosome; nucleus; cytoplasm	metabolic process; response to stimulus; regulation of biological process
31	•D3ZCX4	Uncharacterized protein OS=Rattus norvegicus PE=3 SV=1 - [D3ZCX4_RAT]	GILGYTEDQDVSCDFNNNSHSSTFDAGPGIA LNDNFVK	C13(Nitrosyl)	catalytic activity		metabolic process
32	•D3ZG72	Uncharacterized protein OS=Rattus norvegicus PE=4 SV=1 - [D3ZG72_RAT]	IHTGEKPYECDVCGK	C10(Carbamidomethyl); C13(Nitrosyl)	protein binding		
32	•D3ZG72	Uncharacterized protein OS=Rattus norvegicus PE=4 SV=1 - [D3ZG72_RAT]	LNVPVCQQCLLFK	C6(Carbamidomethyl); C9(Nitrosyl)	protein binding		

Table S9

Direct detection of proteins S-nitrosylated upon BDNF-treatment of neurons

★ transcription factor

• also present in CysNO-treated neurons

56 SNO-sites on 39 proteins

Hit Number	Accession	Description	Sequence	Modifications	Molecular Function	Cellular Component	Biological Process
1	•P45592	Cofilin-1 OS=Rattus norvegicus GN=Cfl1 PE=1 SV=3 - [COF1_RAT]	HELQANCYEEVKDR	C7(Nitrosyl)	protein binding	nucleus; cytoplasm; cytoskeleton; membrane	cellular component movement; metabolic process; transport; cell organization and biogenesis; response to stimulus; regulation of biological process
2	•F1LTP6	Enolase (Fragment) OS=Rattus norvegicus PE=3 SV=1 - [F1LTP6_RAT]	VNQIGSVTESLQVCK	C14(Nitrosyl)	metal ion binding; catalytic activity		metabolic process
3	D4A2L9	F-box and leucine-rich repeat protein 19 (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Fbxl19 PE=4 SV=1 - [D4A2L9_RAT]	MKQSCLLRQCTAPVLPHTAVCLLCGEAGK	C5(Carbamidomethyl); C10(Carbamidomethyl); C21(Nitrosyl)	DNA binding; protein binding; metal ion binding		metabolic process
4	•F1LP06	Fructose-bisphosphate aldolase (Fragment) OS=Rattus norvegicus GN=Aldoal1 PE=3 SV=1 - [F1LP06_RAT]	THTGEKPYQCKQCGK	C10(Nitrosyl); C13(Carbamidomethyl)	catalytic activity		metabolic process
4	•F1LP06	Fructose-bisphosphate aldolase (Fragment) OS=Rattus norvegicus GN=Aldoal1 PE=3 SV=1 - [F1LP06_RAT]	SHTGEKPYQCKECGK	C10(Nitrosyl); C13(Carbamidomethyl)	catalytic activity		metabolic process
4	•F1LP06	Fructose-bisphosphate aldolase (Fragment) OS=Rattus norvegicus GN=Aldoal1 PE=3 SV=1 - [F1LP06_RAT]	SHTGEKPYECKQCGK	C10(Nitrosyl); C13(Carbamidomethyl)	catalytic activity		metabolic process
4	•F1LP06	Fructose-bisphosphate aldolase (Fragment) OS=Rattus norvegicus GN=Aldoal1 PE=3 SV=1 - [F1LP06_RAT]	ALSDHHVYLEGTLLKPNMVTPGHTCTQK	C25(Nitrosyl)	catalytic activity		metabolic process

5	•F1LU03	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) OS=Rattus norvegicus PE=3 SV=1 - [F1LU03_RAT]	GILGYTEDQVVSCNFNSNSHSSTFDAGASIALNDNFVK	C13(Nitrosyl)	catalytic activity		metabolic process
6	•D3ZQ40	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus PE=3 SV=1 - [D3ZQ40_RAT]	IVSNVSCTTDCLAPLAK	C7(Nitrosyl); C11(Carbamidomethyl)	catalytic activity		metabolic process
7	•D4A3W5	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus PE=3 SV=1 - [D4A3W5_RAT]	GILGYTKDQVVSCYFNSNHSSTFDAEAGIALNDNFVK	C13(Nitrosyl)	catalytic activity		metabolic process
8	Q5QD51-3	Isoform 3 of A-kinase anchor protein 12 OS=Rattus norvegicus GN=Akap12 - [AKA12_RAT]	TETAPETHAYDSQTQVPAMQADSQGAQQMLDKNESCQDETPSAAAQR	M19(Oxidation); M29(Oxidation); C36(Nitrosyl)	protein binding	cytoplasm; cytoskeleton; membrane	transport; regulation of biological process; response to stimulus
9	P97836-8	Isoform 6 of Disks large-associated protein 1 OS=Rattus norvegicus GN=Dlgap1 - [DLGP1_RAT]	LSSAVEVSSCITTYKK	C10(Nitrosyl)			cell communication
10	F1LM94	Kinesin-like protein KIF2C OS=Rattus norvegicus GN=Kif2c PE=3 SV=1 - [F1LM94_RAT]	TCMIAMISPGISSCEYTLNTLR	C2(Nitrosyl); M3(Oxidation); M6(Oxidation)	catalytic activity; motor activity; nucleotide binding; protein binding		cellular component movement
11	P98158	Low-density lipoprotein receptor-related protein 2 OS=Rattus norvegicus GN=Lrp2 PE=1 SV=1 - [LRP2_RAT]	YCVVDTGTRCNQLQFTCLNGHCINQDWK	C10(Nitrosyl); C17(Nitrosyl); C22(Carbamidomethyl)	receptor activity; metal ion binding; protein binding; transporter activity	cytoplasm; membrane; endosome; endoplasmic reticulum; Golgi	metabolic process; transport; cell proliferation; response to stimulus; regulation of biological process
12	Q6AY73	Lymphocyte antigen 6 complex, locus E OS=Rattus norvegicus GN=Ly6e PE=2 SV=1 - [Q6AY73_RAT]	NNINCLWPVSCSSTDNYCITLSAAAGFGNVNLGYTLNKGCSPTCPRENININLGVASVNSYCCQSSFCNFSTAGLGLR	C44(Carbamidomethyl); C62(Carbamidomethyl); C68(Nitrosyl)			metabolic process; transport
13	Q5Q0T9	Meteorin OS=Rattus norvegicus GN=Metrn PE=2 SV=1 - [METRN_RAT]	MLVAALLCALCCGLLAASARAGYSEDR	C8(Nitrosyl); C11(Carbamidomethyl); C12(Carbamidomethyl)		extracellular	development; cell differentiation; regulation of biological process

14	Q64119	Myosin light polypeptide 6 OS=Rattus norvegicus GN=Myl6 PE=1 SV=3 - [MYL6_RAT]	MTEEEVEMLVAGHEDSNGCINYEELLR	M8(Oxidation); C19(Nitrosyl)	catalytic activity; motor activity; metal ion binding; structural molecule activity		metabolic process; cellular component movement
15	•G3V918	Phosphoribosylglycinamide formyltransferase, isoform CRA_a OS=Rattus norvegicus GN=Gart PE=3 SV=1 - [G3V918_RAT]	ISNAAVSINDHTALARFCKDEK	C18(Nitrosyl)	catalytic activity; nucleotide binding; metal ion binding	cytoplasm	metabolic process; response to stimulus
15	•G3V918	Phosphoribosylglycinamide formyltransferase, isoform CRA_a OS=Rattus norvegicus GN=Gart PE=3 SV=1 - [G3V918_RAT]	ISNAAVSINDHTALARFCK	C18(Nitrosyl)	catalytic activity; nucleotide binding; metal ion binding	cytoplasm	metabolic process; response to stimulus
16	F1LNJ2	Protein Ascc3l1 OS=Rattus norvegicus GN=Ascc3l1 PE=4 SV=1 - [F1LNJ2_RAT]	TEAEQCKNLELK	C6(Nitrosyl)	nucleotide binding; DNA binding; catalytic activity; protein binding; RNA binding	nucleus; spliceosomal complex; membrane	metabolic process; cell differentiation
17	A7M778	Protein Krt86 OS=Rattus norvegicus GN=Krt86 PE=2 SV=1 - [A7M778_RAT]	GGVVCGDLCVSGTAPAVNTRVCSAPC SGNVVVGTPNACGPCAGAGACSGGC KK	C5(Nitrosyl); C9(Carbamidomethyl); C22(Carbamidomethyl); C26(Carbamidomethyl)	catalytic activity; motor activity; structural molecule activity	cytoskeleton	cell organization and biogenesis
18	F1M1X1	Protein LOC100359483 (Fragment) OS=Rattus norvegicus GN=LOC100359483 PE=4 SV=1 - [F1M1X1_RAT]	VCQCKKPPPPPKPK	C2(Carbamidomethyl); C4(Nitrosyl)	structural molecule activity		
19	D3ZTS7	Protein Olr1443 OS=Rattus norvegicus GN=Olr1443 PE=3 SV=1 - [D3ZTS7_RAT]	TISFLGCAIQAFMFLTLGGSEALMLGFM SYDR	C7(Nitrosyl); M13(Oxidation)	signal transducer activity; receptor activity	membrane	regulation of biological process; response to stimulus
20	D3ZFN4	Protein RGD1561832 OS=Rattus norvegicus GN=RGD1561832 PE=4 SV=1 - [D3ZFN4_RAT]	IHTGEKPYECRDCGK	C10(Nitrosyl); C13(Carbamidomethyl)	metal ion binding		regulation of biological process
21	F1M4C7	Protein RGD1563045 (Fragment) OS=Rattus norvegicus GN=RGD1563045 PE=4 SV=1 - [F1M4C7_RAT]	MCTTVAFTKVNSEDKGALAK	C2(Nitrosyl)			

22	F1LNH0	Protein Sema3g (Fragment) OS=Rattus norvegicus GN=Sema3g PE=4 SV=1 - [F1LNH0_RAT]	VGRVCVNDAGGQR	C5(Nitrosyl)	receptor activity; protein binding	membrane	development
23	•G3V7C6	Protein Tubb2c OS=Rattus norvegicus GN=Tubb4b PE=3 SV=1 - [G3V7C6_RAT]	EAESCDCLQGFQLTHSLGGGTGSGMG TLLISK	C5(Nitrosyl); C7(Carbamidomethyl)	nucleotide binding; RNA binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cell organization and biogenesis
23	•G3V7C6	Protein Tubb2c OS=Rattus norvegicus GN=Tubb4b PE=3 SV=1 - [G3V7C6_RAT]	EAESCDCLQGFQLTHSLGGGTGSGMG TLLISK	C7(Nitrosyl)	nucleotide binding; RNA binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cell organization and biogenesis
24	•Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	ECEHCDCLQGFQLTHSLGGGTGSGM GTLLISK	C2(Nitrosyl); C5(Nitrosyl); C7(Nitrosyl)	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
24	•Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	ECEHCDCLQGFQLTHSLGGGTGSGM GTLLISK	C5(Nitrosyl); C7(Nitrosyl)	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
24	•Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	ECEHCDCLQGFQLTHSLGGGTGSGM GTLLISK	C3(Nitrosyl); C6(Nitrosyl); C8(Nitrosyl)	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
24	•Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	ECEHCDCLQGFQLTHSLGGGTGSGM GTLLISK	C6(Carbamidomethyl); C8(Nitrosyl)	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
24	•Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	MREIVHIQAGQCGNQIGTK	C12(Nitrosyl)	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
24	•Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	ECEHCDCLQGFQLTHSLGGGTGSGM GTLLISK	C2(Carbamidomethyl); C5(Nitrosyl)	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
24	•Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	ECEHCDCLQGFQLTHSLGGGTGSGM GTLLISK	C3(Carbamidomethyl); C6(Nitrosyl); M26(Oxidation)	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis

24	•Q4QQV0	Protein Tubb6 OS=Rattus norvegicus GN=Tubb6 PE=2 SV=1 - [Q4QQV0_RAT]	ECEHCDCLQGFQLTHSLGGGTGSGM GTLLISK	C7(Nitrosyl); M25(Oxidation)	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
25	★D3ZFZ1	Protein Zfp157 OS=Rattus norvegicus GN=Zfp157 PE=4 SV=1 - [D3ZFZ1_RAT]	THTGEKPYECKDCGK	C10(Nitrosyl); C13(Carbamidomethyl)	metal ion binding		regulation of biological process
26	★B1WBX4	Protein Zfp2 OS=Rattus norvegicus GN=Zfp2 PE=2 SV=1 - [B1WBX4_RAT]	IHTGEKPYQCMVCGK	C10(Nitrosyl); M11(Oxidation); C13(Carbamidomethyl)	metal ion binding		regulation of biological process
26	★B1WBX4	Protein Zfp2 OS=Rattus norvegicus GN=Zfp2 PE=2 SV=1 - [B1WBX4_RAT]	IHTGEKPYMCVQCGK	M9(Oxidation); C10(Nitrosyl); C13(Carbamidomethyl)	metal ion binding		regulation of biological process
27	P50398	Rab GDP dissociation inhibitor alpha OS=Rattus norvegicus GN=Gdi1 PE=1 SV=1 - [GDIA_RAT]	FVAISDLYEPIDDGSESQVFCSCSYDAT THFETTCNDIKDIYKR	C21(Nitrosyl); C23(Nitrosyl)	enzyme regulator activity; protein binding	cytoplasm; Golgi	transport; regulation of biological process; response to stimulus
28	Q66H56	TELO2-interacting protein 2 OS=Rattus norvegicus GN=Tti2 PE=2 SV=1 - [TTI2_RAT]	VETAKSSPVCPAWK	C10(Nitrosyl)			
29	•P85108	Tubulin beta-2A chain OS=Rattus norvegicus GN=Tubb2a PE=1 SV=1 - [TBB2A_RAT]	ESESCDCLQGFQLTHSLGGGTGSGMG TLLISK	C5(Nitrosyl); C7(Carbamidomethyl)	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
29	•P85108	Tubulin beta-2A chain OS=Rattus norvegicus GN=Tubb2a PE=1 SV=1 - [TBB2A_RAT]	ESESCDCLQGFQLTHSLGGGTGSGMG TLLISK	C5(Nitrosyl); C7(Carbamidomethyl); M25(Oxidation)	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
30	•Q3KRE8	Tubulin beta-2B chain OS=Rattus norvegicus GN=Tubb2b PE=1 SV=1 - [TBB2B_RAT]	ESESCDCLQGFQLTHSLGGGTGSGMG TLLISK	C5(Nitrosyl); C7(Carbamidomethyl)	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	cellular component movement; metabolic process; cell organization and biogenesis
30	•Q3KRE8	Tubulin beta-2B chain OS=Rattus norvegicus GN=Tubb2b PE=1 SV=1 - [TBB2B_RAT]	FSVCVLGDQQHCDEVK	C4(Carbamidomethyl); C12(Nitrosyl)	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	cellular component movement; metabolic process; cell organization and biogenesis

31	•Q4QRB4	Tubulin beta-3 chain OS=Rattus norvegicus GN=Tubb3 PE=1 SV=1 - [TBB3_RAT]	KECENCDCLQGFQLTHSLGGGTGSGM GTLLISK	C3(Carbamidomethyl); C6(Nitrosyl); C8(Nitrosyl)	nucleotide binding; catalytic activity; structural molecule activity	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis; cell differentiation
32	•P69897	Tubulin beta-5 chain OS=Rattus norvegicus GN=Tubb5 PE=1 SV=1 - [TBB5_RAT]	EAESCDCLQGFQLTHSLGGGTGSGMG TLLISK	C5(Nitrosyl); C7(Carbamidomethyl)	nucleotide binding; catalytic activity; structural molecule activity; protein binding	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
32	•P69897	Tubulin beta-5 chain OS=Rattus norvegicus GN=Tubb5 PE=1 SV=1 - [TBB5_RAT]	EAESCDCLQGFQLTHSLGGGTGSGMG TLLISK	C7(Nitrosyl)	nucleotide binding; catalytic activity; structural molecule activity; protein binding	nucleus; cytoplasm; cytoskeleton; membrane	metabolic process; cellular component movement; cell organization and biogenesis
33	F1LPJ2	Uncharacterized protein (Fragment) OS=Rattus norvegicus PE=4 SV=1 - [F1LPJ2_RAT]	YDPDLFRMALPCLSAIAGALPPDYLDT R	M8(Oxidation); C12(Nitrosyl)	transporter activity; metal ion binding; protein binding	endoplasmic reticulum; membrane	transport; cellular homeostasis
34	•F1LYR7	Uncharacterized protein (Fragment) OS=Rattus norvegicus PE=4 SV=1 - [F1LYR7_RAT]	SEGAIDDSLIGGNACTEGPEGKGTEST VVTGVGIVMNHHLQETSFTK	C15(Nitrosyl)			
35	F1M3P8	Uncharacterized protein (Fragment) OS=Rattus norvegicus PE=4 SV=1 - [F1M3P8_RAT]	EHPSDECGVGVFMGSHFDR	C7(Nitrosyl)	structural molecule activity; protein binding	ribosome	metabolic process
36	•F1M842	Uncharacterized protein (Fragment) OS=Rattus norvegicus PE=4 SV=1 - [F1M842_RAT]	ILMERPTQSNIGIQTMDHSLCAPETVSA ATQTVK	M16(Oxidation); C21(Nitrosyl)	protein binding; DNA binding	chromosome; nucleus; cytoplasm	metabolic process; response to stimulus; regulation of biological process
36	•F1M842	Uncharacterized protein (Fragment) OS=Rattus norvegicus PE=4 SV=1 - [F1M842_RAT]	ILMERPTQSNIGIQTMDHSLCAPETVSA ATQTVK	C21(Nitrosyl)	protein binding; DNA binding	chromosome; nucleus; cytoplasm	metabolic process; response to stimulus; regulation of biological process

37	•D3ZCX4	Uncharacterized protein OS=Rattus norvegicus PE=3 SV=1 - [D3ZCX4_RAT]	GILGYTEDQDVSCDFNNNSHSSTFDA GPGIALNDNFVK	C13(Nitrosyl)	catalytic activity		metabolic process
38	•D3ZG72	Uncharacterized protein OS=Rattus norvegicus PE=4 SV=1 - [D3ZG72_RAT]	LNVPVCQQCLLFK	C6(Carbamidomethyl); C9(Nitrosyl)	protein binding		
39	★Q5FWU5	Zinc finger protein 513 OS=Rattus norvegicus GN=Znf513 PE=2 SV=1 - [ZN513_RAT]	CMRGESGGGGSGGPQGPSDK	C1(Nitrosyl)	DNA binding; metal ion binding	nucleus	metabolic process; regulation of biological process

Table S10
S-nitrosylated members of the BAF Complex
★

Hit number	Uniprot ID	Description	Molecular Function	Cellular Component	Biological Process	1mM CysNO/Cys (Exp A)	1mM CysNO/CysNO-asc (Exp A)	1mM CysNO/Cys (Exp B)	1mM CysNO/CysNO -asc (Exp B)	100uM CysNO/ Cys (Exp C)	100uM CysNO/CysNO -asc (Exp C)	100uM CysNO/Cys (Exp E)	100uM CysNO/CysNO-asc (Exp E)	100uM CysNO/cys (Exp F)	average
36	P86173 ★	Actin-like protein 6B OS=Rattus norvegicus GN=Actl6b PE=1 SV=2 - [ACL6B_RAT]	nucleotide binding	nucleus	cell organization and biogenesis; metabolic process; regulation of biological process	3.9	6.0	4.2	17.1	3.7	2.6	4.0	5.2	10.5	5.7
64	Q91XJ0 ★	Calcium-responsive transcription coactivator OS=Rattus norvegicus GN=Ss18l1 PE=1 SV=1 - [CREST_RAT]	protein binding	chromosome; nucleus	metabolic process; regulation of biological process; cell organization and biogenesis		3.3	2.3						2.8	2.1
460	E9PTG1	Protein Smarca2 OS=Rattus norvegicus GN=Smarca2 PE=4 SV=1 - [E9PTG1_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding	nucleus; cytoskeleton	cell organization and biogenesis; regulation of biological process; metabolic process; cell differentiation	1.2	2.8	2.4	1.7	1.7	7.9			3.6	2.7
465	Q5U3Y2	Protein Smarcd3 OS=Rattus norvegicus GN=Smarcd3 PE=2 SV=1 - [Q5U3Y2_RAT]	protein binding	nucleus; cytoplasm	regulation of biological process; cell organization and biogenesis; metabolic process; cell differentiation	2.6	100.0	5.5	3.1					6.6	19.6
464	D3ZBS9	Protein Smarcd1 OS=Rattus norvegicus GN=Smarcd1 PE=4 SV=1 - [D3ZBS9_RAT]	protein binding; structural molecule activity	nucleus	cell organization and biogenesis; regulation of biological process; response to stimulus	2.4	6.7	100.0	2.0	3.4	4.3		39.7	6.2	18.3
462	Q4KLI0	Protein Smarcb1 OS=Rattus norvegicus GN=Smarcb1 PE=1 SV=1 - [Q4KLI0_RAT]	DNA binding; protein binding	chromosome; nucleus	cell organization and biogenesis; regulation of biological process; cell differentiation; metabolic process	6.2	4.8	100.0	4.0				10.3	100.0	32.2
463	D3ZJU5	Protein Smarcc1 OS=Rattus norvegicus GN=Smarcc1 PE=4 SV=1 - [D3ZJU5_RAT]	DNA binding; protein binding	chromosome; nucleus	cell organization and biogenesis; regulation of biological process; response to stimulus	1.4	2.9	3.2			3.1			3.7	2.4

Table S11
S-nitrosylated members of the NuRD Complex

★

Hit number	Uniprot ID	Description	Molecular Function	Cellular Component	Biological Process	1mM CysNO/Cys (Exp A)	1mM CysNO/CysNO-asc (Exp A)	1mM CysNO/Cys (Exp B)	1mM CysNO/CysNO -asc (Exp B)	100uM CysNO/ Cys (Exp C)	100uM CysNO/CysNO -asc (Exp C)	100uM CysNO/Cys (Exp E)	100uM CysNO/CysNO-asc (Exp E)	100uM CysNO/cys (Exp F)	average
269	B2GV01	Metastasis-associated gene family, member 2 OS=Rattus norvegicus GN=Mta2 PE=2 SV=1 - [B2GV01_RAT]	DNA binding; protein binding; catalytic activity; metal ion binding	nucleus; membrane	regulation of biological process; metabolic process; cell organization and biogenesis	1.4	3.1	2.0	1.5	2.4	9.2			2.4	2.7
237	F7ENH8	Histone deacetylase OS=Rattus norvegicus GN=Hdac2 PE=3 SV=1 - [F7ENH8_RAT]	DNA binding; protein binding; catalytic activity; RNA binding	chromosome; nucleus; cytoplasm	regulation of biological process; response to stimulus; cell organization and biogenesis; metabolic process; cell differentiation	1.9	3.0	2.8	1.6	2.8	3.9		7.3	2.9	2.9
238	Q71UF4	Histone-binding protein RBBP7 OS=Rattus norvegicus GN=Rbbp7 PE=2 SV=1 - [RBBP7_RAT]	RNA binding; protein binding	nucleus	regulation of biological process; metabolic process; cell organization and biogenesis; response to stimulus	2.3	5.1	6.5	5.5				4.5	52.0	10.8
373	E9PU01	Protein Chd4 OS=Rattus norvegicus GN=Chd4 PE=4 SV=2 - [E9PU01_RAT]	protein binding; DNA binding; catalytic activity; nucleotide binding; metal ion binding	nucleus; cytoplasm	metabolic process; cell organization and biogenesis; regulation of biological process; response to stimulus	0.7	2.1	1.7	1.7	1.8	5.0		8.7	3.4	2.8
271	F7EY92	Methyl-CpG binding domain protein 3 (Predicted), isoform CRA_a OS=Rattus norvegicus GN=Mbd3 PE=4 SV=1 - [F7EY92_RAT]	DNA binding; nucleotide binding; protein binding	chromosome; nucleus; cytoplasm	regulation of biological process; cell organization and biogenesis; response to stimulus; metabolic process	3.2	5.3	3.5	0.7					3.3	2.7
436	B5DFB2	Protein Rbbp4 OS=Rattus norvegicus GN=Rbbp4 PE=2 SV=1 - [B5DFB2_RAT]	DNA binding; protein binding; catalytic activity	nucleus	metabolic process; cell organization and biogenesis; response to stimulus	2.4	5.1	6.8	5.7				100.0	18.5	19.8
372	F1LPP8 ★	Protein Chd3 (Fragment) OS=Rattus norvegicus GN=Chd3 PE=4 SV=2 - [F1LPP8_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding; metal ion binding	nucleus; cytoplasm; cytoskeleton	metabolic process; cell organization and biogenesis; regulation of biological process	0.8	1.9	1.4	1.7	3.1	7.1		11.4	3.2	3.4
236	Q4QQW4	Histone deacetylase 1 OS=Rattus norvegicus GN=Hdac1 PE=1 SV=1 - [HDAC1_RAT]	DNA binding; protein binding; catalytic activity	chromosome; nucleus; cytosol	regulation of biological process; response to stimulus; metabolic process; cell differentiation; cell organization and biogenesis	2.0	2.9	2.7	1.3	2.8	3.7		7.2	3.0	2.8
87	D3ZR50 ★	Chromodomain-helicase-DNA-binding protein 5 OS=Rattus norvegicus GN=Chd5 PE=4 SV=1 - [D3ZR50_RAT]	DNA binding; catalytic activity; protein binding; nucleotide binding; metal ion binding	nucleus	metabolic process; regulation of biological process	0.6	1.9	1.4		1.5	4.8		8.7	3.3	2.8

Table S12

Nuclear proteins shown to be S-nitrosylated *in vivo*

Reference	Protein	Stimulus for nitrosylation	S-nitrosylation detected in	Stimulus for nitrosylation (II)	S-nitrosylation detected in (II)
(Doulias et al. 2013)	Brachyury protein;T	basal	wt mouse brain		
(Doulias et al. 2013)	Cullin-associated NEDD8-dissociated protein 1;Cand1	basal	wt mouse brain		
(Gräff et al. 2014)	Histone Deacetylase 2; HDAC2	memory recall	Hippocampus		
(Okamoto et al. 2014)	Myocyte Enhancer Factor; MEF2C	Alzheimer's disease post mortem brains	whole brain tissue	mouse model of stroke	ipsilateral cortex
(Xu et al. 2013)	Glyceraldehyde-3-Phosphate Dehydrogenase; GAPDH	Cocaine exposed rats	striatum		
(Raju et al. 2015)	Androgen receptor;Ar	basal	wt mouse brain		
(Raju et al. 2015)	Four and a half LIM domains protein 1;Fhl1	basal	wt mouse brain		
(Raju et al. 2015)	NAD-dependent protein deacetylase sirtuin-2;Sirt2	basal	wt mouse brain		
(Raju et al. 2015)	Protein DJ-1;Park7	basal	wt mouse brain		